Laboratory & Diagnosis

Official Journal of the Iranian Association of Clinical Laboratory Doctors

Vol. 18, No. 72, Supplement Issue September 2026

Iranian Scientific Association Of Clinical Laboratory Doctors

CONGRESS ABSTRACTS



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Laboratory & Diagnosis

Official Journal of Iranian Association of Clinical Laboratory Doctors

Supplement issue for QICL 23

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The Message from the Congress Chairman



Dr. Fariba Shaygan
DCLS

Distinguished colleagues, esteemed professors, respected researchers, and professionals in the field of laboratory sciences, It is with great honor that I announce the 17th International and 23rd National Congress on Quality Improvement in Clinical Laboratories, to be held with the scientific theme: From Precision to Prediction: The Role of the Laboratory in the Future of Health This congress will take place from 1-4 September, 2026, at the Milad Tower International Convention Center, Tehran.

The congress has been designed and planned with the aim of elucidating the strategic role of medical diagnostic laboratories in the transformation of the health system, from accurate diagnosis toward prediction, decision support, and intelligent interventions.

The scientific themes of the congress reflect a comprehensive and forward-looking spectrum of challenges and opportunities in laboratory sciences. Innovative topics such as artificial intelligence in laboratory diagnostics, evidence-based medicine, intelligent molecular diagnostics, modern virology, the microbiome, molecular biomarkers, standardization, quality improvement, and accreditation occupy a central place in the scientific program, highlighting the decisive role of laboratories in strengthening national and international trust in health outcomes.

Within this framework, the First Extracellular Vesicles Symposium will be held concurrently with the congress as a pioneering scientific event. Focusing on the latest research achievements and diagnostic and therapeutic applications of extracellular vesicles, this symposium will outline new horizons in future medicine, next-generation diagnostics, and personalized medicine, while fostering effective interaction among basic, clinical, and laboratory researchers.

In addition, the Iran Clinical Lab Expo, as the technological and industrial component of this event, will provide a valuable platform for showcasing capabilities, innovations, equipment, and advanced laboratory solutions, thereby creating an effective link between knowledge, technology, and the delivery of standardized, high-quality diagnostic services.

Undoubtedly, medical diagnostic laboratories in Iran have faced numerous challenges in recent years under difficult and complex conditions. Nevertheless, the professional resilience, scientific commitment, and exemplary sense of responsibility of the laboratory community have ensured the continued delivery of accurate, standardized, and reliable diagnostic services—an invaluable asset that plays an undeniable role in safeguarding public health and sustaining the health system, and one that deserves sustained attention, support, and reinforcement at decision-making and policy levels.

It is hoped that this congress, through the active participation of professors, specialists, managers, and industry stakeholders, will provide an effective opportunity for knowledge exchange, the presentation of challenges, collective reflection, and the proposal of practical solutions, and will represent a lasting step toward improving the quality of laboratory services and shaping a smart, sustainable, and science-based future for public health.

The Message from the Congress Scientific Chair



Dr. Ahmad Gharehbaghian
DCLS, Ph.D

Dear Participants, Esteemed Colleagues and Honored Guests,
It is with great pride and pleasure that I, as the Scientific Secretary of the 17th Quality Improvement Congress, extend a warm welcome to each of you.
This year, our congress theme is “From Precision to Prediction: The Laboratory's Role in the Future of Health,” a theme that envisions a bright and transformative future for laboratory sciences.
In an era where technology is advancing at an unprecedented pace, the role of laboratories has evolved beyond delivering accurate and reliable results toward prediction, prevention, and personalized health care. The convergence of artificial intelligence, big data, and next-generation diagnostic technologies has positioned the laboratory at the heart of forward-looking medical decision-making.
This congress presents a valuable opportunity to discuss the latest scientific achievements, existing challenges, and future prospects together. From keynotes and workshops to innovative research presentations, all are designed to advance quality and excellence in laboratory services.
I hope this gathering will not only foster knowledge and experience exchange but also pave the way for more effective collaborations among professionals, researchers, and industry leaders in the field.
Thank you for your valuable presence, and I wish you all a fruitful and inspiring congress.

The Message from the Congress Executive Chair



Dr. Mahmoud Javid
DCLS

The The 17th International & 23rd National Congress on Quality Improvement in Clinical Laboratories stands as the country's largest and most prominent annual gathering in the field of laboratory medicine. Held at the beginning of the Iranian Solar Hijri year and bringing together the latest scientific advances and developments from around the world, the Congress provides a unique platform for laboratory professionals from academic, governmental, and private sectors to come together, exchange knowledge and experience, renew professional relationships, and establish new connections.

Such a valuable opportunity deserves thoughtful planning. Throughout the four days of the Congress, the Congress mobile application and program booklets will serve as essential guides for making the most of your time. A truly rewarding experience begins with a clear understanding of the scientific program-including the themes of the panels and workshops, their dates and times, and the distinguished faculty members presenting at each session. With 25 scientific panels and approximately 40 workshops, featuring leading Iranian and international experts, the Congress offers an extraordinary breadth of topics and perspectives.

Will you explore the laboratory aspects of geriatric medicine, or focus on laboratory accreditation? Will you examine the challenges of laboratory economics and management, or turn your attention to the laboratory diagnosis of myocardial infarction, tumors, allergic disorders, thrombosis, parasitic diseases, viral infections, and many other conditions? Will you explore the fascinating relationship between the immune system, reproduction, and disease, or examine strategies for laboratory test utilization and productivity management? Will you delve into the rapidly expanding field of microbiome research, or discover the latest advances in newborn screening?

Perhaps gene therapy will capture your interest, or perhaps you will immerse yourself in the complex world of hematologic malignancies and hemoglobin disorders. You may choose to explore platelet disorders and non-malignant white blood cell disorders, investigate emerging challenges in immunohematology, or discover the transformative potential of artificial intelligence in laboratory medicine.

And among this rich scientific program, do not miss one of the Congress highlights of this year: the First Symposium on Extracellular Vesicles. With distinguished experts and an

emerging field of major scientific importance, this symposium promises to be one of the unique features of this year's Congress.
The Congress Poster Exhibition offers yet another opportunity for scientific discovery. Every year, the first floor of the Milad Tower International Convention Center comes alive with research findings, innovative ideas, and professional experiences presented through scientific posters.
Although posters may speak quietly, they often have much to say.
Take the time to walk through the exhibition, explore the presented research, exchange ideas with fellow researchers, and discover perspectives and experiences beyond the formal scientific sessions. The opportunity is certainly worth your time.

The Quality Improvement Congress is not merely a premier scientific gathering. It is also a valuable opportunity to discover the latest technologies, diagnostic solutions, instruments, reagents, and products available in the field of laboratory medicine, presented by leading Iranian and international brands.
The synergy between up-to-date scientific knowledge and the latest technological developments gives the Iran Clinical Lab Expo (ICLE) its distinctive character.
With the participation of approximately 240 reputable companies, ICLE provides a comprehensive platform for laboratory professionals, decision-makers, laboratory managers, and healthcare organizations to explore emerging technologies, compare products and services, and establish direct professional connections with leading companies in the field.
Equally valuable is the opportunity to interact directly with distinguished laboratory medicine experts, experienced laboratory managers, industry specialists, and government officials.
The presence of leading companies alongside a large and diverse professional audience, the wide range of products and technologies on display, a dynamic competitive environment, extensive professional networking, and the opportunity to discover innovative solutions from newly established companies all contribute to making the Congress Exhibition one of the most significant events in Iran's laboratory medicine calendar.
For the first time, a laboratory-inspired interactive installation will be created at the entrance of Milad Tower, offering visitors and passersby an opportunity to experience the world of laboratory medicine in an engaging and accessible way.
Visitors will be able to participate in simple laboratory activities, including blood group testing, and explore microscopic images of blood cells. This hands-on experience will offer a glimpse into the fascinating world of laboratory diagnostics and may inspire visitors to learn more about the vital role laboratories play in modern healthcare.
Before leaving, visitors will also have the opportunity to take a memorable photograph wearing a white laboratory coat alongside distinguished figures from the field of diagnostic medicine a symbolic and lasting souvenir of their encounter with laboratory science.
Finally, we must not overlook another important tradition of the Congress: the Hakim Jorjani
Festival and the ceremony honoring a Distinguished Figure in Laboratory Sciences.

The festival provides an opportunity to recognize excellence, innovation, dedication, and outstanding achievements across different areas of laboratory medicine.
The festival categories include:
Outstanding Laboratory Medical Director
Outstanding Laboratory Staff
Outstanding Student Scientific Work
Outstanding Innovator and Technology Developer
Outstanding Book
Outstanding Blood Bank
Although reaching every colleague may require extensive communication—including emails, official correspondence with universities and relevant organizations, text messages, and telephone calls—we believe that recognizing and celebrating excellence is well worth the effort.

We sincerely hope that the active participation of all members of the laboratory medicine community, healthcare professionals, academic institutions, governmental organizations, and industry partners will contribute to making the Quality Improvement Congress an even more successful and memorable event.

Let us come together to share knowledge, celebrate innovation, strengthen professional relationships, and advance the quality of laboratory medicine.

And above all, let us keep alive the memory of our friends, colleagues, and healthcare heroes who stood beside us in previous years and whose dedication and contributions continue to inspire the laboratory medicine community.

The Message from the Congress International Secretary Chair



Dr. Alireza Lotfikian
DCLS

Dear colleagues, students, and esteemed researchers,
It is with great pride that I announce the 17th International Congress and 23rd National Congress for the Promotion of Quality in Iran's Medical Diagnostic Laboratory Services, held under the scientific theme:
"From Accuracy to Prediction: The Role of the Laboratory in the Future of Health"
I am pleased to inform all those interested and active in the field of Iranian laboratory sciences that this congress will be held from Shahrivar 10–13, 1405 (August 2026) at the Milad Tower International Convention Center in Tehran. It has been designed and planned with the aim of clarifying the strategic role of medical diagnostic laboratories in the transformation of the healthcare system — moving from precise diagnosis toward prediction, intelligent decision-making, and knowledge-based interventions.
The scientific themes of this congress cover a comprehensive and forward-looking range of challenges and opportunities in laboratory sciences. Emerging topics such as artificial intelligence in laboratory diagnostics, evidence-based medicine, intelligent molecular diagnostics, modern virology, the microbiome, molecular biomarkers, standardization, quality improvement, and accreditation highlight the laboratory's decisive role in building national and international trust in health outcomes.
Given the growing importance of this field, the First Symposium on Extracellular Vesicles will also be held alongside the congress. Focusing on the latest research achievements and the diagnostic and therapeutic applications of extracellular vesicles, this symposium will chart new horizons in the future of medicine, next-generation diagnostics, and personalized medicine, and will foster effective interaction among researchers in basic, clinical, and laboratory sciences.
On the international front, distinguished scientific authorities and experts in laboratory sciences from Canada, Australia, Brazil, Germany, India, Turkey, Tunisia, Nepal, and Taiwan — who have expressed interest in presenting on the congress's core topics — have been invited. These experts will deliver their presentations online, an approach that extends the boundaries of knowledge and scholarly exchange beyond geographical limitations.

Congress Main Topics

Abnormal Hemoglobin Syndromes	Prof. A. Azar-Keivan Prof. H. Najm-Abadi
Artificial Intelligence in the Clinical Laboratory: From Algorithm to Clinical Trust	Dr. M. R. Bakhtiari
Cell Therapy and Gene Therapy: From Laboratory Standards to Clinical Impact	Prof. A. Haji-Fathali Prof. H. Abolghasemi
Challenges in Immunohematology	Prof. A. Gharehbaghian
Clinical Translation of Reproductive Immunology in Laboratory Medicine	Dr. A. A. Delbandi
Coagulation Disorders & Thrombosis	Prof. P. Eshghi Dr. M. Shahbazi
Diagnostic Methods of Prevalent Parasitic Diseases in Iran	Prof. M. Moheb-Ali
Diagnosis and Therapy Monitoring in Acute Hematopoietic Neoplasms	Dr. A. Eghbali Dr. B. Poopak
Geriatric Medicine and the Role of Medical Diagnostic Laboratories in Promoting Healthy Aging in Iran	Dr. S. M. Bloorchi
Hereditary and Acquired Disorders of Platelets: Laboratory Diagnosis & Therapeutic Strategies	Prof. M. Faranoush Prof. M. Hamidpour
Immune System Dysregulation in Diseases	Prof. N. Rezaei
Intelligent Molecular Diagnosis in Cancer and Infectious Diseases	Dr. E. Maserrat
Laboratory Economics in Normal and Crisis Conditions	Prof. A. R. Olyaei-manesh Prof. A. Akbari-Sari Dr. Gh. R. Hamzelou
Microbiomes and Their Impact on Health and Disease	Prof. M. Rahim-khani
Molecular and Epigenetic Biomarkers in Allergic Disease	Prof. A. R. Ranjbar
Non-Malignant Leukocyte Disorders	Prof. S. Alavi Dr. S. Hosseini
Phylogenetic Studies of Viruses and Recent Advances in Virology	Dr. S. Soltani
Productivity Management in Rational Selection of Laboratory Tests with an Evidence-Based Laboratory Medicine Approach	Dr. A. R. Lotfi-kian
Quality Improvement in the Clinical Biochemistry Section (Department) of the Laboratory	Prof. Kh. Adeli
Selected Articles: Applied Research from the Laboratory to the Clinic	Dr. M. Vanaki
The Clinical Importance and Application of Accurate Measurement of Low Hormone Levels	Dr. H. Bayat
The impact of Laboratory Accreditation on the International Credibility and Acceptance of Laboratory Results	Dr. A. Shirin Dr. Sh. Hemati
The Role of Medical Laboratories in Screening and Diagnosing Diseases in Newborns	Dr. M. R. Mahdavi-Amiri
The Role of Medical Laboratories in the Diagnosis and Monitoring of Common Diseases	Dr. M. Shanaki
The Role of the Laboratory in Diagnosing Heart Attacks	Dr. R. Mohammadi

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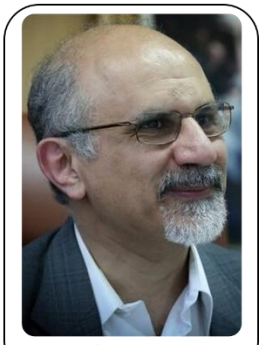

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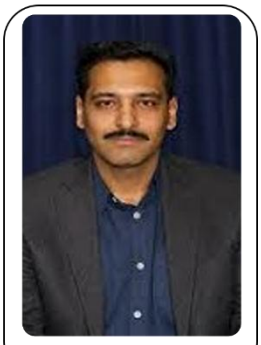

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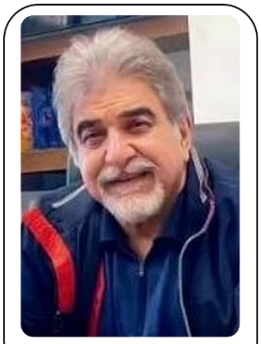

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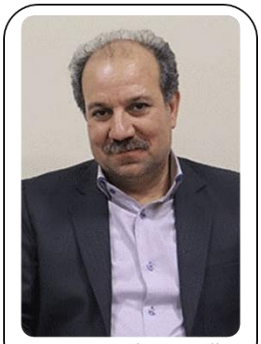

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ABSTRACTS

The 17th International & 23rd National Congress on Quality Improvement in Clinical Laboratory

Oral Presentation

Abnormal Hemoglobin Syndromes

O1-O4

O1

The Role of Blood Transfusion in Abnormal Hemoglobin Syndromes

Azita Azarkeivan 1 *

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Introduction: Hemoglobinopathies are disorders in which globin chains in the structure of hemoglobin are either poorly formed or not formed at all due to genetic mutations, causing chain imbalance and premature destruction of RBCs (hemolysis), causing anemia in the patient. Findings: In these patients, depending on the type of mutation and severity of hemolysis, we have low Hb level that can be so severe which the patient needs blood transfusion in childhood or in milder forms the patient needs to blood transfusions in adulthood due to bone marrow hyperactivity. In addition to hemoglobin levels, other clinical signs such as skeletal deformities, osteoporosis, heart failure symptoms, and increased pulmonary artery pressure can be indications for starting blood transfusion. Discussion: According to the genetic nature of hemoglobinopathies, blood transfusion therapy is a long-term treatment, sometimes lifelong. Therefore, when deciding to start blood transfusion, the patient's RBC subgroups should first be determined, and if the patient has a specific subgroup, the blood transfusion should be performed according to the patient's blood group from the beginning. Also Leukoreduced RBC should be used for the patient to prevent the blood transfusion reactions. Conclusion: Recently, the use of leukoreduced and Kell negative blood and use of Matched RBC subgroups are the rules of blood transfusion for patients requiring continuous blood transfusions

Keywords: Blood Transfusion, Abnormal Hemoglobin Syndromes, Leukreduced RBC, Hemoglobin

O2

Differential Diagnosis of Thalassemia Minor and Iron Deficiency Anemia

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The differential diagnosis between beta-thalassemia minor (a mild inherited carrier state) and iron deficiency anemia (IDA) (an acquired condition due to iron depletion) represents a common and critical clinical challenge. Both conditions present with an identical initial pattern on a routine complete blood count (CBC): microcytic, hypochromic anemia. Misdiagnosis carries significant risks: inappropriate iron supplementation in a thalassemia carrier can lead to iron overload and toxicity, while overlooking iron deficiency may result in missing a serious underlying cause, such as occult malignancy or chronic blood loss. A successful diagnostic approach follows a stepwise algorithm: 1. Clinical Assessment: History (family history in thalassemia; bleeding or pica in IDA) and physical exam provide initial clues. 2. Routine Laboratory Tests (CBC & Smear): Intelligent analysis of specific parameters is key: RBC count (normal/high in thalassemia; low in IDA), RDW (normal in thalassemia; typically high in IDA), and discriminant indices (e.g., Mentzer Index) guide the next step. 3. First-Line Specialized Tests: Assessment of iron status (low ferritin, high TIBC in IDA; normal or reversed pattern in thalassemia) is crucial. 4. Confirmatory Tests: Hemoglobin electrophoresis is the gold standard for confirming beta-thalassemia minor (elevated HbA2 > 3.5%), with molecular genetic testing available for complex or alpha-thalassemia cases. Modern diagnostic strategies are now enhanced by novel parameters such as reticulocyte hemoglobin content (Ret-He) and soluble transferrin receptor (sTfR), which improve accuracy in ambiguous cases or in the setting of concurrent inflammation. The core takeaway is imperative: Never initiate treatment based on CBC alone. Adherence to this structured diagnostic roadmap enables accurate differentiation, ensures appropriate management, and prevents potential harm to the patient.

O3

How Extracellular Vesicles Are Redefining the Diagnostic Landscape

Amir Hassan Zarnani 1 *

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Extracellular vesicles (EVs) are rapidly reshaping the diagnostic paradigm, offering a compelling alternative to conventional tissue biopsies and diagnostic methods through the rise of minimally invasive liquid biopsies. Secreted by nearly every cell type, these vesicles act as sophisticated messengers in intercellular communication, carrying a complex molecular payload comprising proteins, lipids, and various nucleic acids such as mRNA, miRNA, and DNA that closely reflects the biological state of their cells of origin. Their remarkable stability across a range of biofluids, combined with their ready accessibility in circulation, makes them uniquely suited for real-time, repeated monitoring of disease progression. Thanks to recent breakthroughs in isolation techniques, characterization methods, and high-throughput omics technologies, EVs are now being rigorously evaluated as promising tools for assessing biomarkers across a broad spectrum of diseases, with particularly encouraging progress in oncology, neurodegenerative disorders, and cardiovascular medicine. In this presentation, I synthesize the current state of EV-based diagnostics, emphasizing how key technological innovations are bridging the gap between basic biology and clinical application. Indeed, I go on to highlight the distinct advantages that EVs hold over traditional biomarkers to facilitate early detection, sharpen prognostic accuracy, predict therapeutic outcomes, and track recurrence with greater sensitivity. I will argue, EVs are poised to become cornerstones of next-generation precision medicine, fundamentally redefining how we detect, classify, and manage diseases.

Keywords: Extracellular Vesicles, Medical Laboratory, Diagnosis, Diseases, Early Detection

O4

Hemoglobinopathies: from Clinical and Paraclinical Assessments to Molecular Diagnosis

Gholamreza Bahoush 1 *

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Hemoglobinopathies are a group of inherited disorders caused by structural abnormalities or imbalanced production of the globin chains of hemoglobin. Moving from the bedside (clinical presentation) to the laboratory (diagnostic confirmation) is a classic paradigm in hematology. Clinical clues that raise suspicion before any blood is drawn; the patient's story and physical exam often provide the first critical hints. They include evaluation for ethnicity, family history, age at presentation, chronic fatigue, poor growth, and transfusion dependency pallor, high-output cardiac murmur, Jaundice, dark urine, recurrent painful vaso-occlusive crises, leg ulcers, gallstones, extramedullary hematopoiesis and bone expansion, hepatosplenomegaly. Sickle-specific findings are dactylitis, splenic sequestration, and acute chest syndrome. If any such picture emerges, the next step is the laboratory. First-line tests (CBC and reticulocyte count) are widely available and, when interpreted together, strongly suggest a hemoglobinopathy. Peripheral blood smear is the bridge between bedside and specialized tests. Iron studies are essential to rule out iron deficiency, which also causes microcytosis. Once the CBC and smear point toward a hemoglobinopathy, the next step is definitive identification of the abnormal hemoglobin. Hemoglobin Electrophoresis and HPLC/Capillary Electrophoresis. These are the cornerstone investigations. They separate hemoglobins based on charge or retention time. Results are interpreted considering age (normal HbF is high at birth) and transfusion status. High-performance liquid chromatography (HPLC) or capillary electrophoresis are currently the gold standard, providing precise quantification of HbA, HbA2, HbF, and variant peaks. Finaly, molecular diagnosis can be helpful for mild asymptomatic microcytosis with normal paraclinical assays.

Keywords: Hemoglobinopathy, CBC, Hemoglobin Electrophoresis

Artificial Intelligence in the Clinical Laboratory: From Algorithm to Clinical Trust

O5-O7

O5

Applications of Deep Learning Algorithms in the Detection of Abnormal Blood Cells

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Background: Manual microscopic examination of peripheral blood smears for abnormal cell morphology remains time-consuming and subject to inter-observer variability. Supervised deep learning models have shown promise in automating this task; however, their performance is fundamentally constrained by the availability of large, expertly labeled datasets of pathological samples, which are scarce, costly to annotate, and inherently biased toward previously observed disease categories. This conceptual work addresses that limitation by proposing a generative artificial intelligence framework for anomaly detection that does not require labeled pathological data. Methods: We propose a generative modeling framework, such as a convolutional autoencoder or generative adversarial network, trained exclusively on microscopic images of morphologically normal blood cells. Under this design, the model learns a compact latent representation of normal cell morphology rather than a decision boundary between disease classes. At inference, each input cell image would be reconstructed or scored against the learned normal distribution, and a statistical deviation metric, such as reconstruction error or latent-space distance, would be used to quantify departure from normal morphology. Cells whose deviation scores exceed a threshold estimated from the normal-sample distribution would be flagged as anomalous. Discussion: By learning only the distribution of normal cell morphology, the proposed approach is expected to identify abnormal cells as statistical outliers, including rare or previously uncharacterized abnormality types that a supervised classifier, limited to its labeled training categories, would be unable to recognize. This property is particularly relevant in hematology, where the diversity of pathological presentations makes exhaustive labeled coverage impractical. Analogous generative anomaly-detection strategies have demonstrated feasibility in other areas of medical imaging, supporting the plausibility of this approach for blood cell analysis, although its performance in this specific application has not yet been empirically established. Conclusion: Generative AI-based anomaly detection, trained solely on normal cell morphology, represents a promising conceptual alternative to supervised classification for identifying abnormal blood cells, potentially reducing dependence on scarce, expert-labeled pathology datasets. Future work will focus on implementing this framework and validating it on real peripheral blood smear datasets to assess its diagnostic performance and clinical utility.

Keywords: Deep Learning, Anomaly Detection, Blood Cells, Generative AI, Unsupervised Learning

O6

Artificial Intelligence for Predicting and Monitoring Immune Responses to HPV Vaccination

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Abstract: Human papillomavirus (HPV) is a major infectious cause of cancer worldwide, and prophylactic vaccination represents the most effective strategy for preventing HPV infection and associated malignancies. Although currently available HPV vaccines induce robust and durable immunity, the magnitude and kinetics of vaccine-induced immune responses may vary among individuals. Artificial intelligence (AI) and machine-learning approaches offer an emerging framework for integrating multidimensional immunological data, including neutralizing antibody responses, B- and T-cell phenotypes, cytokine profiles, and transcriptomic and proteomic signatures. By identifying complex patterns and interactions that may remain undetected by conventional analytical methods, these approaches could facilitate the characterization of vaccine responsiveness, identify biomarkers associated with durable immunity, and support longitudinal monitoring of immune responses following vaccination. Translation of such strategies into research and clinical practice, however, requires rigorous pre-analytical and analytical standardization, assay harmonization, robust quality control, model interpretability, and independent validation across diverse populations. Integrating AI with systems vaccinology may therefore advance HPV vaccine assessment beyond conventional single-marker approaches toward multidimensional and predictive immune profiling, providing a framework for precision vaccination and data-driven monitoring of vaccine-induced immunity.

Keywords: Human Papillomavirus, Artificial Intelligence, Machine Learning, Immune Monitoring, Systems Vaccinology, Precision Vaccination

O7

The Future of Medical Laboratory Results Interpretation: The Role of Artificial Intelligence in Clinical Decision-Making

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Background & Rationale: Clinical laboratory results are central to medical decision-making, yet their interpretation is often fragmented across individual analytes, reference intervals, and isolated clinical observations. The growing volume and complexity of laboratory data create an opportunity for Artificial Intelligence (AI) to move laboratory medicine from simply reporting results toward intelligent, context-aware interpretation. AI-Enabled Approach: This presentation explores how AI can assist laboratory professionals and clinicians by recognizing complex relationships among biomarkers, identifying subtle abnormalities, detecting clinically relevant trends over time, and integrating laboratory findings with available demographic and clinical information. Rather than interpreting each result independently, AI can help construct a more comprehensive view of the patient's laboratory profile and generate context-aware insights to support differential diagnosis, risk stratification, early detection, and clinical decision-making. As a complementary application, AI-assisted analysis of External Quality Assessment/Proficiency Testing (EQA/PT) data may identify persistent bias, analytical drift, unusual performance patterns, and peer-group deviations, strengthening the analytical foundation of trustworthy clinical interpretation. Clinical Implications & Discussion: The clinical value of AI depends not only on model performance, but also on data quality, validity, generalizability, transparency, and appropriate human oversight. AI should therefore augment rather than replace professional expertise, helping connect results that are often interpreted separately and revealing clinically meaningful patterns that may otherwise remain unnoticed. Conclusion: AI has the potential to redefine laboratory result interpretation—from isolated numerical outputs to integrated, longitudinal, and clinically contextualized information. Its ultimate value lies not in automating professional judgment, but in making interpretation more comprehensive, consistent, timely, and clinically meaningful. The future of laboratory medicine begins with algorithms, but it reaches its destination only through clinical trust.

Cell Therapy and Gene Therapy: From Laboratory Standards to Clinical Impact

O8-O10

O8

The Role of Next Generation Laboratory Technologies in Diagnosis, Monitoring and Clinical Decision Making

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Introduction: Recent advances in next-generation technologies have fundamentally transformed laboratory medicine and its role in diagnosis, monitoring, and clinical decision-making. The integration of advanced automation, molecular diagnostics, artificial intelligence, and digital data management systems has repositioned clinical laboratories as key contributors to precision and personalized medicine. Methods: This work presents a conceptual and analytical review of emerging laboratory technologies. The reviewed domains include total laboratory automation, next-generation sequencing (NGS), artificial intelligence–based laboratory data analysis, smart laboratory information systems (LIS), and advanced point-of-care technologies. Emphasis was placed on their impact on diagnostic accuracy, patient monitoring, and clinical decision support. Results:The analysis indicates that implementation of next-generation laboratory technologies leads to improved diagnostic accuracy, reduced turnaround time, minimized analytical errors, and enhanced clinical interpretation of laboratory data. Machine learning algorithms enable hidden pattern recognition, disease trajectory prediction, and assessment of therapeutic response. In addition, point-of-care and microfluidic technologies strengthen the laboratory–clinic interface. Discussion and Conclusion: Next-generation technologies have transformed laboratory medicine into an active and decision-oriented discipline within healthcare systems. However, challenges related to standardization, algorithm validation, data quality, and ethical and regulatory considerations remain critical. Strategic and responsible integration of these technologies will shape the future of laboratory medicine and enhance patient-centered clinical outcomes.

Keywords: Next Generation Laboratory, Diagnosis, Monitoring, Clinical Decision Making

O9

Predictive Biomarkers of Therapeutic Resistance in Immunotherapy and Targeted Therapies

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Background: Although immune checkpoint inhibitors, monoclonal antibodies, CAR-T cell therapies, and molecularly targeted agents have transformed the therapeutic landscape of hematologic malignancies and solid tumors, primary and acquired resistance remain major barriers to durable clinical responses. Accumulating evidence indicates that treatment resistance is driven by a complex interplay among genomic heterogeneity, clonal evolution, epigenetic reprogramming, metabolic adaptation, and immune dysfunction. Identification of predictive biomarkers is therefore critical for patient stratification, response monitoring, and precision-guided therapeutic interventions. Methods: A comprehensive review of contemporary literature was performed, focusing on genomic, transcriptomic, epigenomic, proteomic, metabolomic, and tumor microenvironment-associated biomarkers implicated in resistance to immunotherapy and targeted therapies. Particular emphasis was placed on evidence derived from acute leukemias, lymphoid malignancies, multiple myeloma, and translational immuno-oncology studies. Results: Multiple mechanisms of resistance have been identified, including impaired antigen presentation through HLA class I downregulation and β2-microglobulin loss, alterations in JAK/STAT signaling, and activation of PI3K/AKT/mTOR, MAPK, and WNT/β-catenin pathways. In hematologic malignancies, therapy-driven clonal evolution, antigen escape characterized by loss or decreased expression of CD19 and BCMA, immune checkpoint upregulation (PD-L1, TIM-3, LAG-3, and TIGIT), and T-cell exhaustion have emerged as major determinants of resistance to cellular and antibody-based immunotherapies. Furthermore, enrichment of regulatory T cells, myeloid-derived suppressor cells, and tumor-associated macrophages contributes substantially to an immunosuppressive microenvironment. Emerging technologies, including next-generation sequencing, single-cell multiomics, circulating tumor DNA analysis, and spatial transcriptomics, have enabled high-resolution characterization of resistance-associated molecular signatures. Conclusion: Therapeutic resistance represents a dynamic evolutionary process shaped by reciprocal interactions between malignant clones and the immune microenvironment. Consequently, reliance on single biomarkers is unlikely to provide sufficient predictive accuracy. Integrative multiomic approaches incorporating genomic, transcriptomic,

immunologic, and spatial data hold considerable promise for improving patient selection and treatment optimization. The incorporation of dynamic biomarkers such as circulating tumor DNA and measurable residual disease assessment, together with artificial

intelligence-driven predictive models, is expected to accelerate the implementation of precision immuno-oncology and next-generation transplantation strategies.

Keywords: Drug Resistance, Immunotherapy, Targeted Therapy, CAR-T Cells, Tumor Microenvironment, Precision Oncology

O10

Immune Monitoring of Patients Undergoing Cellular Therapies: The Role of the Laboratory in Early Detection of Adverse Effects and Decline in Therapeutic Efficacy

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Background: Multiple myeloma (MM) is described by clonally expanding plasma cells within the bone marrow (BM). An essential phase in developing myeloma is the evasion and inhibition of antitumor immunity. MM cells reproduce and proliferate almost exclusively in the BM niche, emphasizing how vital the microenvironment is for promoting cancer progression. The distinctive bone marrow milieu that regulates the progression of myeloma disease involves interactions between plasma and stromal cells, and myeloid and lymphoid cells. These cells affect the immune system independently or because of a complicated web of interconnections, which promotes disease development and immune evasion. Due to the importance of these factors in the onset of disease, various therapeutic strategies have been created that either target or improve the immunological processes that influence disease progression. Regulation of Immune by Immunotherapy in Multiple Myeloma including Chimeric Antigen Receptor (CAR)-T Cell Therapy, B-Cell Maturation Antigen (BCMA) CAR-T, Non-BCMA CAR-T that can be detected by flowcytometry. Several studies demonstrated that CD19 CART cells with anti-BCMA therapies showed promising efficacy in treating MM. Materials and Methods: PB collected from patients & normal control. Cells were stained with anti-human monoclonal antibodies (CD4), CD8, CD28, CD19, and analyzed using flow cytometry. Results: There were significant differences between the rate of Myeloma cells in patient after immunotherapy and cell therapy Conclusion: BMA myeloma cell measurements are not likely to be used as a biomarker for prediction of response to therapy, Treg-mediated inhibition of antitumor immunity has led to an increased frequency of Tregs, widely regarded as a sign of poor prognosis, MM patients showed fewer CD4+ T cells in peripheral blood, connected to a reduced CD4/CD8 T-cell ratio compared to control healthy individuals Favorable prognostic indicators have been linked to the surge in T-cell counts in MM patients.

Keywords: Multiple Myeloma Immune Cells, B-Lymphocyte, Regulatory T Cells, Immunotherapy

Challenges in Immunohematology

O11-O15

O11

Patient Blood management in elective surgery

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Background: Patient Blood management (PBM) is a multifaceted and multidisciplinary approach based on scientific evidence to improve the outcome of patients. Methods: In this narrative review, databases including Embase, Scopus, Google Scholar, Google, Science Direct, ISI Web of Knowledge, and PubMed were searched to obtain the associated literature in print. The key words were: PBM, clinical practice, evidence-based management, blood product use, anemia, perioperative bleeding, implementation of PBM, and patient outcome. Results: The PBM Principles in pre-, intra-, and post-operative periods are including: preoperative evaluation for diagnosis and treatment of anemia, decreasing intraoperative bleeding, and rising tolerance to anemia.1- Identification, diagnosis, and treatment of anemia and should be considered before and throughout surgery, and even after it. The hematopoiesis status in elective surgery patients should be optimized and then prepared for surgery.2- Coagulation status should be monitored (eg, point of care tests), and its disorders treated before, during, and after surgeries with emphasis on exact monitoring and proper use of instruments and interventions to support the patient's homeostasis (eg, minimally invasive surgical techniques, maintenance of normothermia during surgery and coagulation factors, and pharmacological agents such as tranexamic acid.3- Comprehensive use of effective methods to maintain patients' own blood, such as precise surgical technique, use of autologous methods such as acute normovolemic hemodilution (ANH), intra-, and post-operative cell recovery(cell salvage), and minimization of iatrogenic blood loss. Conclusion: It should be noted that Continuous evaluation and monitoring of surgical patients to estimate bleeding, blood clotting, and acute anemia is essential perioperatively, in many cases, may be treated with iron replacement with or without concomitant use of bone marrows stimulating drugs. The goal of this strategy is to maintain patients' own blood for better outcomes such as: decrease of length of ICU and hospital stay, reduction of blood use and transfusion complications.

Keywords: Blood Transfusion, Blood Loss Surgical, Anemia

O12

Rare Blood Groups and Their Challenges

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The definition of a rare blood donor varies by country and depends on the ethnic makeup of the population. However, in many countries, an individual is recognized as a rare blood donor when RBCs are negative for high-prevalence antigens with an occurrence less than 1 in 1000 (but 4 in 1000 in France and 1 in 100 to 1 in 1000 in Japan) or for multiple common antigens with an occurrence that varies from 1 in 200 to 1 in 1000. However, when those numbers jump to 1 in 10,000 is considered extremely rare. When a patient must receive rare blood for a transfusion, time is of the essence because the blood is usually needed that day or night. Finding rare blood used to be a time-consuming ordeal. At any given hospital or blood center, requests for rare blood were relatively infrequent, so each facility had to find rare donors on its own when the need arose. To assist in the supply of rare blood, the International Panel of Rare Blood Donors, also called the International Donor Panel (IDP), was established in 1965 by the ISBT. Many centers have developed programs to identify, freeze, and store rare blood to meet local transfusion needs. Iranian Blood Transfusion Organization (IBTO) is the sole organization providing blood services to hospitals and other medical centers throughout Iran. It has already established a rare blood group program and bank several years ago. As a reference center, the immunohematology laboratory of the IBTO has been responsible for identifying and providing compatible blood for patients with rare blood types and for multiply transfused patients, such as those with thalassemia who have developed several clinically important antibodies. Routinely rare blood bank carries out programs of typing RBC antigens in large cohorts of donors for finding rare blood groups by testing people from specific geographical areas or populations, and mainly through focusing donor screening on different ethnic backgrounds may yield the most productive approach. Patients with a rare blood group are mostly found in routine antibody screening for blood transfusion, antenatal antibody screening, or family members. All people who are eligible at a later date to be allogenic or autologous donors should be encouraged to donate and have their blood frozen for future needs. To meet the requests of patients with rare blood types, IBTO decided to regularly screen blood donor samples received randomly from selected blood centers in 31 provinces at the Immunohematology Reference Laboratory in Tehran for rare blood types.

Keywords: Rare Blood Groups, Blood Transfusion, Rare Blood Group Bank

O13

Immunohematology Challenges in Multi Transfused Patients

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Background: Blood transfusion is a life-saving treatment for many patients, including thalassemia. However, patients who are repeatedly and long-term dependent on blood transfusions (Multi-Transfused Patients) are exposed to significant immunological complications. The most important of these complications is the development of alloantibodies against red blood cell antigens present in donated blood. The occurrence of alloantibodies not only complicates and costs the process of finding compatible blood, but also increases the risk of delayed hemolytic reactions (DHTR). The aim of this article is to systematically review the main challenges of immunohematology in thalassemia patients and provide scientific and practical solutions for their prevention and management. Method: In this article, a review was conducted by searching reputable databases including PubMed, Scopus, ScienceDirect and Web of Science between 2010 and 2025. The inclusion criteria for articles were focusing on epidemiology of Alloantibodies, laboratory challenges, strategies for managing challenges and new laboratory diagnostic methods in patients with multi transfusions. Results: The prevalence of alloantibodies in patients with multi transfusions has been reported to be on average 20-30%. The most common alloantibodies in the thalassemia population are against the Rh systems (E, e c, C) and Kell (K). The main laboratory challenges in these patients are panreactivity (due to the presence of multiple alloantibodies and HTLA antibodies), evanescent antibodies (leading to unexpected delayed hemolytic reactions), and autoantibody interference (making it very difficult to identify underlying alloantibodies). Conclusion: The findings of this review highlight the inherent complexity of managing patients with multi transfusions. The key point is that prevention is much more effective and less expensive than treatment of complications resulting from alloantibody formation. A policy of preventive matching, although costly and time-consuming in the short term, is cost-effective in the long term by preventing antibody development, reducing emergency searches for specific blood, and preventing mortality from DHTR. Implementing a prophylactic antigen matching policy, especially for Rh antigens (C, c, E, e) and K, significantly reduces the rate of alloantibody formation in thalassemia patients (to below 5%). RBC genotyping is an accurate method for identifying blood group antigens in these patients. This method makes it possible to determine the true phenotype of the patient even in cases of repeated blood transfusions. Developing a database of phenotyped donors at the national level could be an efficient method for managing blood transfusion in these patients.

Keywords: Thalassemia, Blood Transfusion, Alloantibody, Phenotype, Genotype

O14

Laboratory Challenges of Autoantibodies in Immunohematology

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Background: Autoimmune hemolytic anemia (AIHA) is the result of the increased destruction of RBCs in the presence of “warm-” or “cold-” autoantibodies. Multiple triggers can cause the production of autoantibodies, including viral infection, or drugs. Autoantibodies are also often seen in patients who are chronically transfused and become alloimmunized, pregnancy, transplantation, and treatment with cancer immunotherapy. Most patients with AIHA will require transfusion support with red cell products. The presence of autoantibodies can complicate pre-transfusion testing and the safe selection of blood. Methods: This review article was conducted by searching in reputable database between 2015 and 2025. The inclusion criteria for articles were focusing on warm and cold autoantibodies, strategies for pre-transfusion testing and the safe selection of blood in patients with AIHA. Results: The aim of pre-transfusion testing for patients with AIHA is to identify underlying alloantibodies masked with autoantibodies (by adsorbed plasma). Transfusion of antigen matched for more than ABO may eliminates the need for repeat patient transfusion workups. This avoids the use of “least incompatible” can be replaced with “compatible for extended blood group antigens”. Transfusion of RBCs that are selected based on the patient’s extended phenotype can provide a significant measure of safety. The availability of extended antigen typing by DNA-based assay makes this a feasible option. Conclusion: Compatibility using adsorbed plasma or using units “antigen matched for clinically significant antigens” can be replaced by “least incompatible” terminology. Genotyping of patients with AIHA is helpful in guiding transfusion therapy by avoiding alloimmunization and potentially reducing delays in treatment.

Keywords: Autoantibody, Pre-Transfusion Testing, Alloimmunization

O15

Prevalence of Weak D Phenotype in Iranian Blood Donors: Manual and Automated Serologic Approaches

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Background: The serologic prevalence of the Weak D phenotype varies among populations and may be influenced by laboratory methodology. Differences in RhD typing approaches affect the detection of reduced D antigen expression and consequently the reported prevalence. Comprehensive nationwide data remain limited in many regions, including Iran. This study aimed to determine the nationwide serologic prevalence of the Weak D phenotype among Iranian blood donors and to compare detection rates between manual and automated methods. Methods: In this nationwide retrospective cross-sectional study, 1,991,758 blood donors from 31 provinces of Iran were evaluated between December 2022 and December 2023. RhD typing was performed using manual tube testing or automated platforms (Magnet and solid-phase red cell adherence). Prevalence rates were calculated and compared using Chi-square and paired t-tests. Results: Of all donors, 213,693 (10.72%) were Rh-negative. Weak D was identified in 1,001 donors, yielding an overall prevalence of 0.0503% and 0.4684% among Rh-negative donors. No significant difference was observed between manual (0.0491%) and overall automated methods (0.0518%) ($P = 0.409$). However, SPRCA demonstrated a significantly higher detection rate than the Magnet method (0.0619% vs. 0.0445%, $P < 0.001$). In provinces applying both methods concurrently, paired analysis showed significantly higher mean prevalence with automated testing ($P = 0.023$). Conclusion: The nationwide serologic prevalence of Weak D in Iranian blood donors is 0.0503%, placing Iran within the lower range of global estimates. Detection varies by analytical platform, with solid-phase automation demonstrating higher sensitivity. Standardized high-sensitivity RhD typing may improve diagnostic consistency and transfusion safety.

Keywords: Weak D Phenotype, Rhd Typing, Serologic, Prevalence, Blood Donors

Clinical Translation of Reproductive Immunology in Laboratory Medicine

O16-O19

O16

Immunodiagnostic Evaluation in Women with Reproductive Failure

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Background: Immunodiagnostic evaluation in women with reproductive failure refers to assessing immune-related factors that may contribute to recurrent pregnancy loss (RPL), recurrent implantation failure (RIF), or unexplained infertility. The goal is to identify abnormal immune responses that interfere with implantation, placentation, or pregnancy maintenance. The immune system plays a key role in: embryo implantation, maternal–fetal tolerance and placental development. Methods: Immunological testing is usually considered in women with: ≥2–3 unexplained miscarriage, recurrent implantation failure after IVF, unexplained infertility, history suggestive of autoimmune disease. Components of Immunodiagnostic Evaluation are autoimmune and alloimmune factors. Results: Most clinically relevant immune cause of reproductive failure should be evaluated are antiphospholipid antibody syndrome (APS), antinuclear antibodies, thyroid autoantibodies, natural killer (NK) cells. Conclusion: APS is the most important immunological test in reproductive failure. As NK cell evaluation tests have poor reproducibility and lack standardization, is not recommended as routine test.

Keywords: Monoclonal Antibody Research Center, Avicenna Research Institute, ACECR, Tehran, Iran

O17

How Is the Immune System Linked to Reproductive Failure?

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Background: Reproductive failure, including infertility, recurrent pregnancy loss, and implantation failure, is increasingly recognized as a condition influenced by the immune system dysregulation. Successful reproduction requires a finely balanced immune environment that allows tolerance of gametes, embryos, and the semi-allogeneic fetus while still maintaining host defense. Disruption of this balance can contribute to adverse reproductive outcomes. Both innate and adaptive immune components play key roles in reproductive processes. Abnormal activity of uterine natural killer (uNK) cells, altered macrophage polarization, and dysregulated dendritic cell function have been associated with impaired implantation and placental development. Additionally, imbalances in T helper cell subsets, particularly an increased Th1/Th17 response and reduced regulatory T cell (Treg) activity, may promote inflammation and immune-mediated rejection of the embryo. Autoimmune conditions, antiphospholipid antibodies, and abnormal cytokine profiles further link immune dysfunction to recurrent miscarriage and infertility. From a clinical laboratory perspective, immune-related biomarkers—such as autoantibodies, cytokines, complement factors, and immune cell phenotypes—are gaining importance in the diagnostic evaluation of unexplained reproductive failure. Understanding immune mechanisms not only enhances diagnostic accuracy but also supports personalized therapeutic strategies, including immunomodulatory treatments. Conclusion: Reproductive success depends on immune tolerance and controlled inflammation. Immune system disturbances can directly and indirectly contribute to reproductive failure, highlighting the essential role of immunological assessment in reproductive medicine and clinical laboratory practice.

Keywords: Reproductive Failure, Innate and Adaptive Immune System, Immune Dysfunction

O18

From Data to Life: How AI is Revolutionizing the Diagnosis and Treatment of Infertility

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Artificial intelligence (AI) is beginning to influence nearly every step of infertility care, often in ways that feel subtle but meaningful in daily practice. This lecture follows the typical path a couple takes through an infertility clinic and illustrates how AI supports clinicians rather than replacing their judgment. In the male evaluation, AI-based semen analysis, motility assessment, and imaging tools help reduce some of the variability that has long challenged andrology. These systems can highlight patterns in sperm function or testicular imaging that may otherwise be easy to miss, and they increasingly assist with predicting outcomes such as sperm retrieval in non-obstructive azoospermia. On the gynecology side, AI contributes to more consistent monitoring during controlled ovarian stimulation, automates follicle measurements, and helps identify conditions like PCOS or endometriosis using ultrasound or MRI features. In the embryology lab, time-lapse imaging and computer-vision models offer an additional layer of support when selecting embryos, especially when aiming for single-embryo transfer. AI is also starting to influence the less visible but essential parts of clinic life. Tools that structure free-text notes, flag missing information, or assist with documentation can reduce clerical load and create cleaner datasets for clinical decision-making. The lecture also addresses the limitations and ethical questions that accompany these technologies. Ultimately, AI's value in reproductive medicine lies in helping clinicians deliver more consistent, thoughtful, and individualized care to the couples they serve.

O19

The Male Contribution to Infertility: A Look Beyond Conventional Parameters

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According to the World Health Organization (WHO), infertility is defined as a disease affecting approximately 10–15% of couples worldwide. It refers to the inability of a female partner to achieve pregnancy after at least one year of regular, unprotected sexual intercourse. Approximately 50% of infertility cases are attributed to male factors, while the remaining 50% are related to female factors. Conventional diagnostic evaluations can identify the underlying cause in only about 50% of male infertility cases. Non-conventional semen paraments including sperm DNA fragmentation index, oxidative stress and high throughput technologies such as proteomics and metabolomics can bridge the diagnostic gap in idiopathic cases. Among the recognized causes of male infertility, infections of the genitourinary tract play a significant role. Historically, semen was considered a sterile fluid; however, this concept has been revised in recent years. Despite this, culturing microorganisms from semen samples in infertile men remains challenging, and there is substantial overlap in the microbial profiles of fertile and infertile men. With the advent of advanced diagnostic technologies such as next-generation sequencing (NGS), it is now possible to identify and characterize diverse bacterial populations through analysis of bacterial ribosomal genes. Another important aspect in this field is the relationship between the gut microbiome and the microbial communities present in semen and urine. A key question is whether disruption of microbial homeostasis in the gastrointestinal tract can influence the seminal microbiome and ultimately affect male reproductive potential. In this presentation, current evidence and available data addressing this relationship will be reviewed and discussed.

Coagulation Disorders & Thrombosis

O20-O23

O20

Laboratory Diagnosis of Heparin-Induced Thrombocytopenia

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Introduction: Heparin-induced thrombocytopenia (HIT) is a prothrombotic disorder mediated by platelet-activating antibodies against platelet factor 4 (PF4)/heparin complexes. Diagnosis requires integrating clinical findings with laboratory evidence. The "iceberg model" illustrates the relationship between platelet activation assays such as (SRA) and PF4-dependent immunoassays. This study aims to review modern laboratory diagnostic methods for HIT. Methods: This review article, based on data published in reputable hematology journals, examines platelet activation assays including SRA, HIPA, aggregometry, and HIMEA, as well as PF4-dependent immunoassays including EIA, CLIA, and LIA. Results: The serotonin-release assay (SRA), with approximately 95% sensitivity and specificity, remains the gold standard for HIT diagnosis. Enzyme immunoassays (EIAs) demonstrate high sensitivity (97%) but low specificity, particularly with weak-positive results. Automated rapid immunoassays such as chemiluminescence immunoassay (CLIA) and latex immunoturbidimetric assay (LIA) enable real-time diagnosis. CLIA shows 98.5% specificity and LIA shows 94% specificity compared to SRA. Discussion and Conclusion: HIT diagnosis requires a combined approach including clinical and laboratory assessment. Platelet activation assays are essential for HIT diagnosis. Automated rapid immunoassays (CLIA and LIA) with the capability of providing quantitative results offer more accurate post-test probability estimates and can facilitate clinical decision-making for heparin discontinuation or initiation of alternative anticoagulants.

Keywords: Heparin-Induced Thrombocytopenia, Serotonin-Release Assay, Chemiluminescence Immunoassay, Latex Immunoturbidimetric Assay

O21

Diagnosis of Inherited Platelet Disorders by Immunofluorescence Method on Peripheral Blood Smears

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Inherited platelet disorders (IPDs) are rare conditions characterized by thrombocytopenia and platelet dysfunction, causing variable bleeding. Accurate diagnosis is essential to avoid misdiagnosis as immune thrombocytopenia and prevent unnecessary treatments. However, conventional tools like aggregometry, flow cytometry, and next-generation sequencing (NGS) have limitations including high blood volume requirements, poor standardization, and interpretive challenges with genetic variants. This review presents blood smear analysis using light and immunofluorescence microscopy as a practical diagnostic alternative. We summarize technical aspects of blood smear preparation, fixation, and immunofluorescence staining using monoclonal antibodies against platelet cytoskeletal proteins, surface receptors, and granule markers. Characteristic morphological and immunofluorescent patterns observed in various IPDs are described. Light microscopy allows assessment of platelet size, granularity, and morphology, distinguishing giant-platelet disorders (e.g., MYH9-related disease, Bernard-Soulier syndrome) from small-platelet forms (e.g., Wiskott-Aldrich syndrome). Immunofluorescence identifies specific abnormalities: abnormal myosin IIA aggregates in neutrophils (pathognomonic for MYH9-RD), disrupted β1-tubulin in TUBB1-RT and WAS, altered filamin A in FLNA-RT, loss of surface glycoproteins in Glanzmann thrombasthenia and BSS, and reduced granule markers in gray platelet syndrome and storage pool diseases. The method requires <100 µL blood, is suitable for shipped samples and pediatric patients, and guides targeted genetic testing. Blood smear analysis by light and immunofluorescence microscopy is a powerful first-line diagnostic tool for IPDs, offering rapid phenotypic characterization, reducing misdiagnosis, and preventing inappropriate treatments. It should be integrated into diagnostic algorithms alongside genetic testing.

Keywords: Inherited Platelet Disorders, Thrombocytopenia, Blood Smear, Immunofluorescence, Bleeding Diathesis

O22

Laboratory Monitoring of Anticoagulant Drugs: What, When, and How Should We Measure?

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Anticoagulant therapy has evolved substantially, with the increasing use of low-molecular-weight heparins (LMWHs), direct oral anticoagulants (DOACs), and newer anticoagulant agents alongside unfractionated heparin (UFH) and vitamin K antagonists. Although routine laboratory monitoring is essential for some anticoagulants, it is unnecessary or potentially misleading for others. Appropriate laboratory assessment therefore requires an understanding of the pharmacology of each drug, the limitations of available assays, and the clinical circumstances in which measurement can meaningfully influence management. This presentation will provide a practical review of laboratory monitoring for currently used anticoagulant drugs, focusing on what should be measured, when testing is indicated, which assay should be used, and how results should be interpreted. For UFH, the roles and limitations of activated partial thromboplastin time (aPTT) and anti-factor Xa assays will be discussed, including factors responsible for discordance between the two methods. Monitoring of LMWH with anti-factor Xa activity will be reviewed, with particular attention to neonates, infants, obesity, renal impairment, extremes of body weight, and other situations in which pharmacokinetic variability may justify measurement. The presentation will then address vitamin K antagonists, emphasizing the international normalized ratio (INR), its appropriate therapeutic targets, and important sources of analytical and biological variability. For DOACs, the concept of “no routine monitoring” will be distinguished from “no possibility of laboratory assessment.” The presentation will review the appropriate use and limitations of drug-specific calibrated anti-Xa assays for factor Xa inhibitors, while explaining why conventional PT/aPTT results should generally not be used to quantify DOAC activity. Special clinical situations requiring consideration of anticoagulant measurement—including major bleeding, urgent surgery, suspected overdose, thrombosis despite therapy, renal dysfunction, extremes of age or body weight, drug interactions, treatment failure, and suspected accumulation—will be highlighted. Particular attention will be given to the challenges of anticoagulant monitoring in children and neonates, in whom developmental hemostasis, variable pharmacokinetics, limited assay standardization, and age-dependent reference ranges complicate interpretation. Finally, the presentation will propose a practical, clinically oriented approach to anticoagulant laboratory testing, emphasizing that the key question is not simply “Can we measure the drug?” but rather “Will measuring the drug change clinical management?”

O23

Diagnostic Algorithms for Thromboembolism and Laboratory Tests

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Based on major guidelines (CHEST 2021, ASH 2020, AHA/ACC/ACCP 2026), the diagnostic algorithm for thromboembolism begins with clinical probability scoring (Wells or Geneva), which determines the subsequent diagnostic pathway. In low or intermediate probability patients, a highly-sensitive D-dimer assay serves as the first diagnostic step, with a negative result safely excluding VTE. Age-adjusted thresholds (age×10 µg/L for patients >50 years), as validated by the ADJUST-PE study, improve specificity and reduce unnecessary imaging. D-dimer is not recommended in high clinical probability patients, who should proceed directly to imaging, with CTPA being the preferred modality and V/Q scanning as an alternative when contraindicated. The laboratory's role extends beyond result reporting to include precise sampling timing and consideration of interfering factors (malignancy, inflammation, pregnancy, anticoagulants) that affect interpretation. Adherence to stepwise algorithms reduces unnecessary imaging by up to 30% and significantly decreases healthcare costs without compromising patient safety. Common clinical errors include ordering D-dimer in high-probability settings or in hospitalized patients with inflammatory conditions, leading to false-positive results and misdiagnosis. Ultimately, an evidence-based stepwise approach, coupled with active clinician-laboratory collaboration, forms the cornerstone of accurate and timely thromboembolism diagnosis.

Diagnostic Methods of Prevalent Parasitic Diseases in Iran

O24-O28

O24

Clinical Features of Human Leishmaniases: Methods and Challenges of Diagnostic Methods

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Leishmaniases are group of parasitic diseases transmitted by various species of Leishmania parasites from infected animals or humans to healthy individuals by some species of sand flies. Clinically, leishmaniases are divided into cutaneous (oriental sore), visceral (kala azar) and mucocutaneous (Espundia) forms, each of which is divided into different subgroups with different pathogenic agents, reservoirs, vectors, clinical characteristics, laboratory diagnosis, control and prevention methods. Some forms of the disease are benign and self-healing, and some are highly malignant and associated with high mortality. Timely diagnosis and treatment of these diseases are very important and decisive. Parasitological (direct exam, culture), biological (inoculation to susceptible laboratory animals and isolation of Leishmania from them), immunological (skin test, serological methods) and molecular assays are used to diagnose leishmaniases. The use of these methods varies depending on the type of leishmaniasis, the stage of the disease, and the status of the host's immune system. Each of these diagnostic methods has advantages and disadvantages that will be discussed and reviewed in this Panel. The diagnostic challenges of each case will be mentioned, separately.

Keywords: Leishmaniasis, Human, Clinical Feature, Laboratory Diagnosis

O25

Diagnostic Methods of Human Intestinal Coccidiosis

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Background: Intestinal Coccidia are unicellular protozoa and belong to the phylum: Apicomplexa. All coccidian parasites have a sexual sporogonic and an asexual schizogonic phase. They live intracellularly, at least during a part of their life cycle. Cryptosporidium spp. Cystoisospora belli, Sarcocystis hominis, Sarcocystis suihominis and Cyclospora cayetanensis are human pathogens. To date, over 47 Cryptosporidium species, approximately 120 genotypes have been recognized. 21 species have been reported in humans worldwide. C. parvum and C. hominis mostly cause human infections (about 95%). These two parasites are transmitted by zoonotic and anthroponotic origin. Diagnosis methods: Laboratory diagnosis is made by demonstration and detection of the oocysts in feces. Microscopy diagnosis is based on concentrated floatation and/or sedimentation. Modified Ziehl-Neelsen, Kinyoun acid-fast, Auramine-rhodamine, Gomori's trichrome and Giemsa staining were recommended for identification of those coccidian parasites. Modified Ziehl-neelsen is more sensitive and the best staining method. Molecular studies are recommended and have shown two genotypes (I & II) for some species of Cryptosporidium. Rapid test kits are available for diagnosis of Cryptosporidium Spp. C. cayetanensis is a specific species in human host. Prevalence rate of disease is unknown. Autofluorescence characteristic is differential diagnosis. The egg shapes of C. belli Oocysts in fresh stool is immature and change to mature form outside of the body. Misdiagnosis is a problem in laboratories but floatation method with zinc sulfate or sugar syrup is recommended. Sporocyst of S. hominis and S. suihominis is usually seen in the human infected feces. The disease may or may not have any symptoms.

Keywords: Intestinal Coccidiosis, Diagnostic Methods, Human

O26

New Laboratory Methods for The Diagnosis of Human Parasitic Infections

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Rapid and accurate diagnosis of parasitic diseases remains a major challenge for healthcare systems, particularly in developing countries. Traditionally, laboratory diagnosis of parasitic infections has relied on microscopic examination of clinical specimens such as blood, stool, and tissue samples. Although these methods continue to serve as reference standards in many laboratories, they are highly dependent on operator expertise, are time-consuming, and are prone to human error, which represent significant limitations. In recent years, substantial advances have been achieved in the laboratory diagnosis of parasitic pathogens. In addition to immunological assays based on parasite-specific antigens and antibodies, and a wide range of molecular techniques with high sensitivity for detecting parasitic DNA, the application of biosensors as emerging diagnostic technologies has attracted increasing attention in the field of medical parasitology. Moreover, remarkable progress in artificial intelligence has opened new avenues for improving the detection and diagnosis of medically important parasites.

Keywords: Parasitology, Biosensors, New Diagnostic Methods, Artificial Intelligence

O27

New Methods for the Diagnosis of Human Cystic Echinococcosis

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The diagnosis of Cystic Echinococcosis (CE) is evolving from reliance on classical clinical evaluation, imaging, and conventional serology toward an integrated, multi-layered precision framework. While imaging, particularly ultrasound with WHO staging, remains the diagnostic backbone, new technologies are redefining the field. Novel tools such as recombinant antigen–based serology, circulating parasite cfDNA, parasite-derived microRNA and exosome biomarkers, AI-assisted imaging, rapid diagnostic tests and point-of-care platforms promise earlier detection, accurate assessment of cyst viability, and reliable treatment monitoring. At the highest resolution, next-generation sequencing (NGS) provides great insight into parasite genotypes, transmission dynamics, host–parasite interactions, and biomarker discovery. The future of CE diagnosis lies in integrating imaging, molecular biomarkers, and omics technologies within AI-supported decision systems, enabling personalized patient management and more effective population-level control.

O28

Advancements in Diagnosis of Cutaneous Leishmaniasis: from Microscopy to Molecular tools

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Cutaneous leishmaniasis (CL) remains a major global public health threat, particularly in Iran, affecting 18,000-23,000 children annually in rural areas, causing disfiguring scars, stigma and, economic losses. Its variable clinical forms mimic bacterial, fungal, or mycobacterial infections, leading to frequent misdiagnosis. The traditional diagnostic method is Giemsa-stained smear microscopy, the gold standard of CL diagnosis, that achieves 70-80% sensitivity in acute cases, but is invasive and painful with risk of co-infections, less sensitive in chronic lesions with low parasite loads, operator-dependent, and unable to differentiate between Leishmania species. In contrast, molecular tools like PCR and LAMP provide >90% sensitivity and point-of-care potential. PCR targets kDNA and ITS effectively but requires thermocyclers and sequencing for species ID, and is hampered by low DNA yields, contamination risks, and high costs limiting its field use in resource-poor areas. We developed a non-invasive tape disc sampling combined with LAMP for Leishmania tropica detection. Among 35 L. tropica patients, 35 non-L. tropica patients, and 35 healthy controls, it achieved 100% sensitivity and specificity. Visual results appear in < 30 minutes without PCR equipment, which makes it ideal for endemic regions. In conclusion, in response to the urgent need for accurate, rapid, and cost-effective diagnostic methods tailored to resource-poor settings, our tape-disc LAMP offers a practical solution but requires further investigation to validate performance across larger cohorts, diverse Leishmania species, and varied field conditions. Interim strategies should integrate patient clinical history, microscopy, and molecular confirmatory for reliable CL diagnosis.

Keywords: Cutaneous Leishmaniasis, Gold Standard Diagnosis, L. Tropica, LAMP, PCR

Diagnosis and Therapy Monitoring in Acute Hematopoietic Neoplasms

O29-O33

O29

Diagnosis and Therapy Monitoring in Acute Hematopoietic Neoplasms

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Minimal or measurable residual disease (MRD) is recognized as the most sensitive indicator for assessing treatment response and prognosis in acute leukemias. Using various advanced methods, residual leukemic cells can be detected at levels far below the threshold of conventional morphology, providing an independent prediction of relapse risk and overall survival. The main techniques include multiparametric and next-generation flow cytometry, quantitative PCR, and next-generation sequencing (NGS), offering sensitivities ranging from 10^{-4} to 10^{-6}. Key MRD assessment time points include the end of induction and consolidation in ALL, and after two induction cycles, at the end of consolidation, and before and after transplantation in AML. MRD results play a critical role in risk stratification, guiding targeted therapeutic decisions, selecting candidates for transplantation, and monitoring after treatment. Structured application of MRD leads to more precise patient management and improved clinical outcomes. Regular MRD monitoring is an effective tool for detecting early molecular relapse and enables timely intervention. Overall, MRD represents a cornerstone of personalized medicine in acute leukemias and plays a major role in improving survival and treatment results.

O30

Review of Some Challenging Hematologic Neoplasm

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The purpose of this study (oral presentation) is to show diagnostic challenges in hematological pathology particularly in myeloid neoplasm by reviewing some cases. Basically, in order to report a hematologic malignancy, we need to incorporate differnt data including morphology, flow cytometry, immunohistochemistry, and genetics. Specifically, for the final classification of a myeloid neoplasm, we need to consider two major classifications; WHO and ICC. Nowadays, genetic study including Cytogenetics and NGS are the cornerstone of the final diagnosis; having these pieces of information are crucial for further management of patients consideing the most recent developement of targeted therapy and precision medicine. In this presentation, I will show the major differences between WHO and ICC classification in terms of myeloid neoplasm. Also, I will show some of my real cases in order to demonstrate diagnostic steps toward a final report for each and individual cases. Best regards, Maryam pourabdollah.

Keywords: Myeloid Neoplasm

O31

Clinical, CBC, and Molecular Findings in Acute Leukemias: Insights and Advances

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Abstract: Acute leukemias, a group of rapidly progressing hematologic malignancies, are characterized by an uncontrolled proliferation of immature blood cells. Early diagnosis and accurate classification are crucial for determining the prognosis and tailoring treatment strategies. This presentation explores the spectrum of findings from clinical features to complete blood count (CBC) and molecular markers in acute leukemias, highlighting advances in diagnostic and therapeutic approaches. Clinical Findings: Acute leukemias often present with nonspecific symptoms such as fatigue, fever, pallor, bleeding, and recurrent infections. The clinical diagnosis is supported by physical examination findings, including hepatosplenomegaly and lymphadenopathy. In pediatric populations, the rapid onset of symptoms necessitates prompt recognition and intervention. CBC Findings: The CBC remains a cornerstone in the initial evaluation of suspected acute leukemia. Key findings include: Leukocytosis or leukopenia with a predominance of immature blasts Anemia due to impaired erythropoiesis Thrombocytopenia as a result of bone marrow failure in some cases, a “leukemic hiatus” or the presence of auer rods in the cytoplasm of blasts may provide additional diagnostic clues. Molecular and Genetic Findings: Molecular and genetic testing plays an essential role in subclassifying acute leukemias, guiding treatment decisions, and predicting prognosis. Commonly identified genetic abnormalities include: Philadelphia chromosome (BCR-ABL1 fusion) in acute lymphoblastic leukemia (ALL) FLT3 mutations and NPM1 mutations in acute myeloid leukemia (AML) Gene rearrangements, such as those involving MLL and RUNX1, that can influence therapeutic strategies Advancements in next-generation sequencing (NGS) have revolutionized the detection of both well-established and novel mutations, providing a deeper understanding of disease biology and enabling precision medicine. Conclusion: The integration of clinical features, CBC findings, and molecular diagnostics is essential for the comprehensive management of acute leukemias. As research continues to evolve, novel biomarkers and therapeutic targets are expected to enhance outcomes, particularly for pediatric patients. A multidisciplinary approach that combines clinical acumen with cutting-edge laboratory diagnostics is crucial in improving survival rates and reducing treatment-related toxicities.

Keywords: Acute Leukemia, Clinical Findings, Complete Blood Count, Molecular Diagnostics, Pediatric Hematology

O32

Diagnosis and Classification of Acute Leukemias and Their Challenges

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Acute leukemias are aggressive hematologic malignancies characterized by the clonal proliferation of immature myeloid or lymphoid precursor cells within the bone marrow, peripheral blood, and extramedullary tissues. Precise diagnosis and classification of acute leukemias are critical for risk stratification, prognostic assessment, therapeutic selection, and monitoring of measurable residual disease (MRD). Recent advances in integrated diagnostics—including multiparametric flow cytometry, cytogenetics, fluorescence in situ hybridization (FISH), next-generation sequencing (NGS), and transcriptomic profiling—have substantially transformed the diagnostic landscape of acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL). Contemporary classification systems, particularly the most recent edition of the World Health Organization (WHO) Classification and the International Consensus Classification (ICC), increasingly emphasize molecular and genomic alterations as defining disease entities. Despite these advances, significant challenges persist, including genetic heterogeneity, clonal evolution, lineage ambiguity, overlapping immunophenotypic features, and disparities in access to advanced molecular technologies across healthcare settings. Furthermore, the rapid discovery of novel biomarkers and targetable mutations continues to reshape disease taxonomy, complicating standardization and clinical implementation. This review summarizes current diagnostic approaches and evolving classification criteria for acute leukemias, highlights the impact of emerging molecular technologies, and discusses the major clinical and laboratory challenges that hinder accurate, timely, and universally applicable diagnosis in modern hematopathology.

Keywords: Malignancy, Classification, Acute Myeloid Leukemia, Acute Lymphoblastic Leukemia

O33

Standardization of Hematology Reports in Acute Leukemias for Therapeutic Decision-Making

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Background: Acute leukemias are among the most important hematologic malignancies, in which rapid diagnosis and accurate therapeutic decision-making play a crucial role in prognosis and the selection of appropriate treatment strategies. Accurate diagnosis requires the integration of clinical, morphological, hematological, immunophenotypic, cytogenetic, and molecular findings. The diversity of disease subtypes, fragmentation of diagnostic information, and the lack of an integrated structure for reporting hematology laboratory results may pose challenges to the interpretation of findings and effective communication between the laboratory and the clinical team. Therefore, developing a standardized and structured reporting framework may facilitate the organization of information and support clinical decision-making. Methods: In this study, scientific literature and evidence related to the principles of reporting and standardization of hematological findings in acute leukemias were reviewed. The major components contributing to diagnostic interpretation, disease classification, assessment of treatment response, and measurable residual disease (MRD) monitoring were evaluated. The main components of the report were considered to include clinical and hematological information, morphological findings and blast percentage, immunophenotyping, cytogenetic findings and molecular abnormalities, as well as measurable residual disease assessment. The role of each of these components in diagnosis, classification, prognosis, and therapeutic decision-making was also evaluated. Results: The review of the literature indicated that comprehensive and standardized reports should present key hematological findings along with morphological information, blood cell counts, blast percentage, immunophenotyping results, and cytogenetic and molecular findings within an integrated framework. The integration of these data may contribute to more accurate diagnosis, appropriate disease classification, assessment of treatment response, identification of prognostic factors, and guidance toward targeted therapies. Conclusion: Standardization of hematology reports in acute leukemias, by establishing a common language between the laboratory and the clinical team, may play an important role in facilitating the interpretation of results and therapeutic decision-making. The development of structured, evidence-based reporting frameworks represents an important step toward improving the quality of diagnostic services and the management of patients with acute leukemias.

Keywords: Acute Leukemia, Report Standardization, Hematology, Therapeutic Decision-Making

Geriatric Medicine and the Role of Medical Diagnostic Laboratories in Promoting Healthy Aging in Iran

O34-O35

O34

Biomarkers in Neurodegenerative Disorders

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Background and Objective: Alzheimer's disease (AD) is the leading cause of dementia worldwide. For decades, definitive diagnosis has relied on clinical assessment and invasive or expensive techniques such as positron emission tomography (PET) imaging and cerebrospinal fluid analysis. Recently, blood-based biomarkers have emerged as a minimally invasive, cost-effective, and scalable approach, offering significant potential for early detection and disease monitoring. This review summarizes recent advances in blood-based biomarkers of Alzheimer's disease and highlights their clinical implications. Methods: This narrative review focuses on recent studies investigating plasma biomarkers, including amyloid beta (Aβ), phosphorylated tau, neurofilament light chain (NfL), and glial fibrillary acidic protein (GFAP). Advances in ultrasensitive analytical technologies are also discussed. Results: The plasma Aβ42/40 ratio demonstrates high diagnostic accuracy for detecting cerebral amyloid pathology and shows strong concordance with amyloid PET imaging. Integration of this ratio with APOE ε4 genotype has enabled the development of the Amyloid Probability Score. Plasma phosphorylated tau isoforms, particularly P-tau181 and P-tau217, increase during preclinical stages of AD and reliably predict progression from mild cognitive impairment to Alzheimer's disease. Plasma NfL reflects the rate of neurodegeneration, while GFAP serves as a marker of reactive astrogliosis, providing complementary diagnostic value. Conclusion: Blood-based biomarkers represent a paradigm shift in the diagnosis and monitoring of Alzheimer's disease. Although challenges related to assay standardization and clinical validation remain, multi-marker plasma panels are likely to play a central role in future precision medicine approaches for Alzheimer's disease.

Keywords: Alzheimer's Disease, Blood-Based Biomarkers, Amyloid Beta, Phosphorylated Tau, Neurodegeneration

O35

The Frailty Index Based on Laboratory Test Data as A Tool to Investigate the Impact of Frailty on Health Outcomes

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Frailty is a rising global health issue in ageing society. Easily accessible and sensitive tools are needed for frailty monitoring while routine blood factors can be potential candidates. Methods: Data from 1907 participants (aged 60 years or above) were collected from the 4th to 9th wave of the English longitudinal study of ageing. 14 blood factors obtained from blood tests were included in the analysis. A 52-item frailty index (FI) was calculated for frailty evaluation. Logistic regression and Cox proportional hazards analysis were used to explore the relationships between baseline blood factors and the incidence of frailty over time respectively. All analyses were controlled for age and sex. Results: The mean age of participants was 67.3 years and 47.2% of them were male. Our study identified that 8 blood factors (mean corpuscular hemoglobin, HDL, triglyceride, ferritin, hsCRP, dehydroepiandrosterone, hemoglobin, and WBC) involved in inflammatory, nutritional and metabolic processes were associated with frailty. The combined model with these 8 blood factors had an AUC of 0.758 at cross-sectional level. In the Cox proportional hazards analysis, higher triglyceride (HR: 1.30, 95%CI: 1.07 ~ 1.59), WBC (HR: 1.16, 95%CI: 1.05 ~ 1.28), and lower HDL (HR: 0.58, 95%CI: 0.38 ~ 0.90) at baseline were linked to greater risk of developing frailty within 10 years. Compared to adults without abnormal blood factors at baseline, the hazard ratios of participants with two or more abnormal blood factors were almost twofold higher in developing frailty over time. Conclusion: Routine blood factors, particularly triglyceride, HDL and WBC, could be used for frailty screening in clinical practice and estimate the development of frailty over time.

Keywords: Frailty Detection, Blood Factors

Hereditary and Acquired Disorders of Platelets: Laboratory Diagnosis & Therapeutic Strategies

O36-O39

O36

Antiplatelet Drugs, Principles of laboratory monitoring and clinical Application of the Results

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Coagulation consists of two types: primary and secondary. Primary coagulation includes humoral (fibrinogen and VWF) and cellular (platelets, white blood cells and vascular endothelium) factors. Secondary coagulation also includes humoral (coagulation factors F-I to F-XIII) and cellular (platelets, red blood cells and white blood cells) factors. Primary coagulation acts as a precursor to secondary coagulation and also as the main element of coagulation in high-pressure vessels such as arteries and plays an important role in the formation of atherosclerotic plaque. In fact, platelets can cause the formation of atherosclerotic plaque, coronary artery occlusion and ischemia and infarction in the heart due to scavenging OX-LDL and their transfer to the subendothelium and activation in high-Shear stress. Therefore, antihypertensive and antiplatelet drugs play an important role in preventing the occurrence of plaque and preventing coagulation and occlusion at the site of the plaque. Platelet metabolism and function depend on the cyclooxygenase pathway, Pro-G, purinergic receptors P2Y12, GP-IIb/IIIa, and calcium, so their inhibition by NSAIDs, corticosteroids, thienopyridine drugs, or anti-receptor antibodies can advance clinical and therapeutic goals by disrupting platelet function. Any drug interaction requires laboratory monitoring, which for platelet inhibitory drugs, either expensive HPLC-based TDM tests are used to directly measure the serum level of the drug or tests based on the effect of the drug on platelet function such as Bleeding Time and PFA-100 tests, aggregometry tests, and sometimes thrombo-elastogram (TEG/ROTEM). This article will discuss the principles and basics of the tests, as well as their clinical application and interpretation.

Keywords: Atherosclerotic Plaque, Myocardial Infarction, Antiplatelet Drugs, Drug Monitoring, Laboratory Tests

O37

Platelet Function Testing Based on Modern Diagnostic Methods: Advantages, Limitations, and Clinical Applications

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Introduction: Platelets play a pivotal role in primary hemostasis, and abnormalities in platelet function may result in either bleeding complications or thrombotic events. Consequently, accurate assessment of platelet function has become increasingly important for the diagnosis of bleeding disorders, monitoring of antiplatelet therapy, and management of patients with cardiovascular diseases. Recent advances in platelet function testing technologies have significantly improved diagnostic accuracy and facilitated more informed clinical decision-making. Methods: Current platelet function assessment methods include light transmission aggregometry (LTA), platelet function analyzer (PFA-100/200), impedance aggregometry (Multiplate®), VerifyNow®, thromboelastography (TEG®), rotational thromboelastometry (ROTEM®), and flow cytometry. LTA remains the reference standard for evaluating platelet function; however, its clinical utility is limited by labor-intensive sample preparation, prolonged turnaround time, and incomplete standardization across laboratories. In contrast, point-of-care (POC) assays such as PFA, VerifyNow, and Multiplate offer rapid testing and greater operational simplicity, although their results may be influenced by pre-analytical variables and patient-specific factors. Flow cytometry provides highly sensitive assessment of platelet activation markers and is particularly valuable in pediatric patients and individuals with thrombocytopenia. Furthermore, emerging microfluidic technologies, which simulate physiological blood flow conditions, have opened new avenues for the rapid and accurate diagnosis of platelet function disorders. Results: The clinical applications of platelet function testing include the diagnosis of inherited and acquired platelet disorders, evaluation of responsiveness to antiplatelet therapy, management of patients undergoing cardiovascular interventions, prediction of perioperative bleeding risk, and quality assessment of platelet transfusion products. Discussion and Conclusion: Despite substantial technological advances, the selection of an appropriate platelet function assay should be guided by the clinical objective, availability of laboratory resources, and inherent limitations of each methodology. Future developments in standardized, automated, machine learning–based, and artificial intelligence–driven platforms are expected to transform platelet function testing and further enhance precision diagnostics in hematology.

Keywords: Platelet Function Testing, Light Transmission Aggregometry, Flow Cytometry, Point-Of-Care Diagnostics

O38

Platelet Exhaustion: Interpretation of Laboratory Findings and Clinical Impacts

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Abstract: Platelets may exhibit distinct pro-aggregatory, pro-inflammatory, and pro-coagulant phenotypes throughout their lifespan, ultimately progressing toward a pro-apoptotic state. These sequential changes occur during ageing or in response to stimuli of varying strength and duration. While platelet phenotypic and functional changes can be simulated in vitro or ex vivo, pathophysiological changes occurring in vivo may lead to progressive platelet clearance by the reticuloendothelial system and consequent thrombocytopenia. Sustained and overwhelming activation, however, may also cause premature and irreversible functional and structural damage, largely because anucleated platelets have limited capacity to renew their metabolic and energetic resources required for functional recovery. This impairment may represent a state of platelet exhaustion, in which platelets, despite sufficient circulating numbers, exhibit impaired responsiveness to further stimuli. Platelet storage lesion provides a well-established ex vivo model of this condition. The clinical significance of platelet exhaustion remains insufficiently explored. Our previous studies linked oxidative and metabolic alterations during platelet storage to receptor shedding, impaired platelet function, and reduced post-transfusion efficacy, while our work in immune thrombocytopenia suggests that platelet count alone may not fully reflect disease status or treatment response. These findings support further investigation of platelet exhaustion as a clinically relevant functional state and its potential contribution to disease pathophysiology and treatment response.

Keywords: Exhaustion, Immune Thrombocytopenia, Metabolism, Platelet, Platelet Function, Storage Lesion, Treatment Response

O39

Thrombocytopenia as a Diagnostic Clue to Hereditary Storage Disorders: Beyond Immune Thrombocytopenia

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Thrombocytopenia is one of the most common hematologic abnormalities encountered in childhood, and in an otherwise well child it is often attributed to immune thrombocytopenia (ITP). Although this is frequently an appropriate initial consideration, persistent or unexplained thrombocytopenia should not always be regarded as an isolated hematologic disorder. The presence of splenomegaly, hepatomegaly, anemia, leukopenia, skeletal abnormalities, growth impairment, bone pain, or other systemic manifestations should prompt reconsideration of the diagnosis and raise the possibility of an underlying hereditary or metabolic disorder. Hereditary storage disorders, particularly lysosomal storage diseases, represent an important but sometimes overlooked cause of thrombocytopenia. These disorders are characterized by the progressive accumulation of undegraded substrates within cells, particularly macrophages and other cells of the reticuloendothelial system. Their hematologic manifestations are heterogeneous and may result from hypersplenism and splenic sequestration, infiltration or dysfunction of the bone marrow, impaired hematopoiesis, chronic inflammation, or a combination of these mechanisms. Thrombocytopenia may therefore be an early and clinically important manifestation, sometimes preceding the recognition of more characteristic systemic features. Among these disorders, Gaucher disease is one of the most important diagnoses to consider. Deficiency of lysosomal acid β-glucosidase results in the accumulation of glucosylceramide and related substrates within macrophages, producing the characteristic multisystem phenotype. Hematologic abnormalities commonly include thrombocytopenia and anemia, with leukopenia occurring in more advanced disease. Splenomegaly is particularly characteristic and may be substantial. The degree of thrombocytopenia may vary according to the extent of splenic involvement and disease burden. Although hypersplenism and sequestration are important mechanisms, bone marrow involvement and abnormalities of hematopoiesis may also contribute. Skeletal manifestations, including bone pain, bone crises, osteopenia, osteonecrosis, pathological fractures, and characteristic radiographic abnormalities, provide additional diagnostic clues. Other lysosomal storage disorders may also present with thrombocytopenia, particularly when significant splenic involvement is present. Acid sphingomyelinase deficiency, for example, may cause thrombocytopenia as part of a broader phenotype characterized by hepatosplenomegaly and multisystem involvement. Niemann-Pick disease and

other inherited metabolic disorders may similarly produce cytopenias through splenic sequestration or reticuloendothelial involvement. The clinical presentation can vary considerably with the specific disorder, disease subtype, age at onset, and degree of organ

involvement. Consequently, the absence of a classic phenotype should not completely exclude a storage disorder. The distinction from ITP is particularly important in children with chronic or atypical thrombocytopenia. In uncomplicated ITP, thrombocytopenia is generally isolated, and significant hepatosplenomegaly or progressive systemic abnormalities are unusual. In contrast, a child with persistent thrombocytopenia accompanied by marked splenomegaly, anemia, leukopenia, hepatomegaly, skeletal abnormalities, growth impairment, or unexplained bone pain warrants a broader diagnostic evaluation. Failure to achieve an expected response to conventional ITP-directed treatment may provide an additional clue, although treatment response alone should never be used to establish or exclude the diagnosis of a storage disorder.

Immune System Dysregulation in Diseases

O40-O43

O40

Microbiome Analysis and Its Impact on Immune- Mediated Diseases

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Background: The human microbiome-comprising trillions of microorganisms that inhabit the gut, skin, respiratory tract, and other mucosal surfaces-plays a fundamental role in shaping host immunity and maintaining physiological homeostasis. Advances in high-throughput sequencing technologies and multi-omics approaches have enabled comprehensive microbiome analysis, revealing intricate interactions between microbial communities and the immune system. Dysbiosis, characterized by alterations in microbial diversity and composition, has been increasingly associated with the pathogenesis of immune-mediated diseases, including inflammatory bowel disease, rheumatoid arthritis, multiple sclerosis, asthma, and type 1 diabetes. Method: This review has used original articles data to uncover mechanisms by which commensal microbes influence immune development and function, such as modulation of regulatory T cells, production of short-chain fatty acids, maintenance of epithelial barrier integrity, and regulation of pro-inflammatory signaling pathways. Conclusion: These insights have highlighted the microbiome as both a biomarker and a potential therapeutic target in immune-mediated disorders. Emerging interventions—including probiotics, prebiotics, dietary modulation, fecal microbiota transplantation, and microbiome-derived metabolites—demonstrate promising avenues for restoring immune balance and reducing disease severity.

Keywords: Microbiome, Immune- Mediated Diseases, Immune system Regulation, Inflammation

O41

Laboratory evaluation of rheumatologic diseases

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Rheumatic diseases present a diagnostic challenge, as no single laboratory test is diagnostic, and results must always be interpreted in the context of the clinical phenotype. In this talk we briefly review different categories of laboratory tests that are used in the diagnosis and follow-up of rheumatologic diseases. We begin by acute-phase reactants (ESR and CRP) and their interpretation, then examine the core autoantibody panel, including ANA and its sub-serologies (anti-dsDNA, anti-Sm, anti-Ro/SSA, anti-La/SSB), RA-associated antibodies (rheumatoid factor and anti-CCP), ANCA, and antiphospholipid antibodies. We then continue with complement pathway assessment (C3, C4, CH50), alongside organ-specific monitoring including renal, muscular, and synovial fluid evaluation. In addition to routinely performed tests, emerging technologies are reshaping the field: multiplex bead-based autoantibody arrays enable simultaneous detection of many antibodies from a single small sample; the type I interferon gene signature assay offers a promising biomarker for lupus activity and therapeutic response; high-throughput proteomics and phage-display platforms (e.g., PhIP-seq, NAPPA) enable discovery of novel disease-specific antibody signatures; and artificial intelligence algorithms now assist in integrating laboratory data with clinical features for diagnosis and flare prediction. The objective of this presentation is to offer general practitioners a practical overview of laboratory tests used in rheumatologic disease, and, for specialists, to underscore the capabilities that emerging technologies and advanced data analysis now bring to the field.

Keywords: Rheumatology, Laboratory Tests, ANA, ENA, Multiplex Assays, Type I Interferon Gene Signature

O42

Autoinflammatory Disorders: Current Concepts in Diagnosis and Precision Treatment

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Background: Autoinflammatory disorders (AIDs) are a heterogeneous group of diseases caused by dysregulation of the innate immune system, characterized by recurrent episodes of sterile inflammation, fever, elevated acute-phase reactants, and variable multisystem involvement. Advances in molecular genetics and immunopathology have substantially improved disease classification and expanded the understanding of inflammasome-, interferon-, and NF-κB-mediated disorders. The emergence of precision medicine has transformed the diagnostic and therapeutic approach to these conditions. Methods: This narrative review summarizes current evidence from international guidelines and high-quality publications, including EULAR/PReS recommendations, Gene Reviews, and recent peer-reviewed literature published through 2026. Emphasis was placed on laboratory-based diagnosis, biomarker-guided evaluation, genetic testing strategies, and targeted therapeutic interventions. Results: A systematic diagnostic approach integrating clinical phenotype, inflammatory biomarkers, and molecular genetic testing enables early and accurate diagnosis. Conventional inflammatory markers, serum amyloid A, ferritin, interferon signatures, IL-18, and CXCL9 provide valuable information for disease activity assessment and therapeutic monitoring. Next-generation sequencing, whole-exome sequencing, and somatic mosaicism analysis have significantly increased diagnostic yield in genetically heterogeneous disorders. Treatment has shifted from empirical immunosuppression toward mechanism-based therapies, including colchicine, IL-1 inhibitors, TNF inhibitors, IL-6 inhibitors, JAK inhibitors, and interferon-γ blockade in selected conditions, resulting in improved disease control and prevention of irreversible organ damage. Conclusion: A phenotype-driven, laboratory-supported, and genetically informed strategy is essential for the optimal management of autoinflammatory disorders. Precision diagnosis facilitates individualized targeted therapy, minimizes disease-related complications, and improves long-term clinical outcomes. Future integration of genomic technologies with functional immune assays is expected to further advance personalized care for patients with autoinflammatory diseases.

Keywords: Autoinflammatory Disorders, Innate Immunity, Precision Medicine, Targeted Therapy, Genetic Diagnosis.

O43

Approach to Patient with Inborn Errors of Immunity

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Inborn Errors of Immunity (IEIs) are a heterogeneous group of inherited disorders, characterized by increased susceptibility to recurrent severe infections, autoimmune diseases, lymphoproliferation and malignancies. IEIs should not be considered as rare conditions anymore, while the number of diagnosed patients has significantly been growing up during recent years. Nevertheless, because of inadequate medical awareness, including in pediatricians, it is estimated that a significant number of patients with IEIs are not recognized. There are more than 500 different types of IEIs have been identified. Although our understanding on IEIs is rapidly improving, there is still a delay in diagnosis of patients with IEIs, which leads to an increased rate of morbidity and mortality among the affected individuals. Suspicious to certain IEIs should be made according to their clinical phenotypes. Meanwhile the first step in the diagnostic process starts from a limited set of simple screening tests, which are available in most hospitals. Meanwhile definite diagnosis usually can only be made by genetic diagnosis, where it could change the treatment protocols based on the patients' conditions.

Intelligent Molecular Diagnosis in Cancer and Infectious Diseases

O44-O47

O44

Artificial Intelligence from Data to Data-Driven Medical Decisions in Future Laboratories

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Background: This study emphasizes the importance of data in accurate medical decision-making and its role in early diagnosis and cost reduction. The convergence of big data, artificial intelligence, and machine learning has created a major transformation in disease diagnosis, patient monitoring, and clinical research. The use of laboratory data and intelligent algorithms improves the accuracy, speed, and quality of medical decision-making and moves toward smarter medicine. Method: The method of this study is based on a comprehensive review of recent articles and research in the field of big data, artificial intelligence, and machine learning in medical laboratory sciences. The path of evolution from raw data to data-driven medical decision-making in future laboratories was examined and content analysed based on reliable sources, focusing on emerging technologies and the centrality of artificial intelligence. Methods: The methodology of this study is based on a comprehensive review of recent articles and research in the field of big data, artificial intelligence, and machine learning in medical laboratory sciences. The path of evolution from raw data to data-driven medical decision-making in future laboratories was examined and content analysed based on reliable sources, focusing on emerging technologies and the centrality of artificial intelligence. Findings: The findings show that the evolutionary process of artificial intelligence has an important place in the transformation of data-driven medicine. Innovative applications of machine learning in laboratory data analysis and clinical decision-making are described, and deep learning is introduced as an advanced approach in disease prediction and treatment personalization. The future vision of medical sciences and laboratories is also outlined with a focus on smart technologies, and the role of big data in improving the quality of medical services is considered. Conclusion: In conclusion, AI combined with big data can be the foundation for more accurate medical decision-making and digital transformation of laboratories. The use of intelligent algorithms increases the quality of healthcare services, improves the speed of diagnosis and treatment, and ultimately paves the way for more efficient and smarter medicine and laboratories.

Keywords: Artificial Intelligence, Data, Data-Based Decision, Laboratory, Medicine

O45

Artificial Intelligence Role in Molecular Diagnosis

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Background: Molecular diagnosis relies on genomic, proteomic, and metabolomic data to enable precision medicine. However, exponential growth of high-dimensional datasets from next-generation sequencing and mass spectrometry has exceeded conventional interpretative capacity. Artificial intelligence (AI) and machine learning (ML) have emerged as transformative solutions for rapid, accurate diagnosis of genetic disorders, cancer subtypes, and infectious diseases while enabling novel biomarker discovery. Methods: A narrative review synthesized peer-reviewed literature on AI/ML applications in molecular diagnostics, genomic variant interpretation, proteomic analysis, and metabolomic biomarker discovery in clinical settings. Results: Machine learning models achieve high performance for pathogenic variant identification in hereditary cancer genes, surpassing conventional interpretation. AI-assisted exome sequencing achieves 30–50% diagnostic solve rates for rare genetic diseases, with nanopore sequencing enabling diagnosis within eight hours. Integrated AI systems accurately predict tissue of origin in cancers of unknown primary, facilitating targeted therapy selection. Convolutional neural networks demonstrate superior breast cancer detection compared to human pathologists. Multi-omics integration discovers novel biomarker signatures for disease stratification and treatment response prediction. Real-world implementations (PathAI, Tempus, Guardant360) demonstrate clinical utility. Implementation barriers include data heterogeneity, algorithmic bias, model interpretability limitations, and regulatory validation requirements. Conclusion: AI represents a paradigm shift enabling extraction of actionable clinical intelligence from complex molecular datasets. Future advancement depends on continuous learning systems, explainable AI frameworks, diverse training datasets, ethical frameworks addressing bias and privacy, and global data-sharing initiatives promoting equitable access to AI diagnostic innovations across healthcare systems.

Keywords: Artificial Intelligence, Deep Learning, Molecular Detection, Multi-omics, Oncology

O46

Precision Medicine in Oncology: A Comprehensive Review on Integrating Molecular and Clinical Data for Enhanced Therapeutic Decision-Making

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Introduction: The convergence of high-throughput molecular profiling and comprehensive clinical data represents the foundation of precision oncology. This paradigm shift aims to decipher tumor heterogeneity and deliver personalized, effective therapies by moving beyond a one-size-fits-all approach. Methods: This study is a narrative review based on a synthesis of key scientific literature in precision oncology. The methodology involved identifying, evaluating, and integrating findings from relevant articles and major projects to construct a conceptual framework. This framework outlines the core processes, tools, and practical applications of integrating molecular and clinical data for therapeutic decision-making. Results: Application of this integrated strategy yields significant clinical impact. Functional precision medicine tumor boards in acute myeloid leukemia (AML) report objective response rates up to 59% in refractory disease. Large-scale consortia (e.g., AACR GENIE) demonstrate actionable findings in >30% of profiled tumors. Tools like ex vivo drug sensitivity testing (DSRT) and knowledge bases (e.g., OncoKB) are critical for translating molecular alterations into treatment decisions. Conclusion: While transformative, challenges remain, including data interpretation complexity, clonal evolution, and regulatory hurdles. Future advancements hinge on artificial intelligence, single-cell technologies, and expanded data sharing. A robust, interdisciplinary framework for data integration is therefore indispensable for realizing the full promise of precision medicine, ultimately enabling tailored therapeutic strategies that improve individual patient outcomes in oncology.

Keywords: Precision Oncology, Data Integration, Molecular Profiling, Personalized Therapy, Biomarkers

O47

Artificial Intelligence for Disease Trajectory Prediction Using Multimodal Data

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Background: Accurate prediction of disease trajectories is a core objective of precision and preventive medicine. Conventional statistical models often face limitations in capturing the complexity, heterogeneity, and longitudinal nature of contemporary healthcare data. Recent advances in artificial intelligence (AI) have enabled the integration of multimodal data sources, creating new opportunities for more comprehensive and informative prognostic modeling. This presentation synthesizes current evidence on the application of AI for disease trajectory prediction using multimodal healthcare data, with a focus on clinically relevant use cases across different disease domains. Methods: A narrative review of peer-reviewed studies was conducted, examining classical machine learning and deep learning approaches applied to multimodal datasets. The reviewed studies primarily integrate clinical variables, medical imaging, longitudinal electronic health record (EHR) data, and molecular information to model disease trajectories over time. Results: Across a range of conditions—including infectious, chronic, and neurodegenerative diseases—AI models leveraging multimodal data have been shown to improve the prediction of disease severity, progression patterns, and transitions to advanced disease stages when compared with conventional approaches. Conclusion: Overall, AI-driven multimodal disease trajectory prediction represents an important advancement toward predictive and personalized healthcare. Continued integration of diverse data sources into AI-based models is expected to further enhance their clinical utility and relevance in real-world healthcare settings.

Keywords: Artificial Intelligence, Disease Trajectory Prediction, Multimodal Data, Precision Medicine, Prognostic Modeling, Machine Learning

Laboratory Economics in Normal and Crisis Conditions

O48-O49

O48

The Role of Scientific Associations of Iranian Medical Diagnostic Laboratories in Improving Budgeting, Tariff Setting, Quality, and Access to Enhanced Services in Normal and Crisis Conditions

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The objective of this speech is to elucidate the frameworks for economic reporting to promote transparency and trust among stakeholders, clarify the role of professional/scientific associations in improving coordination, standardization, and sustainability of the supply chain, and present practical solutions for associations, members, and stakeholders. In this speech, the following key messages will be conveyed to the panel audience, which mainly consists of laboratory managers, supply chain managers (companies), and policymakers in the field of medical laboratories: Scientific associations can serve as a reliable bridge between science and policy in practice. Budgets and tariffs should be aligned with valuable evidence and quality standards to improve access and clinical outcomes. Transparency, public reporting, and stakeholder participation are essential and strategic imperatives. Investment in quality leads to long-term savings and the reduction of unnecessary costs. Fair access to diagnostic services, as a health right, is fundamentally an economic and social issue.

O49

The Impact of Digital Transformation and New Technologies (Artificial Intelligence, Automation, Data Integration) on Improving the Economic Resilience of Labor

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The Transition to an Integrated Network: The national laboratory network, comprising approximately 6,500 medical diagnostic laboratories with a diverse composition—including about 600 public health centers, nearly4,000private laboratories, and various other centers located within hospitals and limited surgery clinics—constitutes the backbone of health data production. Today, connecting these centers to one another and aligning them with the "National Health Database "transcends a mere technological necessity for cost optimization; it has become a binding legal obligation. Article69of the "Seventh Five-Year Development Plan "has delineated a clear roadmap for establishing a smart health information system, in which diagnostic laboratories occupy a central position. Data Standards: An End to Inconsistency: One of the most significant barriers to deriving meaning from health data was the problem of disorder in data recording, marked by the existence of over12,000data fields in the list of prescribable tests and the absence of adherence to a unified model. To address this challenge, a joint effort between the General Department of Laboratory Affairs of the Ministry of Health and the Center for Statistics and Information Technology Management led to the development and notification of "National Standards for Data Fields. "In this process, the "Data Exchange Performance Scorecard "has been operationalized not merely as a reporting tool,but as a "Performance Measurement Document "for laboratories, enabling the monitoring of online, real-time data transmission concurrent with service delivery. Laboratories are currently within a legal transition period; surpassing this deadline signifies the adoption of a "standard language "for data exchange—an event that will bring years of data heterogeneity to an end. Clinical Synergy and the "Hub & Spoke "Model: With the aggregation of information in the National Health Database and its linkage to citizens 'national identification codes, the "long-standing aspiration of an interconnected laboratory network "is being realized. This targeted access to patient records—subject to access levels, patient consent, and confidentiality requirements—enables the technical supervisor to enhance the accuracy of result verification by reviewing indicator trends and clinical information, prevent unnecessary repetition of tests, and minimize errors arising from incomplete interpretation. Furthermore, this infrastructure facilitates the implementation of the "Hub & Spoke "model(central and satellite centers).Under this model, satellite laboratories can refer specialized samples to centralized reference laboratories, resulting in:1-Reduced operational

costs and optimized reagent utilization(preventing the waste of consumables in low-volume runs).2-Savings in capital expenditures(CAPEX)by eliminating the need to procure

expensive equipment in small centers.3-Enhanced productivity and the transformation of heavy fixed costs into manageable variable costs. Data-Driven Governance and Territorial Planning-At the macro level, managerial processing systems possess the capability to combine and analyze multiple vital indicators simultaneously. Through the analysis of demographic profiles, disease burden(epidemiology), referral patterns, and capacity assessment, health system managers can conduct dynamic needs assessments for each region. This “smart dashboard ”determines which regions should be prioritized for the establishment of new laboratories and how specimen transport routes should be reinforced. Conversely, transparency in financial data (fixed and variable costs, depreciation, and profit margins per test) provides a powerful instrument for defending the laboratory profession before the Supreme Insurance Council. Access to standardized, real-world data from6,000centers empowers the Ministry of Health and professional associations to base laboratory tariffs on genuine economic realities—a development that safeguards the economic resilience of this industry against crises. Artificial Intelligence: Decision-Support Assistant and Policy Maker: Artificial intelligence operates on two distinct levels:1-At the operational level(Internal Lab Operations):Serving as an assistant to the technical supervisor, AI enhances process accuracy and safety through the analysis of result trends, identification of pre-analytical errors, intelligent resource management, and demand forecasting. It is emphasized that all outputs of this technology serve solely as decision-support tools, with final decisions always resting with the technical supervisor.2-At the governance level (National Health Governance):Data mining at the national scale is employed for real-time epidemic monitoring, equitable resource allocation, and the refinement of macro health policies. Future Outlook: The Center for Monitoring Service Management-The future of laboratories is not confined to test performance alone. With the emergence of molecular technologies, rapid smart tests, biosensors, and home-based tools, healthcare is transforming from “episodic visits ”in to a “continuous, data-driven flow. ”In this new paradigm, laboratories are gradually evolving from sites of test performance in to “centers for the management of continuous monitoring services”—centers where data interpretation, monitoring guidance, and the coordination of therapeutic interventions play a central role in enhancing citizens ’quality of life. Success in this scientific and economic competition hinges upon readiness to embrace this new generation of knowledge-based services.

Microbiomes and Their Impact on Health and Disease

O50-O53

O50

Future of Microbiome - Based Prevention and Treatment

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The human microbiome, with particular emphasis on the gut microbiota, is increasingly recognized as a central determinant of healthy aging and longevity. Through complex host–microbe interactions, the microbiome regulates immune homeostasis, metabolic flexibility, low-grade chronic inflammation, and cellular signaling pathways associated with aging processes. A diverse and resilient microbiome contributes to disease prevention by maintaining epithelial barrier integrity, modulating immune responses, and reducing oxidative stress, all of which are critical factors in extending healthspan. Age-related dysbiosis has been linked to the development of chronic non-communicable diseases such as metabolic syndrome, neurodegenerative disorders, cardiovascular disease, and immune dysfunction. Emerging therapeutic strategies—including precision nutrition, targeted probiotics and prebiotics, lifestyle interventions, and microbiome-based therapeutics—offer promising avenues for personalized longevity medicine. Integrating microbiome profiling into preventive healthcare frameworks may play a pivotal role in promoting sustained physiological resilience and extending healthy lifespan.

O51

Gut Microbiota and Chronic, Metabolic and Mental Disorders

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In past centuries, bacteria were considered a potential threat to health, it is now well known that under normal conditions in some parts of the body, such as the intestine, there is a community of microbes, mainly composed of non-pathogenic microorganisms, which are relevant to inhibit the development of several chronic diseases. The development of an organism is significantly influenced by its microbiota, the interplay between the gut microbiota and brain development during infancy is a growing area of research that highlights the critical role of microbial communities in neurodevelopment. Methods: In this study, a systematic review of clinical studies and experimental research conducted on the gut microbiome and its influence on the human physiological and metabolic systems and other microbiome-based strategies is conducted. also, other studies published regarding the effect of disruption in the gut microbiota on the development of chronic diseases were considered. Results: Early in life, the gut microbiome plays a critical role in developing various physiological processes, including immune system maturation and brain development. On the other hand, some studies have shown that disruption of the gut microbiota (induced by fast food diets and sedentary lifestyles) may lead to excessive production of reactive oxygen species (ROS) and contribute to increased oxidative stress. Evidence suggests that disruptions in the gut microbiota during critical developmental can lead to negative neurodevelopmental outcomes, including increased risks for conditions such as autism spectrum disorders and attention deficit hyperactivity disorder. Furthermore, this review discusses the mechanisms underlying the microbiome-gut-brain axis and emphasizes the importance of early nutrition and environmental factors in establishing a healthy microbiome that supports optimal brain development. Research suggests that early life stressors can disrupt the colonization and diversity of gut bacteria, potentially affecting the development of the immune system and neurobiological pathways associated with stress responses. These changes in microbial composition are associated with a variety of adverse outcomes, including increased susceptibility to anxiety and other mental health disorders. On the other hand, excessive dietary fat consumption is strongly associated with an increased risk of various chronic diseases, such as obesity,

diabetes, metabolic liver disorders, cardiovascular disease, chronic intestinal inflammation, and some cancers. A significant portion of the adverse effects of high-fat diets on disease risk are mediated through changes in the gut microbiota. In particular, high-fat diets are

associated with reduced microbial diversity, overgrowth of Gram-negative bacteria, and changes at multiple taxonomic levels. These microbial changes affect intestinal metabolism of small molecules, which subsequently increases intestinal permeability, exacerbates inflammatory responses, disrupts metabolic functions, and disrupts signal transduction pathways in the host. As a result, diet-induced changes in the gut microbiota play a critical role in the initiation and progression of chronic and metabolic diseases such as cancer and diabetes. Conclusion: Diseases associated with gut microbiota dysbiosis increased oxidative stress and may have physiological effects on other systems such as the brain, cardiovascular organs, and metabolism-related tissues, preventing hypertension and the development of metabolic diseases and psychiatric disorders. Furthermore,it is suggested that probiotic interventions could serve as a promising adjunctive therapy to counteract the negative effects of a high-fat diet.

Keywords: Gut Microbiota, Mental Disorders, Dysbiosis, Diabetes, Chronic Diseases, Cancer

O52

Understanding the Types of Microbiomes and Their Impact on the Immune System and Physiological Function

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Background: Microorganisms, including bacteria, viruses, fungi, protozoa, and archaea, constitute a fundamental component of biological systems and play a pivotal role in human health. Beyond their well-established association with infectious diseases, microorganisms are now recognized as key regulators of immune function and physiological homeostasis. Understanding the diversity of microbiological types and their interactions with the host immune system is essential for advancing preventive, diagnostic, and therapeutic approaches in modern medicine. Methods: This study is based on a comprehensive narrative review of current scientific literature, including original and review articles, clinical studies, and experimental research focused on microbiology, immunology, and host–microbe interactions. The most important types of microbiomes in the human body are oral microbiome, nasal microbiome, skin microbiome, lung microbiome, genital microbiome, and gut microbiome. Relevant data were analyzed to evaluate the effects of different classes of microorganisms on immune responses and physiological functions. Results: The findings demonstrate that commensal and symbiotic microorganisms, particularly the human microbiota, contribute significantly to immune system development, immune tolerance, and regulation of inflammatory pathways. These microorganisms support epithelial barrier integrity and influence metabolic and neuroimmune functions. In contrast, pathogenic microorganisms were found to disrupt immune balance, induce inflammatory responses, and impair normal physiological processes through direct tissue damage and immune-mediated mechanisms. Conclusion: Microorganisms exert both beneficial and detrimental effects on the immune system and physiological function, depending on their type and host interaction. A deeper understanding of these relationships provides a foundation for microbiome-targeted therapies and immunomodulatory strategies in clinical practice.

Keywords: Microbiology, Immune System, Microbiota, Host–Microbe Interaction, Physiological Function

O53

Novel Therapies Such as Fecal Microbiota Transplantation (FMT) and Microbiome-Based Approaches in Disease Treatment

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Background: In recent years, the role of the human microbiome in maintaining health and disease development has gained significant attention. Microbial imbalance (dysbiosis) has been associated with a wide range of conditions, including antibiotic-resistant infections, inflammatory bowel diseases, metabolic disorders, and certain neurological conditions. Consequently, novel microbiome-based therapeutic strategies, particularly Fecal Microbiota Transplantation (FMT), have emerged as promising treatment options. Methods: This presentation provides a systematic review of clinical studies and experimental research related to FMT and other microbiome-based interventions. Peer-reviewed clinical trials, meta-analyses, and international guidelines were evaluated to assess mechanisms of action, procedural methodologies, patient selection criteria, and safety considerations. Results: The findings demonstrate that FMT is highly effective in the treatment of recurrent Clostridioides difficile infection and has shown encouraging outcomes in certain inflammatory bowel diseases, metabolic syndrome, and immune-mediated disorders. In addition, targeted use of probiotics, synbiotics, and engineered microbiota is being developed as complementary or alternative strategies to FMT. Conclusion: Despite its clinical efficacy, several challenges remain, including long-term safety, standardization of protocols, and ethical considerations. Advances in microbiome research and biotechnology may help address these limitations. Microbiome-based therapies, particularly FMT, represent a new frontier in personalized medicine and hold substantial potential as effective therapeutic approaches for the future management of various diseases.

Keywords: Human microbiome, Fecal microbiota transplantation (FMT/EMT), Dysbiosis, Microbiome-based therapies, Personalized medicine

Molecular and Epigenetic Biomarkers in Allergic Disease

O54-O56

O54

The Effect of Environmental Factors on the Regulation and Reprogramming of Gene Expression

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Dr Marzieh Asgharyan, Assistant Professor Allergy and Clinical Immunology, Rasol Akram Hospital, Department of Allergy and Clinical Immunology, School of Medicine, Iran University of Medical Sciences, Tehran, Iran. Introduction: The surrounding environment plays a fundamental role in regulating the expression of genes in allergic diseases, and the increasing prevalence of these diseases in recent decades cannot be explained solely by genetic factors. This article examines epigenetic mechanisms as the main mediators of the effect of environmental factors on the reprogramming of gene expression in human allergy. Three main epigenetic mechanisms, including DNA methylation, histone modifications, and non-coding RNAs, enable the interaction between genetic predisposition and environmental exposures. Methylation at specific gene loci, including associated with regulatory T cell function and immune tolerance and involved in inflammatory responses is associated with impaired immune regulation and increased susceptibility to diseases such as asthma, allergic rhinitis, and atopic dermatitis. Several environmental factors affect the immune system through these mechanisms. Exposure to pollutants (such as diesel particulate matter), tobacco smoke, and some aspects of the diet induce epigenetic changes that lead to polarization of helper T cells toward a Th2 phenotype (allergic pathway) and reduced differentiation of regulatory T cells. In contrast, factors such as maternal and early life microbial diversity, and dietary supplementation with unsaturated fatty acids and vitamin D have a protective role and promote immune tolerance through appropriate epigenetic programming. Understanding these mechanisms will not only help identify new biomarkers for early diagnosis and prediction of disease progression, but also can lead to the optimization of existing treatments and the development of targeted preventive strategies. Despite the advances, heterogeneity of methods and findings, the main challenge remains in the path to clinical application of this knowledge. Result: Environmental factors play a key role in regulating the expression of allergy-related genes through epigenetic mechanisms. Exposure to factors such as pollutants and cigarette smoke increases the risk of allergic diseases by altering immune pathways, inducing Th2 responses,

and reducing regulatory cells. In contrast, microbial diversity, adequate nutrition with vitamin D and fatty acids, and some infections, with their protective effects through

epigenetic reprogramming, enhance immune tolerance. Understanding these interactions will help to develop preventive strategies, although clinical application is challenged by the heterogeneity of methods.

Keywords: Epigenetics, Environmental Factors, Allergy, Gene Expression Recovery, Gene-Environment Interaction

O55

Novel Approaches for Diagnosis of Allergic Diseases

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The diagnosis of allergic diseases has undergone remarkable advances over the past decade, moving beyond conventional methods such as skin prick testing and serum-specific IgE measurement. Recent developments in laboratory medicine have enabled a more precise characterization of allergic sensitization patterns and immune responses, facilitating personalized patient management. This presentation will review emerging diagnostic approaches in allergy, with a particular focus on molecular and component-resolved diagnostics (CRD), which allow identification of sensitization to individual allergenic proteins rather than whole allergen extracts. The role of multiplex allergen testing platforms in evaluating complex sensitization profiles will also be discussed. In addition, recent advances in cellular assays, including the basophil activation test (BAT) and other functional immunologic tests, will be highlighted as valuable tools for assessing clinically relevant allergic reactions and improving diagnostic accuracy in selected patients. The potential contribution of novel biomarkers, omics technologies, and artificial intelligence–based analytical methods in predicting disease phenotypes, severity, and treatment responses will be explored. Special attention will be given to the practical applications of these technologies in routine laboratory settings, their advantages and limitations, and their impact on precision medicine in allergy and clinical immunology. By integrating innovative laboratory techniques with clinical assessment, modern allergy diagnostics are evolving toward more accurate, individualized, and evidence-based approaches. These advances provide laboratory professionals and clinicians with new opportunities to improve diagnostic performance and optimize patient care in allergic diseases.

O56

Skin Microbiome as a Diagnostic and Treatment Tool in Allergic Skin Diseases

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The skin microbiota plays a vital role in maintaining normal skin physiology, while dysbiosis have been linked to atopic dermatitis (AD), psoriasis and acne. In AD we have dry skin, barrier defect, microbial dysbiosis and outgrowth of staphylococcus aures (S. aures). S. aures activate keratinocytes in AD and barrier dysfunction induce dysbiosis. Recent researches have found that S. hominis (skin microbiota) abundance can stabilizes lipids, reduce spongiosis and reverse type 2 inflammation. Drugs that targeted type 2 inflammation such as JAK inhibitors or Dupilumab restore microbiota to a healthy balance and decrease disease severity.

Non-Malignant Leukocyte Disorders

O57-O58

O57

The Role of Acquired Changes in White Blood Cells in Diagnosis and Treatment Monitoring: Novel Approach in Precision Medicine

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Acquired Changes in White Blood Cells: From Biomarker to Treatment Guide In modern precision medicine, moving beyond quantitative white blood cell counts, the functional and acquired status of these cells in response to clinical stimuli is key to effective diagnosis and monitoring. Acquired changes—including phenotypic (e.g., expression of activation markers), metabolic, and functional shifts—provide a dynamic, personalized reflection of the body's interaction with challenges such as inflammation, infection, pharmacological treatments, and physiological stress. In diagnosis, these changes act as sensitive and early signatures. For instance, the rapid upregulation of CD64 on neutrophils is a strong diagnostic marker for bacterial sepsis, offering greater speed and specificity compared to conventional indices like CRP. Similarly, alteration patterns in monocyte surface markers or macrophage phagocytic capacity can delineate the severity of systemic inflammation or the response to a specific pathogen. The transformative application of these changes lies in monitoring treatment response. In managing complex infections, a decrease in activation markers like CD64 or HLA-DR can confirm antibiotic efficacy earlier than clinical symptom improvement or negative blood cultures, enabling timely therapy adjustment. More broadly, monitoring acquired changes induced by immunosuppressants, chemotherapy, or even nutritional interventions allows for precise assessment of therapeutic impacts and side effects (e.g., immunosuppression) at the cellular level. In conclusion, monitoring the dynamics of acquired white blood cell changes represents a novel paradigm in precision medicine. By providing a "live report" on the functional state of the immune system, this approach empowers clinicians to make more targeted diagnoses and guide treatment not based on fixed protocols, but according to each patient's unique, real-time biological response. This path envisions a future where a "functional immune profile" becomes a standard component of monitoring for both acute and chronic conditions.

O58

Advanced Laboratory Tests in Non-Malignant White Blood Cell Changes

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Bakground: Benign leukocyte disorders comprise a group of non-malignant and non-neoplastic conditions characterized by the absence of clonal proliferation, recurrent and non-random cytogenetic abnormalities, genetic rearrangements, and leukemogenic oncoproteins. Nevertheless, patients with these disorders may exhibit moderate to severe quantitative and qualitative alterations in leukocytes. These abnormalities may manifest as quantitative or qualitative changes, including morphological and functional abnormalities, or a combination of both. Differentiating reactive and non-malignant leukocyte alterations from clonal or neoplastic processes, particularly in cases where peripheral blood morphology does not provide definitive findings, remains a major challenge in the hematology laboratory. Methods and Results: Multiparametric flow cytometry, which enables the simultaneous assessment of cellular phenotypic characteristics, antigen expression intensity, and cellular population patterns, has been increasingly employed in the evaluation of these disorders. In addition, nucleic acid-based diagnostic methods and molecular techniques, including real-time PCR, multiplex PCR, and next-generation sequencing (NGS), as well as enzymatic assays, have contributed to the diagnosis and characterization of these conditions. The latest generations of hematology analyzers and artificial intelligence-based diagnostic approaches have also emerged as valuable tools for improving the detection and differentiation of benign leukocyte abnormalities. Conclusion: The future-oriented approach in the hematology laboratory is shifting from reliance on a single diagnostic test toward an integrated, multiparametric, and multiplatform diagnostic strategy. In this approach, cellular, morphological, immunophenotypic, and molecular data are interpreted collectively rather than in isolation. Such an integrated model may improve the diagnostic accuracy of the underlying causes of non-malignant leukocyte abnormalities, reduce unnecessary laboratory investigations, and facilitate more rapid clinical decision-making.

Keywords: Benign leukocyte disorders, Non-Malignant Leukocyte Abnormalities, Molecular Methods, Flow Cytometry

Phylogenetic Studies of Viruses and Recent Advances in Virology

O59-O62

O59

The Development and Validation of Novel Molecular Methods (NGS, CRISPR, LAMP, Multiplex PCR, and Real-Time PCR) for the Diagnosis and Monitoring of Viral Infections

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Viruses are considered among the most important human pathogens due to their high mutation rates, extensive genetic diversity, and remarkable ability to rapidly adapt to host environments. In this context, phylogenetic studies of viruses play a critical role in understanding viral origins, ransmission pathways, genetic evolution, and patterns of spread. Recent advances in molecular virology, particularly the development of nucleic acid–based technologies, have enabled more precise analysis of viral evolutionary relationships and have significantly improved the diagnosis and surveillance of viral infections. Next-generation sequencing (NGS) has emerged as one of the most powerful tools in modern phylogenetic research, enabling whole-genome sequencing of viruses without prior knowledge of target sequences. This technology has been widely applied in the epidemiological surveillance of viruses such as SARS-CoV-2, HIV, influenza viruses, and other emerging pathogens, playing a decisive role in the identification of novel variants, pathogenicity-associated mutations, and antiviral resistance. Data generated by NGS constitute the foundation of phylogenetic analyses, evolutionary tree reconstruction, and the tracking of viral transmission chains. Alongside NGS,real-time PCR (RT-PCR) and multiplex PCR remain the backbone of routine viral diagnostics in clinical laboratories. Real-time PCR, with its high sensitivity and specificity, enables quantitative assessment of viral load and monitoring of treatment responses, while multiplex PCR allows the simultaneous detection of multiple viruses or target genes from a single sample, making it particularly valuable for the differential diagnosis of respiratory and gastrointestinal infections. The loop-mediated isothermal amplification (LAMP)method, as a rapid, cost-effective, and single-temperature technique, has attracted considerable attention for use in resource-limited settings and point-of-care diagnostics. LAMP has demonstrated acceptable performance in terms of sensitivity and speed for the detection of viruses such as Zika virus, Dengue virus, SARS-CoV-2, and HPV. Moreover, CRISPR–Cas–based technologies have emerged as a new generation of molecular diagnostic tools, enabling highly specific detection of viral nucleic acid sequences. Platforms such as SHERLOCK and DETECTR, which combine CRISPR systems with isothermal amplification, have facilitated rapid, accurate, and portable viral diagnostics and show substantial potential for epidemic surveillance.

The validation of these novel molecular methods in terms of sensitivity, specificity, reproducibility, and clinical applicability is a crucial step in translating them from research settings into routine diagnostic practice. Overall, the convergence of phylogenetic studies with advanced molecular technologies offers a new paradigm for accurate diagnosis, continuous surveillance, and effective control of viral infections at the global level.

Keywords: Next-Generation Sequencing (NGS)؛ Viral Phylogenetics؛ Molecular Diagnostics؛ Multiplex and Real-Time PCR؛ Isothermal Amplification (LAMP)؛ CRISPR-Based Diagnostics

O60

Diagnostic Virology in the Post-Pandemic Era

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Severe acute respiratory infections (SARIs)remain a major cause of morbidity and mortality across all age groups worldwide, particularly among children, older adults, immunocompromised individuals, and patients with underlying cardiopulmonary conditions. It is estimated that approximately 30–70% of SARIs are of viral origin, with the most prevalent etiological agents including seasonal influenza A and B viruses, human rhinovirus (HRV), human adenovirus (HAdV), human parainfluenza viruses types 1–4 (HPIVs), respiratory syncytial virus (RSV), and human coronaviruses (HCoVs). In the post–COVID-19 pandemic era, the epidemiology of respiratory viral infections has undergone substantial changes. Disrupted circulation patterns of respiratory viruses, the re-emergence of seasonal pathogens, increased rates of coinfections, and the continuous emergence of novel variants have introduced new diagnostic and surveillance challenges. Consequently, rapid, accurate, and comprehensive identification of the causative agents of SARIs has become increasingly critical not only for individual patient management but also for epidemiological surveillance, healthcare preparedness, and early warning systems for future pandemics. Given the considerable overlap in clinical manifestations of respiratory viral infections, reliance solely on targeted molecular assays such as multiplex PCR and multiplex real-time PCR, despite their high sensitivity, may limit the detection of unexpected or emerging pathogens. In this context, next-generation sequencing (NGS) technologies have gained prominence in the post-pandemic era as essential tools enabling a paradigm shift from targeted to unbiased pathogen detection Third-generation nanopore sequencing offers distinct advantages, including real-time sequencing, high multiplexing capacity, relatively low cost, portability, and minimal laboratory infrastructure requirements, making it particularly suitable for post-pandemic diagnostic virology. Moreover, nanopore-based metagenomic approaches allow the simultaneous and direct detection of viral and bacterial respiratory pathogens from clinical specimens, while also providing valuable insights into viral diversity, genomic variation, and molecular typing. Considering the clinical and epidemiological significance of major SARI-associated viruses—including SARS-CoV-2, influenza viruses, RSV, rhinovirus, adenovirus, and parainfluenza viruses—the implementation of nanopore sequencing–based diagnostic strategies represents a critical advancement in respiratory virus surveillance and diagnostic preparedness in the post-pandemic era.

Keywords: Severe Acute Respiratory Infections (SARI), Diagnostic Virology, Post-Pandemic Era, Next-Generation Sequencing, Nanopore Sequencing, Metagenom

O61

Evaluation and Monitoring of Opportunistic Viral Infections in Transplant Patient

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Opportunistic viral infections represent a significant challenge in transplant medicine, as immunosuppressive therapies predispose recipients to viral reactivation and primary infections that may compromise graft function and patient survival. Over the past decades, advances in molecular diagnostics have improved the detection and management of these infections; however, optimal strategies for surveillance and monitoring remain an area of ongoing research. This study provides a comprehensive overview of the current evidence regarding evaluation and monitoring of opportunistic viruses in transplant patients, with a particular focus on the role of diagnostic viral panels. Key opportunistic viruses, including cytomegalovirus (CMV), Epstein–Barr virus (EBV), BK virus (BKV), JC virus (JCV), adenovirus, and human herpesvirus 6 (HHV-6), are discussed in relation to their epidemiology, pathogenesis, and clinical impact in solid organ and hematopoietic stem cell transplant recipients. The study summarizes current guidelines and consensus recommendations for viral surveillance, highlighting differences in monitoring approaches based on transplant type, timing post-transplantation, and intensity of immunosuppression. Special emphasis is placed on the use of molecular-based diagnostic panels, particularly quantitative and multiplex polymerase chain reaction (PCR) assays, which enable simultaneous detection and viral load quantification of multiple pathogens. These technologies have enhanced early diagnosis, facilitated preemptive therapeutic strategies, and contributed to individualized patient management. The advantages and limitations of panel-based testing, including cost-effectiveness, assay standardization, and clinical interpretation of low-level viremia, are critically reviewed. Furthermore, emerging trends such as next-generation sequencing, biomarker-guided monitoring, and risk-adapted surveillance strategies are explored as future directions in transplant virology. Integrating clinical, virological, and immunological data may improve risk stratification and optimize antiviral interventions. In conclusion, structured evaluation and monitoring of opportunistic viruses using comprehensive transplant patient panels play a pivotal role in contemporary transplant care. Continued refinement of surveillance strategies and diagnostic tools is essential to balance effective viral control with minimization of unnecessary treatment, ultimately improving long-term outcomes in transplant recipients.

Keywords: Opportunistic Viral Infections, Transplant Recipients, Viral Surveillance, Diagnostic Viral Panels, Polymerase Chain Reaction (PCR), Immunosuppression

O62

Development of point of care and rapid tests by using current advancements and nanotechnological approaches for viral infection detection

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Background: Rapid diagnosis of viral infections is a critical and challenging step during clinical management. Using nontechnological approaches for rapid viral detection or point of care testing is a classical way with new advancement during recent years. In this research we tried to introduced new rapid test for clinical virology using nanotechnological approaches. Methods: A literature search using Nanotechnology, rapid tests, point of care testing, viral infections keywords in electronical data bases including Scopus, PubMed and Web of sciences were performed. Results: Current study results highlight the advantages of rapid viral detection by considering regular regulations. An update perspective in this field focused on the molecular rapid tests for clinical virology. Nanotechnological approaches in biosensors, detectors and microfluid systems are considered as a great advancement in this field. Conclusion: In conclusion, using molecular rapid tests for clinical virology is an update and useful method. Current study highly suggests future researches focused on the molecular rapid tests development and clinical validation for diagnostic virology.

Keywords: Nanotechnology, Rapid Tests, Point of Care Testing, Viral Infections

Productivity Management in Rational Selection of Laboratory Tests with an Evidence-Based Laboratory Medicine Approach

O63-O67

O63

Developing Diagnostic Guidelines and the Role of the Laboratory in Integrated Care Pathways (ICP) Laboratory and Clinical Practice

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A large proportion of clinical decisions are based on laboratory test results. However, in traditional models of care, diagnostic services are often delivered in a fragmented manner, leading to delays in diagnosis, repeated testing, and increased healthcare costs. Integrated Care Pathways (ICPs) provide a structured response to these challenges, but they cannot be effective without the active involvement of laboratories. Integrated Care Pathways (ICPs) are evidence-based tools designed to coordinate diagnosis, treatment, and patient follow-up. Within this framework, the laboratory evolves from being a mere provider of numerical results into a clinical decision-making partner. This article focuses on the structural and economic realities of Iran's healthcare system and explains the role of laboratories in designing and implementing localized, cost-effective, and feasible diagnostic pathways.

O64

Threats and Opportunities for Medical Laboratories in the Context of Rational Test Ordering

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Rational laboratory test ordering is a fundamental component of Diagnostic Stewardship and Evidence-Based Laboratory Medicine (EBLM). It directly influences diagnostic quality, patient safety, healthcare expenditure, and laboratory efficiency. The objective is not to reduce testing indiscriminately, but to select investigations that appropriately address the clinical question, pretest probability, and intended clinical decision. This approach is consistent with the quality and competence requirements of ISO 15189:2022 and the risk-management principles outlined in ISO 22367. One important threat is the inappropriate use of tumor markers for screening asymptomatic individuals. For example, routine CA-125 testing for ovarian cancer screening in women at average risk may generate false-positive results and lead to unnecessary imaging or invasive investigations. Similarly, CEA is not an appropriate test for general population screening for colorectal cancer and may result in anxiety and additional diagnostic procedures. These examples emphasize that tumor markers should be requested according to validated clinical indications, such as disease monitoring or assessment of treatment response. Another threat is unnecessary repetition of laboratory testing in hospitalized patients. Repeated blood glucose testing without a clear clinical indication, particularly in clinically stable patients, may increase unnecessary blood sampling and the overall burden of diagnostic phlebotomy. The frequency of glucose monitoring should instead reflect the patient's clinical status, treatment regimen, and risk of dysglycemia. These challenges also represent opportunities for laboratories to enhance clinical value through evidence-based ordering guidelines, reflex-testing algorithms, minimum retesting intervals, clinician education, and LIS-based alerts. The laboratory can therefore evolve from a result-producing service into an active partner in Diagnostic Stewardship. Ultimately, laboratory value should be assessed not by test volume alone, but by the appropriateness, timing, and clinical impact of testing.

O65

The Power of Data Integration: Building Multi-Omics Diagnostic Models for Allergic Diseases

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Allergic diseases affect hundreds of millions of people worldwide. Despite their prevalence, diagnosis and treatment can still be challenging because these conditions arise from complex interactions between genes, environmental factors, immune responses, and the microbiome. Traditional diagnostic methods, such as skin prick testing or measuring specific IgE, provide valuable information but often capture a limited part of the complex biological picture. In recent years, advances in high-throughput technologies have enabled researchers to measure biological systems at multiple molecular levels, including genomics, transcriptomics, proteomics, metabolomics, and microbiomics. Each of these technologies offers a different perspective on disease mechanisms. However, when analyzed separately, they provide only partial insights. This is where data integration becomes essential. Multi-omics integration combines data from several biological layers to create a more comprehensive model of disease. By linking genetic predisposition with gene expression patterns, immune signaling, metabolic profiles, and microbial communities, researchers can uncover relationships that would remain hidden in single-dataset studies. Multivariate data analysis methods (e.g. R mixOmics project) have been developed for the specific purpose of omics data integration. The aim is the development of multi-omics diagnostic as well as pathogenesis models that can improve disease classification, predict disease severity, and individualize treatments. With the advancement of computational tools and data-sharing efforts, multi-omics approaches are likely to become an essential component of next-generation diagnostics for allergic diseases.

Keywords: Omics, Allergy, Genomics, Transcriptomics, Proteomics, Metabolomics

O66

Scientific Principles for Managing Laboratory Test Requests

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The transformation of healthcare systems over the past decade has elevated the role of medical diagnostic laboratories from mere producers of laboratory test results to one of the most important generators of reliable clinical data. In this new paradigm, productivity is no longer measured solely by the number of tests performed or cost reduction; rather, it is evaluated through the quality of generated data, speed of information accessibility, preventable error rates, and impact on clinical decision-making. This presentation examines the future-oriented position of laboratories within the health data production chain and demonstrates how integration among Laboratory Information Systems (LIS), Hospital Information Systems (HIS), and other health information platforms can reduce pre-analytical, analytical, and post-analytical errors, enhance patient safety, and improve organizational productivity. Furthermore, the role of pathology and laboratory sciences in generating standardized, traceable, and artificial intelligence-ready data for precision medicine and population health management is explored. Within this framework, emerging productivity indicators—including data quality, interoperability, clinical turnaround time (Clinical TAT), and clinical value creation—are introduced. The presentation also addresses the challenges of laboratory digital transformation, including fragmented information systems, inadequate data standardization, and organizational resistance. Proposed solutions include data governance, intelligent automation, and performance management based on measurable indicators. Introduction: In recent years, medical diagnostic laboratories have assumed a more strategic role within healthcare systems, evolving from operational service units into centers for the generation of valuable clinical data. This paradigm shift necessitates a redefinition of the concept of productivity in laboratory medicine. Methods: This presentation was developed using an analytical, managerial, and foresight-oriented approach based on the evaluation of digital transformation trends in medical laboratories and the integration of healthcare information systems. Findings: The findings indicate that the integration of LIS and HIS, together with data standardization, plays a significant role in reducing laboratory errors and improving service quality. Moreover, when laboratory data are structured and standardized, they become suitable for applications in artificial intelligence and precision medicine. Discussion and Conclusion: The future of medical diagnostic laboratories depends on a transition from “result generation” to “valuable data generation.” Modern productivity frameworks should focus on data quality, decision-making efficiency, and clinical value creation. In this evolving landscape, laboratories will become one of the fundamental pillars of health data governance.

Keywords: Medical Diagnostic Laboratory, Productivity, Pathology, Digital Health, Artificial Intelligence

O67

Evidence- and Clinically-Based Optimization of Laboratory Test Requests

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Appropriate laboratory test selection is a cornerstone of high-quality healthcare, contributing to cost containment and reduction of diagnostic errors. Guideline-based laboratory medicine offers a systematic framework for guiding both test ordering and interpretation based on the best available evidence. This approach minimizes unnecessary testing while reducing the risk of missed or delayed diagnoses. This presentation will review key principles of optimizing test utilization, including the role of clinical guidelines, decision-making algorithms, and laboratory information system–based interventions. It will also address implementation challenges such as clinician resistance, resource limitations, and the need for continuous education. Ultimately, the goal is to enhance efficiency, improve patient safety, and increase value in healthcare delivery.

Quality Improvement in the Clinical Biochemistry Section (Department) of the Laboratory

O68-O71

O68

Quality-Assured Reference Intervals: from Establishment to Continuous Verification

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Abstract: Reference intervals (RIs) are indispensable to the interpretation of laboratory test results, yet their development and validation remain among the most challenging aspects of laboratory practice. While clinical decision limits guide diagnosis and treatment based on evidence of disease and outcomes, reference intervals describe the expected range of values in a healthy population and therefore require a fundamentally different scientific approach. Inaccurate or poorly validated reference intervals can lead to misclassification of patients, inappropriate clinical decisions, and compromised patient safety. This presentation provides a practical overview of contemporary strategies for establishing and verifying reference intervals in accordance with CLSI EP28-A3c and ISO 15189 recommendations. It discusses the strengths and limitations of direct and indirect approaches, the importance of controlling pre-analytical and analytical variables, and the role of appropriate statistical methods, including partitioning by age, sex, and other biological characteristics. The session also highlights the practical considerations of transferring published reference intervals, verification using the CLSI 20-sample protocol, and the growing value of laboratory information system–based continuous monitoring. Particular emphasis is placed on harmonization, metrological traceability, quality management, and documentation to ensure that reference intervals remain clinically relevant and scientifically robust. By integrating international best practices with practical laboratory experience, this presentation aims to support laboratory professionals in implementing reliable reference intervals that enhance result interpretation, improve harmonization across laboratories, and ultimately contribute to better patient care.

O69

Future Visions of External Quality Assurance and Quality Control-Integrate IQC and EQA

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The talk will describe a possible future use of patient-based data in EQA and QC. We begin by examining what we are trying to achieve with a quality control system and the current problems in the practice of IQC. Then patient-based QC is introduced, with its advantages (commutable and frequent monitoring) and limitations (poorly understood, yields normal values and large numbers of samples). Next, we describe the role of EQA in the Quality Assurance stable, and the current problems with EQA (commutability and traceability). Lastly, I present an 'ideal' system based on a mixture of patient-based QC and EQA.

O70

Standardization, Harmonization, IQC and EQA in Clinical Biochemistry

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Clinical laboratory medicine plays a central role in diagnosis, risk assessment, treatment selection, and monitoring, making the accuracy, comparability, and clinical interpretation of test results essential to patient care. This presentation reviews the integrated quality framework required to ensure reliable laboratory testing across the total testing process, with emphasis on standardization and harmonization, internal quality control (IQC), external quality assessment (EQA), and appropriate reference intervals. Standardization establishes metrological traceability through reference measurement procedures, certified reference materials, calibration hierarchies, and commutable materials, while harmonization supports comparable interpretation when complete reference systems are unavailable. Effective IQC provides continuous monitoring of analytical performance, detects trends and outliers, and supports timely corrective action through risk-based planning, appropriate control materials, statistical tools, and emerging patient-based real-time quality control approaches. EQA complements IQC by assessing interlaboratory comparability and identifying laboratory- or method-specific bias; accuracy-based schemes using commutable samples and reference-assigned targets provide the strongest assessment of true standardization. However, limitations including noncommutable materials, cost, inconsistent participation, and inadequate global access remain important challenges. Post-analytical quality further depends on harmonized units, reference intervals, clinical decision limits, and reporting practices. A practical quality pathway therefore links definition of the measurand and clinical purpose with traceability, performance specifications, risk-based IQC, appropriate EQA, harmonized interpretation, and continuous improvement. Together, these components create an integrated quality ecosystem that supports consistent, clinically meaningful laboratory results across laboratories, methods, instruments, and time. International collaboration through organizations such as IFCC is critical to advancing standardization, harmonization, and equitable access to quality systems.

O71

Continuous Education and Development of Technical Skills in Medical Laboratories

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Introduction & Professional Roles: The Role: Laboratory professionals evaluate patient health using techniques involving blood, DNA, tissue, and cells. They work in laboratories, academia, and industry. Career Progression: The presentation compares roles based on schooling and skills: Assistant: Routine tests, focus on manual dexterity. Technician: Routine tests, QC/special tests, licensure. Medical Technologist: Developing new tests and research. The Need for Education: Rapid advancements in laboratory medicine require constant re-education. IFCC recommends a stepwise approach based on Bloom's Taxonomy (Remembering, Understanding, Applying, Analyzing, Evaluating, Creating). Educational & Practice Needs: The curriculum for modern laboratory practitioners spans eight core areas:1-Quality Management & Compliance: ISO 15189:2022 standards, Internal Quality Control (IQC),External Quality Assessment (EQA),risk management, and uncertainty calculations.2-Clinical Chemistry: Focus on endocrinology, hematology, cardiac markers, and point-of-care testing (POCT).3-Emerging Trends: Integration of Artificial Intelligence (AI),Machine Learning, Genomics/Molecular Diagnostics, and advanced analytical techniques(Mass Spectrometry).4-Specialized Testing: Genetic/Prenatal screening and immunohistochemistry.5-Management & Leadership: Total Quality Management (TQM), Lean Six Sigma, and health economics.6-Case Studies: Practical training in troubleshooting and analytical error management.7-Public Health: Disease prevention, diabetes management, and trauma medicine.8-Innovation:Developing novel biomarkers and sustainable(Green)laboratory practices. The Role of IFCC and EQA: IFCC (International Federation of Clinical Chemistry): The IFCC is instrumental in developing educational materials and position statements to maintain global standards. EQA (External Quality Assessment): Participation is essential for accreditation. EQA programs go beyond simple assessment; they serve as a platform for networking, information sharing, and conducting continuing education activities. Clinical Cases & Practical Application: The presentation emphasizes the use of digital images and photographs to train professionals in: Urinary Sediment: Analyzing crystals (e.g., Calcium Oxalate Dihydrate) using various microscopy techniques (Brightfield, phase-contrast, polarized light). Advanced Diagnostics: Documented cases on Primary Hyperoxaluria Type 1 and identifying Cryptococcus within urinary casts. Competency Benchmarking: Literature shows that ongoing participation in EQA programs improves the accuracy of particle identification (e.g.,

normal vs. dysmorphic RBCs) over time. Conclusion: Continuous education is mandatory to keep pace with the evolution of the field. There remains a significant gap between current

practice and required competencies. EQA programs act as powerful, accessible tools for continuous learning. Integrating education into routine laboratory practice is critical to improving diagnostic quality and patient outcomes.

Selected Articles: Applied Research from the Laboratory to the Clinic

O72

O72

Designing an X-ray Irradiation System for Platelet Products Using a Linear Accelerator Device

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Background: Transfusion-associated graft-versus-host disease (TA-GVHD) is a rare but often fatal complication of transfusion of cellular blood components caused by the proliferation of donor T lymphocytes. X-rays and gamma rays prevent TA-GVHD by inducing direct and indirect DNA damage in donor T lymphocytes, thereby inhibiting their proliferative capacity. Gamma irradiation using dedicated blood irradiators has an established clinical history. In contrast, X-ray blood irradiation has emerged as an attractive alternative to gamma irradiation because it does not require a continuously active radioactive source. However, implementation of this technology requires dedicated blood irradiation equipment and associated infrastructure. In the present study, rather than using a dedicated X-ray blood irradiator, an X-ray irradiation system based on an available linear accelerator (LINAC) at a radiotherapy center was used to irradiate platelet components. A custom-designed and fabricated irradiation phantom was developed for this purpose. By utilizing existing radiotherapy infrastructure, this approach may reduce the need for a dedicated blood irradiator and provide an accessible and potentially cost-effective method for platelet concentrate irradiation. Gamma irradiation was compared with LINAC-generated X-ray irradiation, and their effects on T lymphocytes and platelets were evaluated. Methods: A Perspex irradiation phantom was designed and fabricated to accommodate a single platelet bag for use with the linear accelerator. Platelet concentrates were divided into three groups: X-ray-irradiated, gamma-irradiated, and non-irradiated control groups. To assess the effects of irradiation on T-cell proliferation, mononuclear cells isolated from platelet concentrates were treated with 1% PHA and evaluated using MTT and cell-cycle assays. Following co-culture of responder and stimulator cells using the mixed lymphocyte reaction (MLR) assay, lymphocyte proliferative responses to allogeneic cells were evaluated using the MTT assay, while $CD8^+$ T-cell activation was assessed by flow cytometry based on the early activation marker CD69 and the late activation marker CD25. In addition, platelet activation was evaluated by flow cytometric assessment of P-selectin expression and PAC-1 binding to the activated form of the GPIIb/IIIa receptor. Results: Both X-ray and gamma irradiation significantly inhibited T-cell proliferation. Irradiation disrupted the cell cycle by reducing the proportion of cells

entering the S phase and inducing cell-cycle arrest at the G2 phase. Both irradiation modalities also significantly reduced the proliferative response of lymphocytes to

allogeneic cells and decreased $CD8^+$ T-cell activation. In contrast, neither irradiation method caused significant adverse effects on platelet activation. Conclusion: For the first time, this study demonstrated that a LINAC-based X-ray irradiation system operating at a dose of 30 Gy was comparable to gamma irradiation in terms of safety and efficacy. The proposed system may therefore serve as an alternative approach for platelet component irradiation in settings where dedicated gamma- or X-ray-based blood irradiators are unavailable.

Keywords: X-ray, Gamma Irradiation, Transfusion-Associated Graft-Versus-Host Disease (TA-GVHD), Platelet Concentrate, Linear Accelerator (LINAC), Mixed Lymphocyte Reaction (MLR)

The Clinical Importance and Application of Accurate Measurement of Low Hormone Levels

O73-O75

O73

Clinical Importance and Applications of Measuring Low Concentrations of Steroid Hormones

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Introduction: Steroid hormones are among the principal regulators of physiological processes, including metabolism, reproductive function, stress response, and maintenance of homeostasis. These hormones are normally present in the circulation at very low concentrations, such that even subtle alterations may reflect clinically significant endocrine disorders. Consequently, accurate measurement of steroid hormones at low concentration ranges plays a critical role in the early diagnosis and clinical management of hormonal abnormalities. Methods: This review summarizes current evidence regarding the clinical relevance of measuring low concentrations of steroid hormones and evaluates the analytical methodologies used for this purpose. Particular emphasis was placed on comparing the performance of conventional immunoassays with advanced analytical techniques based on liquid chromatography–tandem mass spectrometry (LC–MS/MS) for the quantification of steroid hormones in low concentration ranges. The applicability of these methods across different clinical settings and special patient populations was also assessed. Results: The reviewed evidence indicates that reduced levels of steroid hormones are of high diagnostic value in conditions such as adrenal insufficiency, hypogonadism, disorders of the hypothalamic–pituitary–gonadal axis, premature ovarian insufficiency, and congenital defects of steroidogenesis. Immunoassay-based methods demonstrate several limitations at low hormone concentrations, including analytical interference and reduced accuracy. In contrast, LC–MS/MS provides superior sensitivity and specificity, enabling reliable and simultaneous quantification of multiple steroid hormones at low circulating levels. Discussion and Conclusion: Accurate assessment of low steroid hormone concentrations is essential for establishing correct diagnoses, monitoring hormone replacement therapies, and optimizing therapeutic dosing, particularly in vulnerable populations such as pediatric patients, older adults, pregnant women, and critically ill individuals. The use of highly sensitive and specific analytical techniques, especially LC–MS/MS, substantially reduces diagnostic uncertainty and improves the quality of clinical decision-making. Overall, the selection of appropriate measurement methodologies is a key determinant in enhancing patient care and advancing clinical endocrinology.

Keywords: Steroid Hormones, Low-Level Hormone Measurement, Endocrine Disorders, Liquid Chromatography, Tandem Mass Spectrometry (LC–MS/MS), Clinical Endocrinology

O74

The Significance and Clinical Application of Measuring Low Hormone Levels

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Background: Accurate measurement of low hormone concentrations in biological fluids plays a crucial role in the diagnosis, monitoring, and management of a wide range of endocrine and metabolic disorders, as well as certain chronic diseases. The sensitivity and specificity of measurement methods directly impact diagnostic accuracy and therapeutic efficacy. Methods: Modern hormone measurement techniques include highly sensitive immunoassays such as ELISA (Enzyme-Linked Immunosorbent Assay), chemiluminescence assays, and mass spectrometry, particularly LC-MS/MS (Liquid Chromatography-tandem Mass Spectrometry). These techniques are capable of detecting and quantifying hormones at very low levels, typically in the femtogram to picogram per milliliter range. The selection of an appropriate method depends on the type of hormone, the sample matrix, and the required sensitivity. Findings: Immunoassay methods like ELISA and CLIA (Chemiluminescence Immunoassay), owing to their ease of execution, relatively low cost, and reasonable speed, are widely employed in routine diagnostics. However, LC-MS/MS, due to its high specificity and ability to differentiate structurally similar molecules, is recognized as the gold standard for measuring numerous hormones, especially steroids and peptides. Furthermore, microfluidic technologies hold significant potential for the future development of rapid, accurate, and low-volume diagnostic kits. Conclusion: The precise measurement of low hormone levels facilitates the early detection of diseases such as adrenal insufficiency, thyroid disorders, and certain types of cancers. Choosing the appropriate diagnostic method, considering sensitivity, specificity, cost, and turnaround time, is essential for ensuring reliable results and making sound clinical decisions. Advances in measurement technologies, particularly LC-MS/MS, have dramatically increased diagnostic precision, paving the way for more targeted therapies.

Keywords: Low-Concentration Hormones, Laboratory Diagnostics, Sensitive Immunoassay, Mass Spectrometry (LC-MS/MS)

O75

Detection Capabilities in the Lower Measurement Range of Analytical Techniques (LOB, LOD, LOQ)

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In this presentation, measurement at low concentration levels (zero and close-to-zero) will be addressed. Although theoretically it is expected that in the “absence” of analyte in the specimen, the measurement method to report a zero result; and in the “presence” of analyte, the measurement method to report a reliable quantitative result, but it does not come true in practice. Therefore, it is necessary that the capabilities of measurement methods at low concentration levels be considered, including: Limit of Blank (LoB)- the highest result that would be provided in the absence of analyte in the specimen; Limit of Detection (LoD)- the least analyte concentration that can reliably identified from the absence of the analyte; and Limit of Quantification (LoQ)- the least analyte concentration that can be quantitatively measured with the “intended analytical quality”. Over this presentation, theoretical and practical aspects of detection capabilities, especially based on CLSI EP17:2012, will be discussed.

The impact of Laboratory Accreditation on the International Credibility and Acceptance of Laboratory Results

O76-O79

O76

A Structured Model for Ensuring the Quality of Results to Meet the Requirements of the ISO 15189 Standard

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Background and Objective: Clause 7.4.1.2 of the ISO 15189 standard states: Results shall be reviewed and authorized for reporting before they are issued. The laboratory shall ensure that authorized personnel review the test results and evaluate them based on internal quality control and, where appropriate, with available clinical information and previous test results. Considering this issue, the final review and control of laboratory results is one of the most critical and important steps in the post-test process. This article aims to introduce a preventive and multi-stage quality control model that minimizes reporting errors by creating different layers of review and checks. Methodology and Methods: In this model, a multi-layered structure is designed in which each result undergoes successive and defined stages of control and checks by different levels of expertise and supervision before final approval. The central core of this model is the response check group. Findings:Implementation of this model over a 10-month period resulted in a significant reduction in potential clinically significant errors. The system also enhanced process transparency, decision traceability, and a culture of collective accountability in the laboratory. Conclusion:The proposed model goes beyond the minimum requirements of the standard, providing maximum protection against reporting errors through intelligent controls at various levels. This model is recommended as a suitable solution for laboratories committed to continuous quality improvement.

O77

The Role of Accreditation in the International Exchange of Laboratory Results

Moslem Barak *

The international exchange of laboratory results is essential for cross-border healthcare services, regulatory cooperation, and global trade. Accreditation provides the internationally agreed mechanism that enables laboratory results to be accepted beyond national boundaries by establishing confidence in their technical validity, impartiality, and reliability. For medical laboratories, this confidence is achieved through accreditation to ISO 15189, while testing and calibration laboratories rely on ISO/IEC 17025. This presentation focuses on how accreditation facilitates the international acceptance of laboratory results through mutual recognition arrangements among accreditation bodies, in particular the ILAC Arrangement. Under this framework, results issued by laboratories accredited to ISO 15189 or ISO/IEC 17025 are recognised internationally as technically equivalent, reducing the need for repeat testing and supporting regulatory reliance across different economies. Drawing on the Global Accreditation Incorporated framework, the presentation highlights how the harmonised application of ISO 15189 and ISO/IEC 17025, together with international peer evaluation of accreditation bodies, ensures the comparability, reliability, and global acceptance of laboratory results. This system sustains trust in the global recognition framework and supports the principle of “accredited once, accepted everywhere.” The presentation concludes by emphasizing accreditation as a cornerstone of the global quality infrastructure, enabling the seamless international exchange of laboratory results while reducing technical barriers to trade and supporting public health and regulatory confidence.

O78

Linking Laboratory Accreditation to Measurable Clinical Outcomes

Vivek Pant *

Laboratory accreditation is often viewed as a formal process of meeting standards and passing inspections. However, its true value lies in its ability to translate structured quality systems into measurable improvements in patient care. Accreditation according to ISO 15189:2022 provides a framework that connects analytical performance, risk management, and continuous improvement with tangible clinical outcomes. This lecture will present a practical framework for linking accreditation activities to measurable indicators of patient impact. Rather than focusing solely on compliance, the session will demonstrate how quality management systems can reduce patient misclassification risk, prevent unnecessary treatment, minimize laboratory related incidents, and improve diagnostic accuracy. Real world examples, with reported cases, from accreditation implementation will illustrate how quality indicators can be reframed in terms of safety, effectiveness, and patient centered outcomes. The presentation will argue that the future of accreditation lies in shifting the central question from “Is the result analytically correct?” to “Is the result clinically useful for this patient?” By integrating risk based thinking, outcome measurement, and clinician engagement, accredited laboratories can move beyond documentation toward demonstrable healthcare value.

Keywords: ISO 15189:2022, Clinical Outcomes, Laboratory Accreditation, Quality Indicators, Patient Safety

O79

The Role of Laboratory Accreditation in the International Exchange of Laboratory Results

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“Accreditation based on international standards is, in fact, the only scientific passport for medical laboratories to enter the global health and trade cycle. This talk will explain how confirmation of technical competence by governing bodies such as ILAC and IAF, beyond being a systemic requirement, creates “mutual trust” at the international level. The main focus is on the strategic role of Mutual Recognition Agreements (MRAs), which, by formalizing laboratory results in member countries, remove technical trade barriers and prevent costly duplication of tests. Through standardization based on ISO 15189, laboratories achieve a common language of quality, which in turn facilitates the exchange of clinical data, supports public health, and improves patient safety on a cross-border scale. This presentation introduces accreditation not as a destination but as a gateway to achieving global acceptance and a powerful presence in the international health system.”

The Role of Medical Laboratories in Screening and Diagnosing Diseases in Newborns

O80-O82

O80

Important Points About Screening and Specialized Tests for Metabolic Diseases in Newborns

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Background: Infant health can be guaranteed through early screening programs and timely interventions. Newborn screening, typically performed in the first days of life via heel prick blood sampling, plays a vital role in the early identification of disorders. These programs include the detection of metabolic diseases (such as phenylketonuria (PKU), galactosemia, and congenital hypothyroidism). In Iran, extensive screening covers more than 40 to 50 metabolic and genetic diseases, with coverage exceeding 95% of births. In the future, screening programs for immune deficiencies (such as SCID or severe combined immunodeficiency) and genetic disorders (such as cystic fibrosis and certain hemoglobinopathies) should also be implemented. Early detection of these disorders allows treatments like special diets, medications, or supportive interventions to prevent irreversible complications such as intellectual disability, physical disability, or death. Gene therapy, as a modern advancement, directly corrects or replaces defective genes and is effective for severe genetic diseases like SMA, hemophilia, or certain immune deficiencies. However, if screening is performed timely and identified issues are followed up (such as dietary therapy in PKU), there is often no need for complex and costly gene therapy at older ages. Early intervention not only prevents disability but also improves quality of life.It is recommended that all parents take screening seriously and, in case of abnormal results, promptly consult metabolic and genetic specialists.

O81

Genetic Screening Methods in Newborn Screening of Inherited Metabolic Disorders: Current Guidelines and Emerging Directions

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Bakground: Biochemical newborn screening (NBS), particularly tandem mass spectrometry (MS/MS), is the foundation of population-based screening for inborn errors of metabolism (IEMs) and is endorsed by international guidelines from the American College of Medical Genetics and Genomics (ACMG), the International Society for Neonatal Screening (ISNS), and the European Society for Newborn Screening (ESNS). However, biochemical screening alone is limited by false-positive results, incomplete disease coverage, and limited genotype–phenotype resolution. Objective: To review guideline-based genetic screening strategies in metabolic NBS and to discuss emerging genomic approaches, with a focus on artificial intelligence (AI). Methods: Guideline-supported molecular approaches—including targeted gene sequencing, next-generation sequencing (NGS) panels, whole-exome sequencing (WES), and copy number variant (CNV) analysis—were reviewed as second-tier or complementary tools following abnormal biochemical screening results. Evidence from recent pilot studies on expanded genomic NBS and rapid genomic testing in neonatal intensive care units was also examined. Results: Targeted molecular testing improves diagnostic specificity and reduces false-positive rates. Expanded NGS-based screening increases diagnostic yield, particularly for disorders with subtle or variable biochemical profiles. AI-based tools show promise in metabolite pattern recognition, variant prioritization, genotype–phenotype correlation, and integration of multi-omics. Conclusion: An integrated model combining biochemical screening, targeted genomic testing, and AI-assisted interpretation represents a future direction for metabolic NBS and should be implemented in alignment with established guidelines and ethical.

Keywords: Newborn Screening, Inherited Metabolic Disorders, Genetic Screening, Artificial Intelligence

O82

Newborn Screening for Severe Combined Immunodeficiency Using TREC Assay: Opportunities and Challenges for Laboratory Implementation

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Severe Combined Immunodeficiency (SCID) represents a group of life-threatening primary immunodeficiency disorders characterized by profound T-cell deficiency and severe susceptibility to infections. Early diagnosis before the onset of clinical manifestations is crucial, as timely hematopoietic stem cell transplantation, gene therapy, or enzyme replacement therapy can dramatically improve survival outcomes. Newborn screening using T-cell Receptor Excision Circle (TREC) quantification has emerged as an effective strategy for the early detection of SCID and other significant T-cell lymphopenias. The TREC assay is performed on dried blood spots routinely collected for neonatal screening programs and provides a sensitive, rapid, and cost-effective approach for identifying infants at risk. Since its first implementation in population-based screening programs, TREC testing has enabled the detection of affected infants prior to the development of severe infections, thereby reducing morbidity, mortality, and healthcare costs. This presentation reviews the biological basis of TREC analysis, current screening algorithms, laboratory quality assurance requirements, interpretation of results, and common causes of false-positive and false-negative findings. In addition, practical considerations for integrating TREC-based screening into national newborn screening programs and the role of molecular genetic confirmation will be discussed. The implementation of SCID newborn screening represents a significant advancement in preventive laboratory medicine and highlights the critical collaboration between immunology, genetics, and clinical laboratories in improving patient outcomes and healthcare quality.

Keywords: Severe Combined Immunodeficiency (SCID), TREC, Newborn Screening, Primary Immunodeficiency, Laboratory Quality Improvement, Molecular Genetics

The Role of Medical Laboratories in the Diagnosis and Monitoring of Common Diseases

O83-O86

O83

Cardiac biomarkaers and Heart Failure Management

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Cardiac biomarkers play a pivotal, but adjunctive, role in the contemporary management of heart failure (HF). This concise summary integrates diagnostic, prognostic, and therapeutic guidance across HF phenotypes. Natriuretic peptides (BNP, NT-proBNP) illuminate myocardial wall stress, enabling differentiation of acute decompensated HF from non-HF etiologies, risk stratification, and monitoring decongestion. Cardiac troponins (hs-cTnI/T) detect myocardial injury and add prognostic value in HF, particularly when trends suggest concomitant ischemia or decompensation. Emerging markers (sST2, Galectin-3, GDF-15, MR-proANP) offer additional risk stratification but remain adjuncts to the core drivers of care. In practice, NT-proBNP/BNP-guided strategies may benefit select populations, with serial measurements guiding volume status and response to therapy, while troponin elevations should be interpreted within the clinical context to distinguish acute coronary events from chronic injury. Biomarkers are most effective when integrated with guideline-directed medical therapy (GDMT) for HF with reduced ejection fraction (HFrEF) or preserved ejection fraction (HFpEF), including ACE inhibitors/ARBs or ARNI, beta-blockers, MRAs, and SGLT2 inhibitors, alongside meticulous diuretic management and comorbidity optimization. Patient-specific factors—renal function, obesity, atrial fibrillation, and age—shape biomarker interpretation and decision-making. Key takeaways BNP/NT-proBNP are central for diagnosis, prognosis, and decongestion assessment; emphasis on serial trends over single values hs-cTn elevations in HF signal myocardial injury and worsened prognosis; employ serial measurements to differentiate acute from chronic processes Biomarkers refine, but do not replace, clinical judgment and hemodynamic assessment within guideline-concordant HF care A multimarker, patient-tailored approach enhances risk stratification and supports GDMT optimization, with ongoing research poised to refine biomarker-guided strategies in HFpEF and precision phenotyping.

O84

Analytical Challenges and Advances in Laboratory Assessment of Thyroid Disorders: The Evolving Role of the Clinical Laboratory Specialist

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Abstract: Accurate laboratory assessment of thyroid disorders is fundamental to clinical decision-making, yet thyroid testing remains vulnerable to significant pre-analytical and analytical challenges. Thyroid-stimulating hormone (TSH) is the primary test for thyroid function evaluation; however, biological variability, sample integrity, heterophile antibodies, biotin interference, and assay-specific calibration differences frequently compromise result reliability. Free thyroxine (fT4) and free triiodothyronine (fT3) immunoassays are particularly susceptible to binding protein abnormalities, non-thyroidal illness, and drug interference, underscoring the need for robust analytical validation and careful method selection. Autoimmune thyroid testing, including thyroid peroxidase antibodies, thyroglobulin antibodies, and TSH receptor antibodies, introduces additional complexity related to assay heterogeneity, limited standardization, and challenges in clinical interpretation. Implementation of comprehensive quality assurance programs, harmonized reference intervals, and method verification strategies is essential to ensure consistency and comparability of results. Recent advances in laboratory medicine have expanded diagnostic capabilities. Liquid chromatography–tandem mass spectrometry (LC-MS/MS) improves analytical specificity for thyroid hormone measurement in selected populations and serves as a reference technique for assay evaluation. In thyroid nodules and cancer, molecular diagnostics and next-generation sequencing (NGS) panels identifying BRAF, RAS, RET/PTC, and other oncogenic alterations support risk stratification and personalized patient management. This presentation highlights the central role of the clinical laboratory specialist in managing assay interference, validating advanced technologies, ensuring quality, and translating complex laboratory data into clinically actionable information.

Keywords: Thyroid Function Testing, Assay Interference, Quality Assurance, LC-MS/MS, Autoimmune Thyroid Disease, Molecular Diagnostics, Thyroid Cancer

O85

Diagnosis and Monitoring of Metabolic Dysfunction Associated Steatotic Liver Disease (MASLD)

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Background: Metabolic dysfunction-associated steatotic liver disease (MASLD), previously termed non-alcoholic fatty liver disease (NAFLD), is defined as steatotic liver disease (SLD) in the presence of one or more cardiometabolic risk factor(s) and the absence of harmful alcohol intake. The spectrum of MASLD includes steatosis, metabolic dysfunction-associated steatohepatitis (MASH, previously NASH), fibrosis, cirrhosis and MASH-related hepatocellular carcinoma (HCC). This joint EASL-EASD-EASO guideline provides an update on definitions, prevention, screening, diagnosis and treatment for MASLD. Case-finding strategies for MASLD with liver fibrosis, using non-invasive tests, should be applied in individuals with cardiometabolic risk factors, abnormal liver enzymes, and/ or radiological signs of hepatic steatosis, particularly in the presence of type 2 diabetes (T2D) or obesity with additional metabolic risk factor(s). A stepwise approach using blood-based scores (such as FIB-4) and, sequentially, imaging techniques (such as transient elastography) is suitable to rule-out/in advanced fibrosis, which is predictive of liver-related outcomes. In adults with MASLD, lifestyle modification – including weight loss, dietary changes, physical exercise and discouraging alcohol consumption – as well as optimal management of comorbidities – including use of incretin-based therapies (e.g. semaglutide, tirzepatide) for T2D or obesity, if indicated – is advised. Bariatric surgery is also an option in individuals with MASLD and obesity.

O86

Key Biomarkers in Diabetes and Diabetic Nephropathy: Applications and Limitations

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Background: Diabetes and its complication, diabetic nephropathy or diabetic kidney disease (DKD), pose a major global health challenge. Early detection and monitoring are crucial to prevent disease progression. While traditional biomarkers such as albuminuria and estimated glomerular filtration rate (eGFR) remain clinical cornerstones, their limitations in sensitivity and specificity have necessitated the search for novel biomarkers. These emerging biomarkers include glomerular injury markers (e.g., negatively charged transferrin), tubular injury markers (e.g., NGAL, KIM-1, and nephronectin), systemic inflammation and fibrosis indicators (e.g., MCP-1, TGF-β, FGF-23, and suPAR), as well as molecular signatures identified through proteomic and metabolomic studies. The primary applications of these biomarkers are detecting kidney injury at a very early stage (even pre-microalbuminuria), enabling more accurate risk stratification for disease progression, categorizing disease subtypes for targeted therapy, and monitoring response to novel treatments (e.g., SGLT2 inhibitors). However, significant translational barriers exist, including patient heterogeneity, influence of comorbidities, challenges in standardization and interpretation, cost, and the pressing need for validation in large, diverse prospective studies. Therefore, despite their transformative potential, the transition to personalized medicine in DKD will require the development of integrated multi-biomarker panels and their fusion with clinical and imaging data into AI-enhanced predictive models. This holistic approach promises to shape the future management of DKD, ultimately improving patient outcomes.

The Role of the Laboratory in Diagnosing Heart Attacks

O87-O90

O87

Challenges in Interpretation of Serum Troponin Results in the Diagnosis of Myocardial Infarction

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Cardiac troponins (cTn), including cardiac (cTnI) and cardiac troponin T (cTnT), are the preferred biomarkers recommended to both rule-in and rule-out of myocardial infarction (MI). Although measuring cTn with high-sensitive techniques has enough analytical sensitivity for rapid diagnosis and high clinical sensitivity, high levels of blood cTn values necessarily do not indicate the occurrence of MI. In addition to acute coronary syndrome which may results to MI, increased blood troponin values may also result from ischemic myocardial injury due to non-coronary syndrome (e.g. hypoxia, shock, anemia, invasive procedures), non-ischemic myocardial damage (e.g. heart failure, myocarditis, pericarditis, renal failure, lung disease, hypothyroidism, sepsis, heavy activity), and analytical problems (e.g. heterophil antibody, calibration error, poor performance). So, abnormal high values of cTn should be interpretated with caution. In this regard, it is recommended to use changes (increasing or decreasing) in blood cTn values, at least 20% between 2 serial values. It is important to note that differences between 2 serial values, may also be due to intra-individual biological variations and analytical variations which are calculated as reference change value (RCV). Because of relatively high intra-individual variations, especially for cTnT, using 20% changes for diagnosis of MI has low specificity. Using higher difference (more than 20%) increases the clinical specificity but also lowers clinical sensitivity.

Keywords: Myocardial Infarction, Cardiac Troponin, Sensitivity, Specificity

O88

Guidelines for the Diagnosis of Myocardial Infarction

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Background: Myocardial infarction (MI) is one of the leading causes of mortality and disability worldwide. Rapid and accurate diagnosis of MI can save patients' lives and prevent long-term cardiac damage. The laboratory plays a vital role in the identification of cardiac biomarkers and in guiding clinical decision-making. Methods: (1) Review of international guidelines (ESC, ACC/AHA). (2) Evaluation of cardiac biomarkers including high-sensitivity troponin I/T and CK-MB, (3) Assessment of blood sampling timing: initial sample at 0 hour, second sample at 3 hours, and third sample at 6 hours after symptom onset. (4) Analysis of the sensitivity and specificity of laboratory tests in early diagnosis. Results: Troponin is the most sensitive cardiac biomarker for the diagnosis of MI, with detectable elevation within 3–6 hours after symptom onset. CK-MB and other biomarkers are complementary and useful in selected clinical situations. Rapid and serial testing facilitates early diagnosis and supports timely clinical decision-making. Conclusion: The laboratory is a vital and irreplaceable tool in the diagnosis of myocardial infarction. Adherence to diagnostic guidelines and standardized sampling protocols improves diagnostic accuracy. Close collaboration between clinical teams and laboratory services leads to faster decisions and reduces diagnostic errors. Ongoing education of laboratory personnel and enhanced coordination with cardiologists are strongly recommended.

Keywords: Myocardial Infarction, Troponin, CK-MB, Laboratory Diagnosis, Guidelines

O89

Novel Biomarkers in the Diagnosis and Evaluation of AMI

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Acute myocardial infarction (AMI) remains a leading cause of death worldwide. Rapid laboratory-based diagnosis is essential for optimal management of these patients. Although high-sensitivity cardiac troponins (hs-cTnT and hs-cTnl) remain the gold standard and diagnostic cornerstone, they have limitations in patients presenting at early stages and in patients with chronic structural or renal disease. In recent years, emerging biomarkers including cardiac myosin-binding protein C (cMyc), copeptin, heart –type fatty acid-binding protein (H-FABP), BB (GPBB), GDF-15, sST2, interleukin-6 (IL-6), myeloperoxidase (MPO), and circulating microRNAs (miR-499, miR-208, miR-1, miR-133) have been investigated in laboratory and clinical research cycles. In this article, we will review the diagnostic value and role of these biomarkers in patient monitoring and follow-up, cost-effectiveness studies, and their technical standardization, and also emphasize that in the future, the path to diagnosis and monitoring will likely include multi-marker panels for personalized AMI management

Keywords: AMI, Novel Cardiac Biomarkers

O90

High-sensitive Measurement Procedure of Troponin vs Its Contemporary Assays

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Background: Acute Coronary Syndrome (ACS) is a leading cause of mortality worldwide, with cardiac troponin serving as the gold standard for diagnosis. High-sensitivity troponin (hs-cTn) assays have revolutionized early detection; however, technological differences among available commercial platforms pose significant challenges for laboratory medicine specialists. Methods: In this review, four major hs-cTn platforms—Abbott ARCHITECT (hs-cTnI), Roche Cobas (hs-cTnT), Siemens ADVIA Centaur (hs-cTnI), and Beckman Coulter Access (hs-cTnI)—were compared regarding analytical specifications, limit of detection (LoD), precision at the 99th percentile, 0-1 and 0-3 hour diagnostic algorithms, and implementation challenges. Results: Limit of detection ranges from 1.1 to 3 ng/L across platforms. The 99th percentile varies from 12 ng/L (Beckman) to 47 ng/L (Siemens). All assays demonstrate >99% sensitivity for Rule-out, while Rule-in specificity ranges from 75–82%. Specific interferences include biotin (Roche), rheumatoid factor (Abbott), and hemolysis (Siemens). Conclusion: The selection of hs-cTn assays should be guided by clinical needs, sample volume, laboratory budget, and team familiarity with the platform. Non-substitution of values from different methods and the need to use method-specific cut-offs are critical for correct interpretation of results. Successful implementation requires rigorous quality control with a CV% of less than 10% at the 99th percentile.

Keywords: High-Sensitivity Troponin, hs-cTnI, hs-cTnT, Acute Coronary Syndrome, 0-1 Hour Algorith

The First Symposium of Extracellular Vesicles

O91-O94

O91

Extracellular Vesicles-Based Therapy: Strategies, Challenges, and Application Prospects

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Extracellular vesicles are nanoscale extracellular vesicles that have emerged as promising tools in advanced therapies due to their unique physical and chemical properties, such as biocompatibility and potential for targeted delivery. Over the past decade, significant progress has been made in understanding their role in drug delivery, gene therapy, tissue regeneration, and immunotherapy. Extracellular vesicles can originate from a variety of cell types, including mammalian and non-mammalian cells, as well as biological fluids. Each type exhibits distinct properties and composition that influence its effects and functions. Therefore, investigating the cargo content of extracellular vesicles could provide opportunities for disease diagnosis and treatment. In addition, extracellular vesicles have been investigated as natural drug delivery vehicles because they can safely navigate extracellular fluids and deliver cargo to target cells with high specificity and efficiency. Despite their promising potential, challenges such as large-scale production, stability in isolation methods, and immunogenicity remain barriers to widespread clinical use. The regulatory landscape and the need for standardized protocols in extracellular vesicle-based therapeutics are also critically discussed. This section aims to provide a comprehensive overview of the progress in extracellular vesicles research, challenges, and future directions, encouraging researchers to further explore the safe and practical application of these approaches in the treatment of various diseases, and providing avenues for future studies.

O92

Current Status and Future of EVs as Diagnosis and Prognosis Biomarkers

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Extracellular vesicles (EVs), which are nanostructures enclosed within a lipid bilayer membrane and released from cells, have garnered significant attention in recent years as novel biomarkers. These particles carry diverse molecular cargo, including proteins, lipids, and nucleic acids, reflecting the physiological and pathological status of their parent cells. The presence of EVs in a wide range of body fluids, including blood, urine, saliva, cerebrospinal fluid, and milk, makes them unique tools for the non-invasive diagnosis of various diseases. These characteristics have positioned EVs as powerful diagnostic tools with high accuracy and sensitivity. In recent years, numerous studies have demonstrated the potential of EVs as diagnostic tools for various diseases. This significant potential has led multiple companies to enter this field and advance EV-based diagnostic products toward commercialization. However, the clinical translation of EV-based biomarkers faces several challenges, highlighting the critical need for developing validated protocols and standardizing methodologies. This specialized workshop will comprehensively examine the current status and future perspectives of EV-based biomarkers in both diagnosis and prognosis. While reviewing the most recent achievements in diagnostic and prognostic applications of EVs, the workshop will also discuss insights gained from the first EV-based diagnostic assays that have received FDA approval. This workshop provides a unique opportunity for dialogue among researchers, laboratory professionals, clinicians, and industry experts to chart a realistic roadmap and accelerate the realization of the promises of EV-based biomarkers.

O93

EVs Engineering for therapeutic delivery and clinical applications

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Extracellular vesicles (EVs) have emerged as a transformative platform in modern biomedicine, offering unique opportunities for therapeutic delivery, immune modulation, and precision medicine. Their intrinsic biocompatibility, ability to cross biological barriers, and capacity to transport complex molecular cargos—including RNAs, proteins, and gene-editing tools—have positioned EVs at the forefront of next-generation therapeutics. Recent advances in EV engineering—encompassing cargo loading, surface modification, targeting specificity, and scalable manufacturing—are rapidly accelerating the transition of EV-based approaches from experimental systems to clinical applications. Engineered EVs are now being explored for the treatment of infectious diseases, cancer, inflammatory disorders, and genetic conditions, highlighting their broad translational potential. Despite this progress, critical challenges remain in standardization, quality control, regulatory alignment, and clinical readiness. Addressing these challenges requires interdisciplinary collaboration that bridges fundamental biology, bioengineering, clinical science, and regulatory expertise. This symposium represents the first dedicated platform of its kind to bring together leading scientists, clinicians, and innovators to critically examine the state of EV engineering with a strong emphasis on therapeutic translation and clinical implementation. By fostering dialogue across disciplines and regions, the meeting aims to catalyze new collaborations, shared standards, and translational pathways that will shape the future of EV-based medicine. In this context, the symposium serves not only as a scientific forum but also as a strategic milestone toward integrating EV engineering into clinically viable and globally relevant therapeutic solutions.

O94

A Critical Comparison of EV Isolation and Characterization Techniques

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Today, due to special role of extracellular vesicles in the treatment and diagnosis of diseases, methods for isolating and characterizing these biological nanovesicles have attracted much attention from researchers. Despite extensive research in this field, unfortunately, scientific communities have not yet reached a single opinion on introducing a standard and reliable method. This workshop is designed to introduce and critically review the latest standards and technological advancements in this field. Participants will become familiar with the principles, advantages, limitations, and applications of novel methods, including polymer-based precipitation, size-exclusion chromatography, and microfluidic techniques. Finally, the challenges of extracellular vesicles purification and characterization will be discussed and analyzed in detail.

Poster Presentation

Abnormal Hemoglobin Syndromes

P1-P4

P1

First Case Report of Hb Archarnes in a Homozygous Genotype in Southern Iran

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Introduction: Hb Archarnes is an unstable hemoglobin variant caused by a point mutation in the β-globin gene (β53(D4) Ala→Thr). It was first characterized structurally and functionally in the 1990s and has been described in a few case reports since then. In this case report we want to introduce a woman diagnosed with Hb Archarnes in a homozygous genotype. Methods: Sanger Sequencing method was applied to detect this variant in HBB gene and analyzed with bioinformatic software and interpreted. Results: The woman is identified with Homozygous genotype of Hb Archarnes (HBB:c.160G>A) in exon 1 of HBB gene and is an unstable hemoglobin variant caused by a point mutation in the β-globin gene (β53(D4)Ala→Thr). All hematologic indices are with normal range with 2.8 amount of Hb A2 and represents no sign or symptoms of anemia. Her husband is a carrier of β-thalassemia with Hb A2 of 4.8. Moreover, earlier research described the variant in association with a β°-thalassemia mutation in compound heterozygosity, producing a thalassemia intermedia phenotype. Conclusion: The homozygous level of Hb Archarnes never has been reported, yet. Our case is phytologically healthy. But their case needs to do a PND test during pregnancy as this hemoglobin in combination of other mutants may lead to a thalassemia phenotype. Introduction: Hb Archarnes is an unstable hemoglobin variant caused by a point mutation in the β-globin gene (β53(D4)Ala→Thr). It was first characterized structurally and functionally in the 1990s and has been described in a few case reports since then. In this case report we want to introduce a woman diagnosed with Hb Archarnes in a homozygous genotype. Methods: Sanger Sequencing method was applied to detect this variant in HBB gene and analyzed with bioinformatic software and interpreted. Results: The woman is identified with Homozygous genotype of Hb Archarnes (HBB:c.160G>A) in exon 1 of HBB gene and is an unstable hemoglobin variant caused by a point mutation in the β-globin gene (β53(D4)Ala→Thr). All hematologic indices are with normal range with 2.8 amount of Hb A2 and represents no sign or symptoms of anemia. Her husband is a carrier of β-thalassemia with Hb A2 of 4.8. Moreover, earlier research described the variant in association with a β°-thalassemia mutation in compound heterozygosity, producing a thalassemia intermedia phenotype. Conclusion: The homozygous level of Hb Archarnes never has been reported, yet. Our case is phytologically healthy. But their case needs to do a PND test during pregnancy as this hemoglobin in combination of other mutants may lead to a thalassemia phenotype.

Keywords: Hb Unstable, Hb a Rcharness, Thalassemia

P2

A Case Report of Combined Severe Iron Deficiency Anemia and Glucose-6-Phosphate Dehydrogenase (G6PD) Deficiency in Pregnancy

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Background: Anemia is a frequent complication of pregnancy, particularly in middle-income countries. It has critical risks for the mother and the fetus. In pregnant women, anemia can reduce cardiac reserve, increase the risk of heart failure, and reduce tolerance to peri- and post-partum hemorrhage. It can also lead to neurodevelopmental delay and preterm birth in the fetus. Thus, early diagnosis and proper management of it are essential. We describe a case of a pregnant woman with complex coexisting forms of anemia. Case presentation: A 31-year-old pregnant woman was seen in the Obstetrics and Gynecology (OBG) clinic for a routine follow-up visit. Her complete blood count showed a severe microcytic-hypochromic anemia with a high red cell distribution width, mild thrombocytosis, and high reticulocyte count. The peripheral smear showed severe anisopoikilocytosis, including ovalocytes, elliptocytes, and fish-shaped red blood cells (rbcs). These suggested the presence of iron deficiency. However, the presence of blister cells, rbc fragments, and bite cells prompted further investigations. Iron studies confirmed severe iron deficiency with a serum iron level of 2 µg/dL. A G6PD assay revealed a significant enzyme deficiency, with the level of enzyme lower than 12 U / g Hb. Discussion: This dual diagnosis has significant implications for pregnancy management. It requires iron repletion and avoiding oxidative triggers to prevent acute hemolytic crisis. Conclusion: This case reminds us that looking beyond obvious findings on the peripheral blood smear can reveal a second underlying condition, ensuring safer care for both mother and baby in OBG clinics.

Keywords: Anemia, Prgnancy, G6PD, Iron Deficiency

P3

Comparison of the Efficacy of Serum Ferritin Measurement Index with MRI Method in Assessing Iron Overload in β -Thalassemia Patients

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Introduction: β-Thalassemia is an inherited hematological disorder resulting from mutations in the β-globin gene, which obligates patients with the major form to receive frequent blood transfusions. Chronic transfusion therapy leads to iron overload, potentially causing severe complications including cardiomyopathy, liver cirrhosis, and cardiac arrhythmias. Regular assessment of the iron burden is crucial for the prevention of organ damage and the timely initiation of iron chelation therapy. Common methods for assessing iron overload include measuring serum ferritin and Magnetic Resonance Imaging (MRI, T2* technique). The objective of this study was to compare the efficacy of these two methods in evaluating iron overload in β-thalassemia patients. Methods: This study was conducted in 2026, utilizing advanced search methodology across reputable databases such as PubMed. Articles published between 2016 and 2026 were selected. Ultimately, from the 21 reviewed articles, 10 were chosen for the final study based on title, abstract, and full text analysis, while strictly adhering to PRISMA guidelines and predefined inclusion/exclusion criteria. Findings: MRI demonstrated the iron levels specifically in the heart and liver tissues, whereas serum ferritin serves as an index of total body iron stores. Conclusion: MRI is a more precise method for assessing myocardial and hepatic iron; however, serum ferritin is a simpler and more generalized marker. Therefore, for preventing complications and ensuring effective monitoring in these patients, MRI is the superior method, and serum ferritin should preferably be used in conjunction with MRI.

Keywords: Beta-Thalassemia, Ferritin, MRI, Iron Overload

P4

Significant Association of Polymorphism in TRIM21 Gene in Iranian Alloimmunization in Thalassemia

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Beta thalassemia is a hereditary hemoglobinopathy and is known as the most common type of hereditary anemia worldwide.Transfusion therapy is crucial for treating Transfusion-dependent thalassemia patients.However, the production of Alloantibodies presents a substantial challenge for these individuals and impacts their quality of. Fifty patients (and fifty control subjects) with beta-thalassemia major who were referred Hospital in Ahvaz received blood and produced alloantibodies. genotyping and primer design were performed to determine the polymorphism in the TRIM21gene using the TETRA-ARMS-PCR technique. A statistically significant difference was observed between the distribution and frequency of the TRIM21 gene in thalassemia patients with alloimmunization and the control group (P=0.016).The frequency of AG allele in thalassemia patients with alloimmunization (38%) was higher than in controls (11%). Considering the significant increase in the chance of alloimmunization in people who carry the AG genotype in the rs660 polymorphism,it can be concluded that this genotype can help in the prognosis before blood transfusion.

Keywords: Thalassemia, Alloimmunization, Polymorphism, TRIM21 Gene

Artificial Intelligence in the Clinical Laboratory: From Algorithm to Clinical Trust

P5-P14

P5

An Integrative Approach Using Artificial Intelligence to Decode Exosomal microRNA Signatures for Early Diagnosis and Risk Stratification of Myelodysplastic Syndromes

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Background: Diagnosing myelodysplastic syndromes (MDS), particularly in early stages, remains clinically challenging. Circulating exosomal microRNAs (miRNAs) offer promise as non-invasive liquid biopsy biomarkers, though the high-dimensional complexity of these data demands advanced analytical approaches. While artificial intelligence (AI) has demonstrated considerable utility in hematological oncology, its application to exosomal miRNA profiling in MDS remains largely unexplored. This review synthesizes current evidence and identifies critical gaps impeding clinical translation. Methods: A comprehensive literature search was conducted using PubMed and Google Scholar. Results: AI models applied to conventional MDS datasets—including bone marrow morphology, cytogenetics, and flow cytometry—have achieved diagnostic accuracies exceeding 90% and enhanced risk stratification, particularly for predicting progression to acute myeloid leukemia and overall survival. Parallel studies profiling circulating exosomal miRNAs in MDS patients have identified dysregulated candidates (e.g., miR-126-5p, miR-1278-5p), several demonstrating strong diagnostic performance with areas under the curve (AUC) reaching 0.99. Critically, however, no studies to date have integrated AI-driven analytical frameworks with exosomal miRNA profiles for MDS diagnosis or prognostication. Key barriers include absent standardized protocols for exosome isolation, miRNA extraction, and data normalization, as well as limited cohort sizes constraining statistical power and hindering development of robust, generalizable AI models. Conclusion: Integrating AI with exosomal miRNA analysis holds significant promise for advancing early MDS diagnosis and risk stratification. Future research must prioritize standardized methodologies and larger, well-characterized cohorts to enable clinically meaningful AI-driven applications.

Keywords: Exosomal Mirna, Artificial Intelligence, AI, Myelodysplastic Syndromes, Liquid Biopsy

P6

Innovative Applications of Artificial Intelligence in Immunohematology: Enhancing Laboratory Quality, Safety, and Decision Support-A Narrative Review

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Background: Immunohematology laboratories play a pivotal role in ensuring transfusion safety and appropriate blood utilization. However, the complexity of immunohematological workflows, reliance on manual interpretation, and inter-operator variability expose these laboratories to pre-analytical, analytical, and post-analytical errors. Such challenges can compromise result accuracy, delay clinical decision-making, and increase the risk of transfusion-related adverse events. In recent years, artificial intelligence (AI), including machine learning, deep learning, and image-based analysis, has emerged as a promising tool to enhance diagnostic precision, laboratory quality management, and risk mitigation in blood transfusion services. Methods: This study was conducted as a narrative literature review. A comprehensive search of PubMed, Scopus, and Google Scholar was performed to identify relevant English-language publications. The search strategy included keywords and combinations of artificial intelligence, machine learning, deep learning, immunohematology, blood group typing, antibody identification, crossmatching, transfusion safety, and laboratory quality. Articles focusing on practical laboratory implementation, performance evaluation, workflow optimization, and quality-related outcomes were selected. The included studies were critically reviewed and qualitatively synthesized to summarize current applications, reported benefits, and existing limitations of AI in immunohematology. Results: AI-based systems achieve high accuracy in automated ABO and RhD blood group typing, with reported performance exceeding 95%, particularly in image-based interpretation of agglutination reactions. Machine learning algorithms have demonstrated the ability to identify complex serological patterns and weak or mixed-field reactions prone to inter-observer variability, improving result consistency and reducing subjective interpretation. In antibody screening and identification, AI-assisted platforms have prioritized clinically significant antibodies, supported expert review, and aided detection of rare or multiple alloantibodies, including anti-Kell and anti-Duffy. AI-supported electronic crossmatching and decision-support systems have reduced turnaround time by up to 30%, minimized manual verification, and enhanced workflow efficiency. Emerging applications extend beyond automation and include predictive models that integrate donor and recipient immunohematological profiles to assess transfusion compatibility, stratify risk of transfusion-related adverse reactions, and guide transfusion strategies in patients with chronic transfusion needs such as thalassemia and sickle cell disease. Deep learning approaches have been successfully applied in automated reading of gel card and tube agglutination images, demonstrating potential for real-time quality control and error

prevention. Collectively, these findings suggest AI can function as an advanced quality assurance tool, contributing to proactive error prevention, standardized interpretation, and enhanced transfusion safety. Challenges remain regarding data standardization, algorithm transparency, clinical validation, regulatory compliance, and ethical considerations. Conclusion: Artificial intelligence represents a valuable and innovative adjunct to conventional immunohematology practices. When appropriately validated and integrated into laboratory quality management systems with continuous expert oversight, AI has the potential to improve diagnostic accuracy, operational efficiency, and transfusion safety, while supporting evidence-based clinical decision-making, proactive risk management, and optimized transfusion strategies in modern transfusion medicine.

Keywords: Artificial Intelligence, Immunohematology, Laboratory Quality, Blood Transfusion, Decision Support Systems

P7

Application of Artificial Intelligence in Enhancing Quality Control of Medical Diagnostic Laboratories

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Background: Medical diagnostic laboratories play a critical role in disease diagnosis, treatment, and monitoring. However, laboratory errors can lead to incorrect diagnoses, inappropriate treatments, and increased healthcare costs. Studies indicate that 60 to 70 percent of laboratory errors occur during pre-analytical and analytical phases. The aim of this study is to present a novel artificial intelligence-based approach to enhance quality control and reduce laboratory errors. Methods: In this study, an intelligent quality control system was designed and implemented using machine learning and deep learning algorithms. The proposed system comprises three main modules: The first module employs Convolutional Neural Networks (CNN) for automatic identification of poor-quality samples (hemolysis, lipemia, and icterus) through image analysis. The second module utilizes Random Forest and Gradient Boosting algorithms to predict instrument deviations and calibration needs. The third module applies anomaly detection techniques to identify unusual and inconsistent results. The dataset included over 50,000 laboratory samples, digital images of specimens, and diagnostic instrument logs. Results: Implementation of the intelligent quality control system resulted in a 58% reduction in pre-analytical errors. The detection accuracy for hemolyzed, lipemic, and icteric samples was 94%, 91%, and 89% respectively, showing significant improvement over traditional methods. In the analytical phase, the system successfully identified 82% of instrument deviations before they could affect patient results. The average time for quality issue detection decreased from 4-6 hours to less than 30 minutes. Additionally, the number of rejected samples due to delayed problem identification decreased by 45%, leading to cost reduction and improved patient satisfaction. Conclusion: Artificial intelligence demonstrates high potential in transforming quality control in medical diagnostic laboratories. Intelligent systems not only increase the accuracy and speed of error detection but also improve overall laboratory productivity by reducing staff workload and operational costs. Integration of these systems with existing laboratory infrastructure can be an effective step toward enhancing patient safety and diagnostic service quality.

Keywords: Artificial Intelligence, Quality Control, Medical Diagnostic Laboratory, Machine Learning, Laboratory Errors

P8

Rapid Identification of Pathogenic Fungi Using Automated Microscopy with Artificial Intelligence-Based Image Analysis

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Introduction: Fungal infections are important challenges They are medical and public health and can have serious and even fatal consequences in patients with immunodeficiency. Common diagnostic methods such as fungus culture and PCR, although accurate, are time-consuming, costly, and human-dependent. These limitations reveal the need to develop new diagnostic technologies. Method: In this study, an intelligent system based on artificial intelligence and automation of light microscope was performed. This system is based on the two main pillars of automating the optical microscope in order to receive and process imaginary information, and the second pillar is the deep artificial intelligence platform for automatic labeling on microscope images. For this system, high speed and automation in the operation of detection and labeling in order to accurately identify fungi from their image, portability of this set and focus automatically in the microscope were considered as mandatory points. In the study, 1,200 images of 10 different genera of fungi, including aspergillus, biopolaris, blastomys, fusarium, penicillium, microspurum, absidia, alternaria, Fonsecaea, Rhizopos was used to train deep artificial intelligence based on deep artificial neural networks. Results: The results showed that the device with artificial intelligence algorithm and average accuracy above 90% was able to identify the type of fungal sex in less than 20 seconds and show it on the display. Human error is one of the outstanding advantages of the device. Discussion and conclusion: Combining automated microscopes with deep neural networks offers a new approach to the diagnosis of pathogenic fungi, which not only reduces the time of diagnosis, but also reduces laboratory costs. Hardware, it is possible to improve the accuracy and cover more aspects. Therefore, this technology can be used as an effective tool in laboratories and health centers.

Keywords: Fungal Infection, Canoe Neural Network, Automatic Microscopy, Rapid Detection

P9

Analysis of Immature Granulocyte Data Based on the MXD Parameter: Evaluating the Performance of Artificial Intelligence Versus Prism

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Background: In recent years, artificial intelligence (AI) and machine learning have increasingly influenced medical data analysis. The emergence of AI-based platforms such as ChatGPT, Grok3, DeepSeek, Gemini, and Perplexity has reduced reliance on conventional statistical software, including SPSS, Prism, and Matlab, due to AI's ability to generate rapid and diverse analytical outputs. This study presents a framework for validating AI tools in counting immature granulocytes using the MXD parameter obtained from the Sysmex XP-300 hematology analyzer. Validation was performed through comparison with peripheral blood smear evaluations and assessment of analytical consistency. Methods: A total of 1,245 blood samples were analyzed and categorized into two groups based on MXD values: less than 10% and greater than 10%. Immature granulocytes were evaluated in both groups, and the distribution of MXD subgroups was recorded. Statistical comparisons between groups were first conducted using Prism software (version 10.4.1) and subsequently replicated using several AI-based platforms. Among all tested tools, only ChatGPT, Grok3, DeepSeek, Gemini, and Perplexity produced valid statistical outputs suitable for comparison. Results: An independent t-test assuming normal distribution and equal variance was applied to unpaired data. Comparison of p-values demonstrated varying levels of agreement with Prism. ChatGPT, Grok3, and DeepSeek showed complete concordance with Prism results (p-value > 0.0001), whereas Gemini and Perplexity demonstrated lower accuracy. Conclusion: The results indicate that ChatGPT, Grok3, and DeepSeek can serve as reliable alternatives to Prism for statistical analysis. Although AI tools show strong potential in medical data analysis, independent validation remains necessary for specific analytical applications.

Keywords: Comparative Analysis, AI, Immature Granulocytes

P10

Multimodal and Interpretable Machine Learning Approaches for Embryo Quality Prediction in IVF: Current Advances and Future Challenges

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Background: Infertility affects 15-20% of couples worldwide, with IVF as the primary treatment. Embryo quality assessment is critical for IVF success, yet traditional morphology-based evaluation suffers from inter-observer variability and limited reproducibility. This review examines advances in multimodal and interpretable machine learning approaches for embryo quality prediction. Methods: A comprehensive literature search was conducted in PubMed and Scopus for studies published between 2020-2025 employing machine learning models with interpretability techniques for embryo assessment, with focus on multimodal architectures combining clinical data and embryo images. Results: Twenty-two studies met inclusion criteria. Multimodal models integrating patient clinical features (age, BMI, hormonal profiles, semen parameters, infertility history) with embryo time-lapse images consistently outperformed unimodal approaches, achieving AUC values of 0.82-0.93 and accuracy up to 91%. Key architectures included FEMI trained on 18 million images, DeFusion networks with decoupling-fusion mechanisms, and dual-branch CNNs processing global and local features simultaneously. For interpretability, SHAP was predominantly used for clinical feature analysis while Grad-CAM provided visual explanations for image-based decisions. Studies have demonstrated that multimodal integration significantly enhances prediction accuracy, and randomized trials have shown deep learning performance comparable to embryologists. Major challenges include limited generalizability across centers, dependence on large annotated datasets, lack of external validation, and clinical adoption barriers due to model opacity. Conclusion: Multimodal interpretable machine learning significantly improves embryo selection in IVF by enhancing accuracy and reducing subjectivity. However, clinical translation requires prospective multicenter validation, data standardization, and user-friendly interpretability tools to foster clinician trust.

Keywords: Machine Learning, Deep Learning, Multimodal Data, Interpretable AI, Embryo Quality, IVF

P11

The Role of Artificial Intelligence in Accelerating Result Interpretation and Improving Communication Accuracy in the Medical Diagnostic Laboratory

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Background: The speed and accuracy of laboratory result interpretation play a vital role in timely diagnosis and the reduction of medical errors. Traditional methods of interpreting laboratory data are primarily based on individual knowledge and experience, facing challenges such as human error, delays in identifying critical values, and a lack of integration with patients' clinical histories. Given the ever-increasing volume of laboratory data and the complexity of relationships between analytes, the need for intelligent tools that can process, analyze, and interpret data in fractions of a second—presenting it in simple language for the physician is more pressing than ever. Artificial intelligence, as one of the leading technologies of the present era, holds significant potential to transform this field and turn laboratories into decision-making units. Methods This study is a narrative review based on a search of reputable databases, including PubMed, Scopus, and the Web of Science, covering the period from 2018 to 2024. The search was conducted using specialized keywords such as "Artificial Intelligence," "Machine Learning," "Clinical Laboratory," "Result Interpretation," "Diagnostic Accuracy," and "Clinical Decision Support Systems." Articles focusing on the application of machine learning algorithms, natural language processing (NLP), and computer vision in interpreting laboratory data and communicating results to the clinical setting were selected for final analysis. Results The findings of this review indicate that artificial intelligence has had a significant impact in three main areas. In the realm of rapid data interpretation, deep learning algorithms can identify hidden patterns in laboratory results, such as the early detection of sepsis from trends in complete blood count data, at a speed surpassing human capability. Regarding error reduction, AI-powered systems have markedly decreased human errors by automatically detecting critical values and flagging abnormal samples, particularly in hematology and microbiology. In terms of effective communication with physicians, tools based on natural language processing convert numerical results into interpretive clinical reports, and when integrated within Clinical Decision Support Systems, they provide diagnostic suggestions or therapeutic recommendations, leading to increased diagnostic accuracy and reduced time to treatment initiation. Conclusion Artificial intelligence, acting as a powerful and intelligent assistant, can fundamentally transform the process of interpreting laboratory results and communicating them to physicians. Implementing this technology not only increases the speed and accuracy of diagnosis but also reduces staff

workload and standardizes reporting. This represents an effective step towards improving the quality of laboratory services and enhancing patient safety. However, challenges such as ethical considerations, data privacy, and the need for algorithm transparency (explainability) must be seriously addressed before widespread clinical adoption. The future of diagnostic laboratories lies in the integration of specialized knowledge with innovative artificial intelligence technologies.

Keywords: Artificial Intelligence, Clinical Laboratory, Result Interpretation, Diagnostic Accuracy

P12

Beyond Automation: Clinical Laboratories Operationalizing Precision Medicine in the in the Age of Artificial Intelligence

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Background: Precision Medicine or Personalized medicine is a longstanding dream of integrating molecular, clinical, and contextual data for improved patient management. Clinical laboratories are central to this transformation, providing the assays that convert biological signals into actionable clinical decisions. However, implementing personalized approaches into routine workflows requires a multidisciplinary team of PhD-trained clinical laboratory scientists and physicians, which has its specific challenges, such as coordination of the team or financial management. The growing area of Artificial Intelligence (AI) agents, which offers interpretable, human-in-the-loop decision support that integrates multi-omics and longitudinal laboratory data to deliver patient-specific interpretations and actionable recommendations, is a possible solution for this problem. Methods: We conducted a comprehensive review of the literature using PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar (2020–2025). Search terms included “personalized medicine,” “pharmacogenomics,” “interpretive reporting,” “machine learning,” “surveillance,” and “outbreak detection.” Titles/abstracts were screened, full texts appraised for methodology and outcomes, and findings synthesized to highlight practical opportunities, barriers, and measurable outcome frameworks. Results: The results have revealed that recently, two high-impact applications have emerged. First, Interpretive reporting assistants—hybrid rule/ML systems that draft evidence-based comments for lipid, endocrine, and pharmacogenomic panels—show promise to standardize reports and reduce clinician cognitive load when coupled with mandatory human sign-off; key measures are concordance with expert interpretation and clinician satisfaction. Second, Lab-based population surveillance—real-time ML on routine test streams can detect aberrant positivity and AMR shifts earlier than traditional systems, improving lead time for public-health response. Cross-cutting challenges include data integration, model explainability, equity/bias, privacy for multi-site model training, and lifecycle governance in light of evolving regulatory scrutiny. Conclusions: To bring personalized medicine into clinical decision-making, clinical laboratories should use systems where people review the AI-generated suggestions, learn from data across hospitals without sharing private records, and have clear rules for enhancing models’ decision-making. They also need simple, standard ways to judge success; for instance, how often AI agrees with experts, whether it helps clinicians make better decisions, how much earlier it detects public-health signals, and whether it works fairly for all groups. Key words: Clinical Laboratory, Precision Medicine, Artificial Intelligence

Keywords: Clinical Laboratory, Precision Medicine, Artificial Intelligence

P13

The Future of Acute Myocardial Infarction Diagnosis: From High-Sensitivity Troponin to Intelligent Machine Learning Algorithms

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Background: Diagnosis of acute myocardial infarction (AMI) is evolving from fixed high-sensitivity cardiac troponin (hs-cTn) thresholds toward machine learning (ML)-based probability models that integrate biomarker dynamics with clinical and electrocardiographic data. This systematic review summarizes the transition from conventional hs-cTn interpretation to intelligent diagnostic algorithms for AMI. Methods: A comprehensive search of major scientific databases identified 111 potentially relevant records. After removal of duplicates and exclusion of studies with overlapping titles, insufficient relevance to the topic, unavailable full text, or other eligibility limitations, studies were screened by two independent reviewers. Data were extracted from eligible studies evaluating ML approaches incorporating hs-cTn, clinical variables, ECG, and/or laboratory parameters for AMI diagnosis. Results: ML-based algorithms consistently demonstrated improved diagnostic performance compared with fixed-threshold strategies. CoDE-ACS achieved external validation AUCs of 0.953–0.959 and increased the proportion of patients classified as low probability at presentation to 61%, compared with 27% using fixed cutoffs, with NPV 99.5%. MI3 enabled rapid 30-minute rule-out with high specificity in patients with indeterminate troponin results. Neural network models and convolutional neural network approaches also improved risk stratification, reduced intermediate classifications, and supported safe early discharge in a larger proportion of patients. Conclusion: ML represents a substantial advance in AMI diagnosis by generating individualized probability scores rather than relying on rigid hs-cTn thresholds. These models improve early rule-out, reduce unnecessary admissions, and enhance clinical decision-making. However, prospective implementation studies and outcome-driven trials are still needed before widespread routine adoption.

Keywords: High-Sensitivity Troponin, Machine Learning, Acute Myocardial Infarction, Diagnostic Algorithms, Systematic Review

P14

Artificial Intelligence in Oncology: Current Applications in Diagnosis and Treatment Monitoring

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Artificial intelligence (AI) is increasingly transforming oncology by improving cancer detection, diagnosis, treatment planning, patient management, and research. Through the analysis of large-scale multimodal datasets, including medical imaging, histopathology slides, genomic profiles, and electronic health records, AI systems enhance clinical decision-making and support precision medicine. In cancer diagnosis, AI-driven imaging tools applied to CT, MRI, PET, and mammography data enable early tumor detection and lesion classification. Systems such as Google Health AI (LYNA), Arterys, and Aidoc demonstrate strong performance in identifying subtle abnormalities, prioritizing high-risk cases, and improving radiology workflow efficiency. In digital pathology, deep learning algorithms analyze whole-slide images to detect malignancies and classify tumor subtypes with high accuracy. Platforms like PathAI reduce inter-observer variability and improve diagnostic consistency, particularly in complex cancers such as breast and prostate cancer. AI also plays a major role in precision oncology by integrating clinical and molecular data to support treatment decisions. Platforms such as IBM Watson for Oncology, DarwinHealth, and Artera AI use evidence-based and genomic approaches to predict therapy response and recommend personalized treatment strategies. Beyond clinical applications, AI supports patient-centered care through digital tools such as Outcomes4Me, which provides symptom tracking, clinical trial matching, and personalized education. AI-driven chatbots further enhance communication between patients and healthcare providers. In research, AI accelerates drug discovery, optimizes clinical trial design, and enables tumor modeling and biomarker identification. Despite its potential, challenges remain, including data heterogeneity, limited interpretability, regulatory issues, and concerns about privacy and generalizability. In conclusion, AI is becoming a key component of modern oncology, offering significant potential to improve diagnostic accuracy, personalize therapy, and advance cancer research.

Keywords: AI, Artificial Intelligence, Oncology, Hematological Malignancy

Cell Therapy and Gene Therapy: From Laboratory Standards to Clinical Impact

P15-P35

P15

A Systematic Review of the Thrombotic Events in Anti-CD19 Chimeric Antigen Receptor T Cell Therapies

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Background: Thrombotic events (TEs) are leading causes of mortality worldwide. In chimeric antigen receptor (CAR) based therapy, T lymphocytes are genetically manipulated to specifically eradicate malignant cells by targeting their surface antigens. In recent years, there have been six commercially approved anti-CD19 CAR T-cell therapies worldwide. CAR-based cell therapies can increase the risk of thrombosis in cancer patients because of the need for long hospitalization, central venous access, and toxicities associated with CAR-based cell therapies. Despite expanding trials on the safety and efficacy of CAR-T cell therapies and approvals for their utilization, their impact on the hemostatic system is poorly defined. The incidence, risk factors, and timing of thrombotic complications in this population have not been systematically evaluated. In this study, we aimed to evaluate the incidence of TEs after CAR-T cell therapies in hematological malignancies. Methods: Two independent authors systematically searched PubMed, Scopus, and Google Scholar by MeSH terms till November 22, 2025. Randomized controlled trials, cohort, and case-control studies were included. But all types of review articles and non-English studies were excluded. Results: 1362 records were retrieved from the literature search. After screening by title and abstract, 1281 records were excluded. The remaining 71 articles were assessed in full-text review; 23 articles were on CD19-targeted CAR-based cell therapies and met our eligibility criteria and were included in the analysis. 5 of them evaluated TEs. One study on 148 patients reported that within 6 months after CAR T cell therapy, 33% of patients undergoing anti-CD19 CAR T-cell therapy had a TEs, 22% of them had an experience of TEs before CAR-T cell therapy. The new TEs occurred in 11% of patients after anti-CD19 CAR T-cell infusion. These TEs were managed with anticoagulation, and no major bleeding events were seen after that. Other studies reported coagulopathy in just 5%, 1,6%, 6,3%, and 1% of their patients. Conclusion: These findings highlight that there is a risk for thrombosis in anti-CD19 CAR-T cell recipients. As these cell-based immunotherapies are getting more used in clinics, there is a need for appropriate monitoring of TEs during

anti-CD19 CAR-T cell therapies and the use of prophylactic anticoagulants. For more evidence-based management, more investigative studies should be conducted in these situations.

Keywords: Thrombosis, Chimeric Antigen Receptor T Cell Therapies, Adoptive Immunotherapy, Systematic Review

P16

Ferroptosis-Engineered Extracellular Vesicles Co-Delivering siGPX4 and Iron Oxide Nanoparticles: In Vitro Evaluation of Ferroptosis Resistance Mechanisms in KG-1Cells

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Background: Acute myeloid leukemia (AML) remains a therapeutic challenge due to resistance mechanisms and limited treatment options. Ferroptosis, an iron-dependent form of regulated cell death, has emerged as a promising therapeutic strategy for cancer treatment. However, cellular resistance mediated by antioxidant systems, particularly glutathione peroxidase 4 (GPX4), significantly limits ferroptosis-based therapies. Extracellular vesicles (EVs) offer biocompatible nanocarriers with inherent targeting capabilities and low immunogenicity. This study investigated the combined delivery of siGPX4 and iron oxide nanoparticles (IONPs) via engineered EVs to overcome ferroptosis resistance in the KG-1 AML cell line. Methods: Extracellular vesicles were isolated from donor cells and engineered to co-encapsulate siGPX4 and IONPs through electroporation. Characterization included dynamic light scattering, transmission electron microscopy, and zeta potential analysis. KG-1 cells were treated with EV-siGPX4-IONP complexes, and ferroptosis induction was evaluated through lipid peroxidation assays, intracellular iron quantification, and reactive oxygen species detection. Gene expression analysis quantified GPX4 knockdown efficiency, while cell viability and morphological changes were assessed using MTT assays and microscopy. Results: Engineered EVs successfully co-delivered siGPX4 and IONPs to KG-1 cells, achieving significant GPX4 downregulation and elevated intracellular iron levels. The combination therapy induced marked lipid peroxidation, mitochondrial dysfunction, and characteristic ferroptotic morphology. Cell viability decreased dose-dependently, with synergistic cytotoxicity observed compared to single-agent treatments. Ferroptosis-specific inhibitors reversed cell death, confirming the mechanism. Conclusion: EV-mediated co-delivery of siGPX4 and IONPs effectively overcomes ferroptosis resistance in KG-1 cells by simultaneously suppressing antioxidant defenses and enhancing oxidative stress, demonstrating potential as a novel therapeutic approach for AML treatment.

Keywords: Extracellular Vesicles, Ferroptosis, Iron Oxide Nanoparticles, Acute Myeloid Leukemia, GPX4

P17

Nanoengineered Exosome-Based PD-1/TIGIT siRNA Delivery System: Comparative Analysis of Checkpoint Relief and Immune Synergy Across HL-60 Cell Line Model with Patient-Derived Primary AML Cells

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Background: Immune checkpoint molecules PD-1 and TIGIT represent critical inhibitory pathways that suppress T-cell activation and enable tumor immune evasion in acute myeloid leukemia (AML). Dual targeting of these checkpoints offers synergistic therapeutic potential, yet effective delivery systems remain challenging. Exosomes, as naturally occurring extracellular vesicles with biocompatibility and low immunogenicity, have emerged as promising nanocarriers for siRNA delivery in cancer immunotherapy. This study developed nanoengineered exosomes co-loaded with PD-1 and TIGIT siRNA and compared their checkpoint inhibition efficacy and immune modulatory effects between the established HL-60 cell line and patient-derived primary AML cells. Methods: Exosomes were isolated from donor cells and surface-engineered with PEG-PEI modifications for enhanced siRNA loading and cellular uptake. Co-encapsulation of PD-1 and TIGIT siRNA was achieved through electroporation. Comprehensive characterization included dynamic light scattering, transmission electron microscopy, and loading efficiency determination. Both HL-60 cells and primary AML samples from patients were treated with engineered exosome-siRNA complexes. Gene knockdown efficiency was quantified using RT-qPCR and Western blotting. Immune synergy was evaluated through T-cell co-culture assays measuring IFN-γ and TNF-α production, cytotoxic activity, and T-cell proliferation. Results: Engineered exosomes demonstrated high siRNA loading capacity (>90%) and efficient cellular internalization in both cell models. Dual PD-1/TIGIT knockdown achieved 60-75% gene suppression in HL-60 cells and 55-70% in primary AML cells. Patient-derived cells exhibited greater heterogeneity in response patterns compared to HL-60 cells. The combination therapy significantly enhanced T-cell-mediated cytotoxicity and cytokine release, with synergistic immune restoration observed in both models, though primary cells showed variable responsiveness reflecting individual patient characteristics. Conclusion: Exosome-mediated dual delivery of PD-1 and TIGIT siRNA effectively relieves checkpoint-mediated immunosuppression in AML models, demonstrating superior immune synergy compared to single-target approaches. Patient-derived primary cells validate clinical translatability while revealing inter-patient variability requiring personalized optimization strategies.

Keywords: siRNA, Exosome, PD-1/TIGIT, Delivery Systems

P18

Transforming Blood Product Waste into Advanced Biomaterials for Regenerative Medicine

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Bakground: Significant volumes of plasma and platelet concentrates are discarded annually worldwide. In high-income countries, platelets constitute the largest share of blood component waste, with expiration rates of 10–22% due to their short shelf life (5–7 days). In developing countries, at least 5 to 8.5 million liters of recovered plasma are destroyed annually. This wastage represents a valuable biological resource rich in growth factors, cytokines, and bioactive vesicles, resulting in a missed opportunity for therapeutic innovation. Method:This article is based on a review of authoritative guidelines and manuscripts (such as those from ISBT and EDQM). The core approach involves a controlled, Good Manufacturing Practice (GMP)-compliant process to convert expired platelets and surplus plasma into high-value products. Key production steps include sample collection, centrifugation, washing, freeze-thaw cycles, and final centrifugation. Quality control is ensured through microbial testing, growth factor concentration measurement (via ELISA), and purity assessments. Findings:Three key products can be derived from this waste: 1. Human Platelet Lysates (HPL): A robust and ethically superior alternative to fetal bovine serum (FBS) for expanding mesenchymal stem cells (MSCs) and immune cells. 2. Serum Eye Drops (SEDs): Produced from surplus plasma for treating severe dry eye disease, outperforming conventional therapies by closely mimicking natural tears. 3. Platelet Extracellular Vesicles (pEVs) and Growth Factor Concentrates: Carriers of proteins, RNA, and signaling molecules for applications in tissue regeneration, neurological disorders, and targeted drug delivery. Establishing a local production chain can significantly reduce waste in blood centers while providing sustainable and cost-effective access to these advanced biotherapies. Conclusion: Despite challenges such as the lack of standardization for HPL and difficulties in defining and quantifying pEVs, solutions like large donor pooling, viral inactivation methods, and purity metrics (e.g., membrane lipid-to-protein ratio) are proposed to mitigate these issues. Converting blood waste into high-value-added products represents not only an economically viable business model aligned with the growing demand for advanced cellular and biological therapies but also has broad impacts on waste reduction, job creation, and healthcare sustainability. Realizing this vision requires investment in GMP-compliant production development, process standardization, and international educational collaboration.

Keywords: Cell Therapy, Gene Therapy, Blood Products, Plasma, platelet, GMP

P19

The Evolving Genetic Landscape of CML: Implications for Resistance and Progression

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Chronic myeloid leukemia (CML) is a myeloproliferative neoplasm characterized by the presence of the Philadelphia chromosome and the BCR-ABL1 fusion gene, which acts as the main oncogenic factor of the disease. According to the 2022 World Health Organization (WHO) classification, CML is classified into two stages based on the percentage of blasts in the peripheral blood and bone marrow—chronic phase and blast phase—and accelerated phase is no longer formally recognized. In contrast, the 2025 European LeukemiaNet (ELN) classification continues to endorse the traditional three-stage model: chronic phase, accelerated phase, and blast crisis. Although BCR-ABL1 initiates the pathogenesis of CML, disease progression to blast phase is largely driven by additional genetic and epigenetic alterations that promote treatment resistance, aggressive behavior, and poor clinical outcomes. Frequent mutations in genes such as ASXL1, TP53, FLT3, RUNX1, and GRB2 play critical roles in leukemic transformation and clonal evolution. These concomitant mutations contribute to increased proliferation, impaired differentiation, genomic instability, and resistance to tyrosine kinase inhibitors (TKIs). FLT3 mutations, particularly internal tandem duplication (ITD) and D835 point mutations, result in persistent activation of the FLT3 receptor. This aberrant signaling results in uncontrolled cell proliferation, resistance to apoptosis, high relapse rates, and reduced overall survival. Importantly, FLT3-ITD mutations also impair myeloid differentiation by altering the expression of key transcription factors such as C/EBPα, thereby increasing blast accumulation. RUNX1 mutations further exacerbate disease progression by inducing transcriptional changes similar to those seen in acute myeloid leukemia (AML) and by disrupting DNA repair mechanisms. As a result, blast-phase CML patients with RUNX1 mutations often exhibit biological and clinical features similar to AML with RUNX1 alterations. The GRB2 gene is also implicated in the pathogenesis of CML through its role in BCR-ABL-mediated Ras signaling. BCR-ABL forms a complex with GRB2 and SOS that facilitates the conversion of Ras from an inactive GDP-bound state to an active GTP-bound form. Overexpression and proliferation of GRB2 increase the formation of this signaling complex, thereby increasing Ras activation, increasing hematopoietic cell proliferation, and disease progression. ASXL1 mutations are involved in hematopoiesis and early leukemogenesis in CML. These changes occur in CML stem cells before BCR-ABL translocation and

contribute to impaired differentiation, particularly in the development of the granulomonocytic lineage. Silencing of the ASXL1 gene has been shown to prevent differentiation of CD34+ progenitor cells, highlighting its role in early disease onset. TP53 abnormalities, including 17p deletions, point mutations, and intronic single nucleotide polymorphisms, are strongly associated with blast crisis and resistance to therapy. The tumor suppressor function of TP53 in BCR-ABL-expressing cells varies depending on the relative expression levels of TP53 and BCR-ABL. Loss of TP53 function is particularly associated with myeloid blast crisis and poor response to therapy.Overall, comprehensive molecular profiling using next-generation sequencing is essential to identify these co-mutations, guide optimal TKI selection, and develop targeted therapeutic strategies beyond BCR-ABL1 inhibition, ultimately improving outcomes for patients with advanced CML.

Keywords: Chronic Myeloid Leukemia, Gene, Mutations, Resistance

P20

Dual-Targeted (CD19/CD20) CAR-NK Cells for B-Cell Malignancies: Advances in Microfluidic-Mediated Gene Transduction

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Natural killer (NK) cells are considered a promising option in cancer immunotherapy due to their intrinsic ability to recognize and eliminate cancer cells. Genetic engineering of NK cells with chimeric antigen receptors (CAR-NK) enhances their cytotoxic potential and enables specific targeting of tumor-associated antigens. Compared to CAR-T cells, CAR-NK cells offer significant advantages, including a superior safety profile with reduced risks of cytokine release syndrome (CRS), immune effector cell–associated neurotoxicity syndrome (ICANS), and graft-versus-host disease (GVHD), as well as the feasibility of allogeneic and off-the-shelf use. Furthermore, they preserve CAR-independent innate cytotoxic mechanisms, which enhances their ability to overcome tumor antigen escape. Despite these advantages, the efficient generation of CAR-NK cells, especially for the simultaneous expression of multiple CARs to enable dual-targeting strategies and address tumor antigenic heterogeneity, faces technical challenges. Conventional gene transfer methods, such as spinoculation, often result in low transduction efficiency, require high multiplicity of infection (MOI), involve extensive consumption of viral vectors, and are limited by vector cargo capacity for delivering large and complex genetic constructs. Microfluidic systems, by enabling precise control over cell and viral particle motion, shear stress, and enhanced cell–virus colocalization at the micron scale, hold the potential to significantly improve transduction efficiency compared to conventional methods. It is anticipated that this technology, by optimizing effective cell–virus interactions, can reduce the required MOI, enhance transduction yield, and shorten the production timeline for multiplexed CAR-NK cells. Therefore, the adoption of novel engineering approaches such as microfluidics represents an important step toward facilitating the scalable, safer, and more efficient production of multi-targeted CAR-NK cells, paving the way for more innovative therapeutic strategies, particularly in B-cell malignancies.

Keywords: CAR-NK, Microfluidics, Transduction, Lentiviral Vectors, Dual Targeting

P21

Reviewing the Standard Quality Control Guidelines for Extracellular Vesicles Entering the Pharmaceutical Production Phase and Clinical Application in Iran

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Extracellular vesicles (EVs) have been identified as a new biological platform in regenerative medicine. However, translation of EVs from the bench to the clinic requires quality control specifications, good manufacturing practice (GMP) requirements, and following the regulatory process. Critical quality attributes (CQAs) include particle size (30–150 nm), cup-shaped morphology, expression of surface markers CD9, CD63, and CD81, product purity, protein and RNA cargo (including miRNA and lncRNA), and biological potency. These parameters have to be assessed using standardized analytical techniques such as nanoparticle tracking analysis (NTA), dynamic light scattering (DLS), transmission electron microscopy (TEM), flow cytometry, and RT-qPCR. In addition, the safety evaluation, such as sterility, bacterial endotoxin tests with a maximum limit of ≤0.125 EU/mL, and mycoplasma, shall comply with pharmacopeial requirements within GMP guidelines, the establishment of qualified master and working cell banks (MCB/WCB), comprehensive process validation, identification of critical process parameters (CPPs) under a Quality by Design (QbD) approach, and stability studies in accordance with the international council for harmonisation (ICH) guidelines are essential. From a regulatory point of view, EV-based products are usually classified as advanced biological therapeutics and involve the submission of a detailed chemistry, manufacturing, and controls document, GLP-compliant preclinical data, and clearance of an investigational new drug application (IND) or equivalent. The integration of manufacturing, quality control, and regulatory strategies is critical to the safety, reproducibility, and therapeutic efficacy of EV-based products in clinical trials.

Keywords: Extracellular Vesicles, Good Manufacturing Practice, Clinical Trials

P22

Potential of Extracellular Vesicle-Derived MicroRNAs in Relieving Diabetic Peripheral Neuropathy: A Systematic Review

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Background and Aim: Diabetic peripheral neuropathy (DPN) provokes axonal degeneration and impairs nerve repair. Some preclinical studies suggest that several extracellular vesicle (EV)-associated microRNAs have neuroregenerative effects in regulating this condition. This systematic review evaluated animal model evidence on the therapeutic potential of exosomal miRNAs in alleviating diabetic peripheral neuropathy. Methods: Following PRISMA 2020 guidelines, a protocol was registered in PROSPERO (CRD420251130044). A comprehensive search of MEDLINE, Embase, and ISI Web of Science was conducted on March 21, 2025. Eligible animal research investigated the effects of EV miRNAs from stem cells, Schwann cells, keratinocytes, or plasma on DPN. Functional, electrophysiological, and histological assessments of nerve regeneration constituted the outcomes. Data were qualitatively synthesized due to heterogeneity. Study quality was assessed using SYRCLE's Risk of Bias Tool. Results: Ten studies met the inclusion criteria. Schwann cell–derived EVs enriched in miR-21, miR-27a, miR-130a, and miR-146a enhanced myelin integrity and nerve conduction, whereas hyperglycemia-induced EVs carried neurodegenerative miR-28 and miR-31a. Stem cell–derived EVs containing miR-130a-3p, miR-146a, let-7a, miR-17, miR-23a, and miR-125b facilitated neurovascularization and mitigated neuroinflammation. Keratinocyte EVs with miR-24a-3p and miR-23/let-7 families supported neural crest cell differentiation. Plasma-derived exosomes from healthy donors with miR-20b-3p exhibited neuroprotection, while exosomal miR-221 and miR-221 from diabetic plasma induced neuroinflammation. Functional recovery was consistently validated by behavioral, electrophysiological, and pathological assessments. Conclusion: EV miRNAs exhibit significant therapeutic potential for enhancing brain function under hyperglycemia. Nevertheless, methodological diversity suggests that animal research with more homogenous methods is necessary to advance clinical translation.

Keywords: Diabetic Neuropathies, Diabetes Complications, Exosomes, MiRNAs, Neurogenesis

P23

Cytoprotective Core-Shell Hydrogels: Enhancing Wharton's Jelly-Derived MSC Viability via Chitosan-Coated Alginate–Hyaluronic Acid Microbeads

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Background: Wharton's jelly-derived mesenchymal stem cells (WJ-MSCs) have gained significant clinical attention in cell-based therapies due to their unique immunomodulatory properties and high regenerative potential. To ensure targeted delivery and protect these cells from the host environment, 3D hydrogel-based encapsulation systems are increasingly utilized. However, conventional hydrogels, often suffer from rapid degradation and mechanical instability. This study aimed to develop a chitosan-coated alginate–hyaluronic acid (Alg-HA) core-shell system to improve scaffold integrity, biocompatibility, and long-term WJ-MSC viability. Methods: WJ-MSCs were characterized by immunophenotyping and multilineage differentiation potential. Core-shell microbeads were fabricated via electrostatic extrusion of an Alginate-Hyaluronic acid blend, followed by Chitosan surface coating. The biocompatibility and cytotoxicity of the hydrogels were evaluated using the MTT assay. Finally, WJ-MSCs were encapsulated within the microbeads, and their long-term viability was assessed at 24, 72, and 120 hours using Acridine Orange/Propidium Iodide (AO/PI) dual staining. All experiments were conducted in triplicate, and statistical analysis was performed using one-way ANOVA with significance set at $p < 0.05$. Results: The MTT assay confirmed the biocompatibility of the composite hydrogels, with no significant cytotoxicity observed. The chitosan-coated group demonstrated significantly higher WJ-MSC viability ($P<0.05$) compared to uncoated Alg-HA scaffolds. While the uncoated group exhibited structural degradation and declining cell survival over 120 hours, the chitosan shell provided superior mechanical stability and a controlled microenvironment, fostering sustained cellular growth and protection. Conclusion: The chitosan-coated Alg-HA core-shell hydrogel serves as a robust, biocompatible platform for stem cell delivery. By enhancing structural integrity and mitigating scaffold swelling, this system significantly improves WJ-MSC survival in 3D environments, offering a promising strategy for advanced cell-based therapies

Keywords: Mesenchymal Stem Cells, Hydrogel, Chitosan, HyaluronicAcid, Cell Therapy

P24

Synthesis and Characterization of a pH-Sensitive Hydrogel Containing CuO-GO Nanocomposite and Human Platelet Lysate as a Carrier of Mesenchymal Stem Cells for Wound Healing Applications

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Background: Wound healing can be enhanced through mesenchymal stem cell (MSC) therapy, which reduces inflammation, promotes angiogenesis, and improves tissue repair. Chitosan-based hydrogels provide a biocompatible carrier for cells, while platelet lysate (PL) supplies essential growth factors to support cell functions. Incorporating copper oxide/graphene oxide nanocomposites (NCs) adds antimicrobial properties, making the hydrogel system a promising platform for advanced wound healing. Methods: The synthesized NCs were characterized using FTIR, DLS, XRD, and SEM techniques. The antimicrobial activity of the nanocomposites was evaluated against Pseudomonas aeruginosa and Staphylococcus aureus. The cytotoxic effects of the NCs and hydrogel on dental pulp stem cells from deciduous teeth (SHEDs) were analyzed using MTT and flow cytometry assays. To evaluate the hydrogel's capability to maintain cell viability over one week, AlamarBlue and DAPI staining assays were performed. Additionally, hemocompatibility tests were conducted on both the hydrogel and the nanocomposites. Results: The hydrogel demonstrated non-toxicity to SHEDs, as confirmed by MTT and flow cytometry assays. It maintained cell viability for over one week, as shown by AlamarBlue and DAPI staining. Antibacterial tests indicated effective inhibition of both gram-positive and gram-negative bacteria by the NC. Hemocompatibility tests confirmed its safety. Conclusion: This hydrogel system demonstrates excellent moisture retention, antimicrobial activity, growth factor delivery, biodegradability, and biocompatibility, making it a potential candidate for use as an advanced wound dressing.

Keywords: Wound Healing, Cell Therapy, Stem Cells, Hydrogel, Nanocomposite, Platelet Lysate

P25

Effect of Interleukin-15 on Activation and Cytotoxicity of Natural Killer Cells

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Background: Acute myeloid leukemia (AML) is a highly aggressive hematologic malignancy that presents considerable therapeutic challenges, particularly in elderly patients, due to the high risks associated with chemotherapy and the scarcity of treatment options. Immunotherapy using natural killer (NK) cells has shown good efficacy as a novel approach. The present study investigates the effect of interleukin 15 treatment on increasing cytotoxic potency and expression of surface markers of NK cells. Methodes: Natural killer cell samples isolated from peripheral blood mononuclear cells of donors were included in the study after examining their viability and percentage of natural killer cells. Natural killer cells were treated with interleukin 15 for 24 hours. After the treatment period, the cells were evaluated for the expression of activation markers (CD69, CD25) and NK-specific markers (CD56, CD16), cytotoxicity through direct killing power against K562 target cells. Results: Natural killer cells treated with interleukin 15 on day 1 after activation had a significant increase in the expression of activation-related factors such as CD69, CD25. Also, following the treatment of this cell, a significant increase in the cytotoxicity against K562 target cells was observed. Conclusion: Overall, this study demonstrates the effect of interleukin 15 on the activation of natural killer cells as a suitable option for increasing the activity of these cells and subsequently increasing the efficiency of these cells against tumor target cells.

Keywords: Natural Killer Cells, Interleukin-15, Acute Myeloid Leukemia

P26

Advancements in gene therapy for human diseases: Trend of current clinical trials

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In an era of rapid scientific advancement, gene therapy has emerged as a groundbreaking approach with the potential to revolutionize the treatment of a myriad of diseases and medical conditions. The trend of current clinical trials suggests that there is growing interest and investment in exploring gene therapy as a viable treatment option. In 2023, a significant milestone was achieved with the approval of seven gene therapies by the Food and Drug Administration (FDA). Projections indicate that between 10 and 20 gene therapies could receive annual FDA approval by 2025. In this review, we conducted a comprehensive analysis of registered clinical trials on Clinicaltrials.gov to determine the progression status of gene therapies. Upon extraction of the data, we conducted a comprehensive analysis of the 2809 included studies. This involved a systematic approach, commencing with an overview, followed by a detailed examination of gene therapy strategies employed in various malignant and non-malignant disorders. Additionally, the study will cover the types of vectors utilized in current trials. Lastly, a meticulous review of 105 phase III-IV clinical trials was conducted to identify potential therapies demonstrating promise. We trust that the comprehensive overview provided will serve as a solid foundation for forthcoming research and study designs, ultimately contributing to the progression of gene therapy and its practical application within healthcare settings. Also, we anticipate that such inquiries will bolster the formulation of practical policies and guidelines for pharmaceutical companies engaged in gene therapy research and development.

Keywords: Gene Therapy, Gene Editing, CRISPR-Cas, Genetic Disorders, Vectors

P27

CRISPR/Cas: A Platform for Precision Diagnostics and Therapeutic Validation in Hematologic Disorders

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The combination of CRISPR/Cas system for genome editing, hematopoietic stem cell biology, and nanomedicine is creating new chances for development of laboratory diagnostics and therapeutics. Using CRISPR/Cas systems to engineer stem cells provides an effective tool for modeling diseases. This allows the generation of isogenic induced pluripotent stem cell lines recapitulate patient-specific hematologic disorders like myeloproliferative neoplasms with specific mutations. At the time non-viral delivery systems such as lipid nanoparticles have demonstrated remarkable efficacy for the in vivo delivery of CRISPR components to HSCs, achieving gene editing in normal and malignant stem cell populations. Lipid nanoparticles that target bone marrow can deliver mRNA to at least 14 types of bone marrow cells types. This can support therapeutic editing for hemoglobinopathies such as sickle cell disease by reactivating fetal hemoglobin. Ribonucleoprotein complexes are an efficient CRISPR format supporting activity and reduce off-target effects, with new delivery methods including nanoparticles and microfluidic-based systems continually being developed. Besides, for diagnosing diseases quantum nanosensors that use CRISPR technology and DNA nanostructures enable sensitive detection of low-abundance biomarkers without amplification. Quantum nanosensors can potentially transform early disease diagnosis and therapeutic monitoring. This integrated platform which combines disease modeling, therapeutic delivery, and diagnostic sensing, brings molecular diagnostics and precision therapeutics into a unify framework for hematologic diseases.

Keywords: CRISPR/Cas, Hematopoietic Stem Cells, Nanosensors, Gene Editing, Laboratory Diagnostics

P28

Exosome Derived Non Coding RNAs: Novel Biomarkers for Precision Diagnosis and Therapy in Leukemia

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Introduction: Exosome-derived non-coding RNAs (ncRNAs) have emerged as vital mediators in the leukemia microenvironment. As stable, non-invasive biomarkers, these molecules offer significant potential for the diagnosis, prognosis, and monitoring of leukemia. This systematic review highlights the potential of exosomal ncRNAs to advance precision oncology and optimize diagnostic and prognostic biomarkers. Method: This systematic review examines the role of exosomes in leukemia, focusing on their ncRNA content and its potential as diagnostic and prognostic biomarkers. A comprehensive search of PubMed, Scopus, Embase, and Web of Science was conducted, according to PRISMA guidelines, with keywords such as leukemia, hematological malignancy, extracellular vesicles, exosome, and tumor-derived exosome/ extracellular vesicles. All English original studies without time limitations were included in our studies. Results: Key findings revealed that exosomal microRNAs, such as miR-532, miR-10b, and miR-21 in acute myeloid leukemia, miR-326 in acute lymphoblastic leukemia, and miR-494 in chronic myeloid leukemia, exhibit significant differential expression between patients and healthy controls, correlating with disease progression, treatment resistance, and survival outcomes. Moreover, long non-coding RNAs and circular RNAs were identified as potential biomarkers in myelodysplastic syndromes and leukemia. These non-coding RNAs have been suggested to be useful as predictive and prognostic biomarkers in AML. Conclusion: These findings highlight the transformative potential of exosomal ncRNAs in precision oncology, offering a novel approach for non-invasive diagnostics, prognostic stratification, and targeted therapies in hematological malignancies. Additional studies are necessary to validate these biomarkers and explore their clinical applications.

Keywords: Exosomes, Non-coding RNAs, Hematological Malignancies, Biomarkers, Liquid Biopsy, Precision Medicine

P29

Folate-Functionalized PAMAM G4 Dendrimer Nanocarrier for Targeted Delivery of Silver and Iron Oxide Nanoparticles to Leukemia Cells

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Background: Cancer remains a leading cause of mortality, and conventional therapies are often limited by targeting efficiency and outcomes. Smart drug delivery systems offer promising strategies to improve therapeutic delivery. This study developed a folic-acid-functionalized polyamidoamine G4 (PAMAM G4) nanocarrier for silver (Ag) and iron oxide (Fe) nanoparticles to leukemia cells. Methods: PAMAM G4 dendrimers were functionalized with folic acid using EDC/NHS-mediated conjugation to produce a folate-targeted platform. Ag and Fe nanoparticles were loaded into PAMAM-FA, followed by dialysis purification and lyophilization. Structural and physicochemical properties were characterized by FT-IR, DLS, zeta potential, TEM, and TGA. Ag release was measured in PBS at pH 7.4, 6.0, and 5.0. Cytotoxicity was examined by MTT assay in NALM-6 and K562 leukemia cells, with HGF normal controls. Apoptosis and cellular uptake in NALM-6 cells were quantified by Annexin V-FITC/PI. Results: Analyses confirmed FA conjugation and efficient metal nanoparticle loading. PAMAM-Ag-Fe-FA had a 235 nm hydrodynamic diameter, +22.5 mV surface charge, 30-90 nm TEM size range, and Ag and Fe contents of 22.5% and 24%, respectively. Ag release was controlled and pH-sensitive, with higher release under acidic conditions. After 24 h of treatment at 400 nM, viability decreased to <40% in NALM-6 and <30% in K562 cells, while HGF cells showed higher viability. PAMAM-Ag-Fe-FA induced >55% apoptosis in NALM-6 cells and >40-fold higher uptake than the non-targeted carrier. Conclusion: Folate-targeted PAMAM-Ag-Fe-FA showed pH-responsive release, enhanced leukemia-cell internalization, potent cytotoxicity, and apoptosis, supporting its potential as a promising targeted co-delivery platform for leukemia therapy.

Keywords: PAMAM, Folic Acid, Silver Nanoparticles, Iron Oxide Nanoparticles, Leukemia

P30

BMMSC-Derived Extracellular Vesicles in Hypoxia-Conditioned Modulate Angiogenesis-Related Gene Expression in Jurkat T-Cells

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Introduction: Bone marrow–derived mesenchymal stem cell (BMMSC)-derived exosomes exhibit notable therapeutic potential through delivery of regulatory RNAs and proteins to tumor cells. Hypoxia significantly influences their composition and biological activity. This study aimed to evaluate how hypoxia alters the biological activity of BMMSC-derived exosomes by comparing exosomes produced under normoxic and hypoxic conditions, and to determine their effects on angiogenesis in Jurkat T lymphoblast cells through analysis of angiogenesis-related gene expression. Method: BMMSCs were cultured under normoxic and hypoxic conditions. Exosomes were isolated from conditioned media by differential ultracentrifugation and characterized using dynamic light scattering (DLS), scanning electron microscopy (SEM), and Western blot analysis of exosomal markers. Jurkat T lymphoblast cells were treated with the isolated exosomes, and angiogenesis-related gene expression was evaluated by real-time PCR. Result: BMMSC-derived exosomes were successfully isolated and characterized by DLS and SEM analyses, revealing a typical spherical morphology with a nanoscale size distribution. Furthermore, Western blot analysis confirmed the expression of CD63 and TSG101 markers, validating the successful isolation and characterization of the exosomes. ANGPT2 expression showed a marked increase in the HC and HN groups compared with NC, NN, and NH groups, with the highest level observed in HN (P-value < 0.001). Although expression decreased in the HH group, it remained elevated relative to the low-expression groups, suggesting enhanced angiogenic and inflammatory activity under Hypoxia conditions. HIF1A expression remained relatively stable across most experimental groups, with only minor fluctuations compared to the control (P-value > 0.05). A slight reduction was observed in the HH1 group, suggesting that the experimental conditions had limited overall impact on HIF1A transcription. Conclusion: Hypoxia enhances the pro-angiogenic potential of BMMSC-derived exosomes by modulating their biological activity and increasing angiogenesis-related gene expression in Jurkat cells. These findings highlight the potential of hypoxia-conditioned BMMSC exosomes as promising candidates for targeted therapeutic strategies.

Keywords: BMMSC, Hypoxia, Extracellular Vesicles, Angiogenesis

P31

Therapeutic Applications of Platelet-Derived Exosomes for Wound Regeneration: A Review of Cell-Based Approaches

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Background: Platelet-derived exosomes are nanosized (30–100 nm) extracellular vesicles enriched with growth factors, regulatory microRNAs, and bioactive lipids that regulate angiogenesis, inflammation, and tissue repair. This narrative review evaluates current evidence on their role and therapeutic applications in wound healing. Methods: A targeted search was performed in PubMed and Scopus up to 2026 using keywords related to platelet-derived exosomes and wound healing. In vitro, in vivo, and review studies were screened and critically reviewed to summarize mechanisms and therapeutic potential. Results: The evidence indicates platelet-derived exosomes accelerate wound healing via interconnected pathways. In ischemic and cutaneous wounds, they enhance fibroblast and keratinocyte proliferation and migration, increase collagen I/III secretion, and support endothelial differentiation, promoting faster closure with reduced scar formation. These effects involve SMAD2, TAK1/p38, RAS/ERK, and Rho/ROCK–YAP signaling. In diabetic wounds, they improve healing by stimulating angiogenesis and regeneration through PI3K/Akt and ERK signaling, and via S1P/S1PR1-mediated mechanisms. In gingival models, they facilitate fibrosis-sparing repair through extracellular matrix remodeling, including increased MMP1 and COL1A1 expression. In burn injuries, combined platelet-derived exosomes and mesenchymal stem cell exosomes reduce inflammation and oxidative stress while enhancing angiogenesis and epithelial regeneration. An early clinical pilot in healthy volunteers reported scarless healing within 30 days after subcutaneous allogeneic platelet exosome injection without serious adverse events. Conclusion: Platelet-derived exosomes are promising cell-free candidates with potential efficacy and safety for acute/chronic wounds, including diabetic, pressure, burns, and gingival injuries. They coordinate inflammation control, angiogenesis, and ECM remodeling, making them valuable in tissue regeneration and cell therapy.

Keywords: Platelet-Derived Exosomes, Cell Therapy, Wound Healing

P32

Safety and Efficacy of CAR-T Cell Therapy in Relapsed/Refractory Acute Myeloid Leukemia: A Systematic Review Based on the Latest Clinical Trial Data

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Background: Patients with relapsed or refractory AML have a poor prognosis and treatment remains challenging. Although CAR-T therapy is established in lymphoid malignancies, its clinical utility in AML remains investigational. Methods: A systematic PubMed search was conducted from inception to May 10, 2026, using terms related to AML and CAR-T-cell therapy. Clinical trials reporting safety or efficacy outcomes were included. Reviews, preclinical studies, and case reports were excluded. Results: Seventeen studies with 257 patients were analyzed. Median age ranged from 3 to 78 years, and 130 patients (58%) were male. Most trials were early phase, predominantly phase I, conducted in the USA (7/17), China (5/17), and Europe (5/17). Target antigens included CD33, CLL-1, CD123, CD7, and NKG2D ligands. Products were autologous in 76% of studies and allogeneic in 24%. Retroviral and lentiviral vectors were used in seven and eight studies, respectively. The mean infused dose was 4.7×10^6 cells/kg. Among 225 efficacy-evaluable patients, overall response rates ranged from 0% to 100%. CRS occurred in 139 patients (62%), mainly grade 1–2; grade ≥3 events occurred in 25% of affected patients. Neurotoxicity occurred in 0–26%, whereas GVHD was uncommon and mainly associated with allogeneic platforms. Post-CAR-T hematopoietic stem cell transplantation was used in 60% of studies, supporting durable remission in some cohorts. Conclusion: CAR-T-cell therapy in AML is feasible and generally tolerable, with heterogeneous but promising antileukemic activity. Durable benefit may depend on optimized antigen selection, enhanced persistence, multi-target or armored constructs, and standardized post-CAR consolidation, particularly allogeneic transplantation.

Keywords: Acute Myeloid Leukemia, Relapsed/Refractory, CAR T Cells

P33

Cyanidin-3-Glucoside Reduces Angiogenesis of Myeloma Cells with HUVECs Mediated by Extracellular Vesicles

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Background: Multiple myeloma (MM) is a neoplastic condition resulting from the uncontrolled expansion of B-cell-derived plasma cells. The importance of angiogenesis in MM development has also been demonstrated. Extracellular vesicles (EVs) have vital functions in interactions between neighboring cells, such as angiogenesis. Cyanidin-3-glucoside(C3G) is a naturally occurring anthocyanin widely found in red and purple fruits, recognized for its potent antioxidant, anti-inflammatory, and potential anticancer activities demonstrated in preclinical studies. The objective of this in vitro study was to examine the transfection and angiogenesis effects of MM-EVs on endothelial cells (ECs) upon treatment with C3G. Methods: Following treatment of multiple myeloma cells (U266) with C3G, MM-EVs were harvested and transmigrated to human umbilical vein endothelial cells (HUVEC) in a co-culture model. After 48 hours of treatment with C3G, VEGF, VEGFR2 and IL6 mRNA levels were evaluated with quantitative real-time PCR from the HUVECs and U266. Likewise, the proliferation of HUVECs treated with C3G-treated MM-EVs was visualized and estimated by tube formation assay. Results: The anti-angiogenic effect of C3G-treated MM-EVs was evident by the decreased expression of VEGF, VEGFR2 and IL-6 at the mRNA levels after internalization of MM-EVs in HUVEC. Furthermore, tube formation assay showed inhibition of HUVEC cell proliferation by C3G-treated MM-EVs compared to control MM-EVs. Conclusion: Our research indicated that MM-EVs derived from C3G-treated myeloma cells inhibited angiogenesis in HUVECs. This phenomenon is coordinated by the internalized C3G treated MM-EVs in HUVECs, and ultimately the reduction of angiogenic factors and inhibition of tube formation.

Keywords: C3G, Extracellular Vesicles, Multiple Myeloma, Angiogenesis

P34

Emerging Non-Coding RNA-Directed Therapeutics in Solid Tumors: A Systematic Review of Clinical Efficacy and Safety

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Background: Non-coding RNA (ncRNA)-directed therapeutics are emerging as precision-oncology strategies that modulate cancer-related pathways through RNA interference, transcript activation, microRNA replacement, and antisense inhibition. However, their efficacy and safety in solid tumors remain unclear. Methods: PubMed was searched from 2010 to May 2026. Eligible studies enrolled patients with solid tumors treated with ncRNA-directed agents and reported safety and/or efficacy outcomes. Reviews, non-peer-reviewed publications, preclinical studies, and reports without extractable clinical data were excluded. Results: Twenty clinical studies involving 728 patients were included. Most were early-phase trials, phase I-containing studies, and were conducted in seven countries, most frequently in the United States. Therapeutic platforms comprised siRNA (10/20), miRNA mimics (3/20), LNA-based inhibitors (3/20), saRNA (2/20), and ASOs (2/20). Targets included KRASG12D/G12D-V, TGF-β1/COX-2, GSTP1, miR-10b, CEBPA, Bcl2L12, Cbl-b, PKN3, miR-34a, PLK1, miR-16, miR-221, STAT3/PD-L1, and survivin/BIRC5. Most agents were administered intravenously using lipid nanoparticles, liposomes, exosomes, minicells, or related systems; intralesional, intratumoral, and ex vivo approaches were less common. Tumor types included pancreatic cancer, hepatocellular carcinoma, non-small cell lung cancer, glioblastoma, mesothelioma, prostate cancer, and mixed refractory solid tumors. Efficacy varied, with stable disease more frequent than objective response. The strongest signals included STP705 histologic clearance (76%), siG12D-LODER response rates up to 63.6%, and MTL-CEBPA plus pembrolizumab partial response (10%). Grade ≥3 treatment-related adverse events occurred in fewer than 40% of patients in most trials. Conclusion: ncRNA-directed therapeutics show encouraging early activity and generally manageable toxicity in refractory solid tumors. Further biomarker-driven trials, improved delivery systems, and rational combination strategies are needed.

Keywords: Non-coding RNA, siRNA, microRNA, Small Activating RNA, Solid Tumors, Systematic Review, Nanoparticle Delivery, Clinical Trials

P35

Harnessing the Synergistic Potential of TRAIL and SAHA To Overcome Apoptosis Resistance in KG-1 Cells

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Acute Myeloid Leukemia (AML) is a complex blood cancer marked by the uncontrolled proliferation of immature myeloid cells. Tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) has been shown to induce apoptosis specifically in cancer cells. However, certain cell lines, such as KG-1, exhibit resistance to TRAIL-induced apoptosis, highlighting the necessity for combination therapies. Histone deacetylase inhibitors (HDACis), particularly Suberoylanilide Hydroxamic Acid (SAHA), have demonstrated promise in enhancing the sensitivity of these resistant cancer cells to TRAIL. This study investigates the combined effects of SAHA and TRAIL on KG-1 cells over 24, 48, and 72 hours. Methods and Materials: KG-1 cells were cultured in RPMI 1640 medium and treated with varying concentrations of SAHA (0.5, 1, 2, 4, and 8 µM). The MTT assay was employed to determine cell viability, identifying 2 µM SAHA as the IC50 at the 24-hour mark. Apoptosis was evaluated using flow cytometry following treatment with 2 µM SAHA alone or in combination with TRAIL (50 nM and 100 nM) at 24, 48, and 72 hours. Additionally, real-time PCR was conducted to analyze the expression levels of key genes involved in apoptosis, including BAX, CASPASE-8, BCL2, NF-kB, and PI3K. Results: The MTT assay confirmed that 2 µM SAHA is the IC50 after 24 hours. Flow cytometry results revealed a significant increase in apoptosis rates in the group treated with SAHA (2 µM) and TRAIL (100 nM), peaking at approximately 84% at the 72-hour time point. In contrast, the TRAIL-only groups showed no significant changes in apoptosis compared to the control. Real-time PCR analysis indicated that the combination therapy notably increased the expression of pro-apoptotic genes (BAX, CASPASE-8) while decreasing the expression of anti-apoptotic and survival genes (BCL2, NF-kB, PI3K), particularly at the 48 and 72-hour intervals. Conclusion: The combination of SAHA and TRAIL significantly enhances apoptosis in KG-1 cells, as evidenced by increased expression of pro-apoptotic genes and decreased expression of anti-apoptotic and survival genes. These findings highlight SAHA's potential to overcome TRAIL resistance in AML by modulating essential apoptotic pathways, suggesting a promising therapeutic approach for this challenging malignancy.

Keywords: AML, TRAIL, SAHA, KG-1, Bax-Bcl-2

Challenges in Immunohematology

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P36

Frequency of Red Blood Cell Antibodies and Their Association with Transfusion History and Clinical Diagnosis

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Background: The formation of unexpected red blood cell (RBC) antibodies is a major concern in transfusion medicine. These antibodies may lead to hemolytic transfusion reactions, delay in providing compatible blood, and increased morbidity in transfusion-dependent patients. Determining the frequency of these antibodies and identifying factors associated with their development are essential for improving transfusion safety. Methods: This descriptive–analytical study was performed on 814 patients referred for pre-transfusion compatibility testing between 2012 and 2024. Demographic characteristics, clinical diagnoses, history of blood transfusion, antibody screening results, and antibody identification findings were collected and analyzed. Statistical analysis was conducted using appropriate tests, and a p-value of less than 0.05 was considered statistically significant. Results: The mean age of patients was 33.46 ± 24.95 years, and 58.2% were female. A history of blood transfusion was reported in 61.5% of patients. The most frequent clinical diagnoses were Thalassemia (31.6%) and other hematologic diseases (15.2%). Forty-seven percent of patients had a positive antibody screening result. Among the identified antibodies, Anti-E (8.8%), Anti-K (6.5%), and Anti-D (6.4%) were the most prevalent, with antibodies of the Rh and Kell systems accounting for the majority of cases. Rare alloantibodies, including anti-Ku, anti-Jk3, anti-Rh17, anti-pp1pk, and anti-H, were identified in ten patients. A statistically significant association was observed between history of blood transfusion and the presence of unexpected antibodies ($p = 0.01$). Conclusion: Unexpected RBC antibodies were commonly detected among transfusion candidates, particularly antibodies belonging to the Rh and Kell systems. A history of blood transfusion was identified as the primary factor associated with antibody development. Routine antibody screening, especially in patients with a prior history of transfusion, is strongly recommended to enhance transfusion safety and prevent adverse transfusion reactions.

Keywords: Unexpected Antibodies, Blood Transfusion, Antibody Screening, Rh System, Kell System

P37

Quality Comparison of the Leukocyte-Reduced Red Blood Cell Products Derived from Different Leukocyte Filtration Sets

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Background: Leukocyte-reduced red blood cell products (RBCs) are among the most widely used blood products in the world. In Iran today, more than half of RBCs are leukocyte-depleted. Given the high consumption of these products, continuous monitoring of all stages of preparation, processing, storage, and infusion is essential to maintain the quality of blood products (1-4). Since different methods and bags are used for leukocyte filtration, this study aims to compare the quality of red blood cell products derived from the various leukofiltration bags used by the Iranian Blood Transfusion Organization. Methods Twelve whole-blood units from continuous male donors with blood group A+ were included in the study. To eliminate donor-related background variables, each unit of whole blood was divided into three equal parts, and each part was filtered using one of the leukofiltration sets studied [Whole Blood Filtration bag (WBF), Red cell Filtration bag of company 1 (C1-RCF), Red cell Filtration bag of company 2 (C2-RCF)]. CPD-SAGM (Saline-Adenin-Glucose-Monitol) was the anticoagulant and preservative solution used in all the units. The prepared RBCs (32 units) were stored at 2-6°C up to 42 days. The RBCs were withdrawn on days 2, 14, 28, and 42 and sampled for erythrocyte indices (Hematocrit, Mean Cell Volume, Mean Cell Hematocrit, Mean Cell Hemoglobin Concentrate), glucose, lactate, LDH (lactate Dehydrogenase), pH, and hemolysis index. Results The Data were analysed by SPSS version 25. A one-way repeated-measures ANOVA was used to compare three product groups on each day. The results are reported as Mean±SD with a 95% confidence interval. The mean difference is significant at the 0.05 level. The results showed that the average erythrocyte indices across the different products did not differ significantly at any of the time intervals

studied (P-value > 0.05). However, the glucose drop rate in WBF-RBCs was significantly higher than that in C1-RCF and C2-RCF products (P-value < 0.001). Also, lactate, LDH, and hemolysis percentage in WBF-RBCs were significantly higher than in C1-RCF and C2-RCF bags (P-value < 0.05). The pH decrease was also significantly greater in WBF bags than in RCF bags on days 14 and 42. WBF-RBCs had a lower pH. Conclusion The results demonstrated that glucose drops faster in WBF-RBCs than in the others, suggesting that erythrocytes were more sensitive and lysed more quickly. The decrease in pH and the increases in lactate, LDH, and the hemolysis index confirmed the greater susceptibility of cells in WBf Products. However, the hemolysis percentage in all the products from different sets remained within the standard range (< 0.8%) throughout storage. Therefore, despite the observed differences, all products met acceptable quality standards for transfusion according to the Iranian Blood Organization.

Keywords: Leukocyte Filtration, Leukocyte-Reduced, Red Blood Cell Products, Quality, Iranian Blood Organization

P38

The TGFβ Signaling Pathway Could be Effective in the Pathogenesis of Human Lymphotropic Virus Type 1 Evidence from a Systems Biology Study

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Background: Human T-cell lymphotropic virus type 1 (HTLV-1) is responsible for two critical human diseases: Adult T-cell leukemia/lymphoma (ATLL) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). Although most cases of HTLV-1 infection are asymptomatic and the prevalence of serious diseases like HAM/TSP and ATLL is not remarkable, their prognosis is poor. It has been assumed that various immunological responses, different interactions between the patient's body and the virus, and clearly the virus itself, are responsible for pathogenesis. To prevent and manage the consequences of this oncogenic virus, we should clearly understand the molecular pathways and interactions between the HTLV-1 virus and human cells. Objectives: In this study, we aim to identify the most essential genes and microRNAs involved in the induction of ATLL disease and its laboratory confirmation. Methods: After a purposeful search in databases and a qualitative review of obtained data, the data were processed using R software, and miRNAs with different expressions (DEMs) were calculated according to the value of logFC. The gene targets of miRNAs were obtained using the miRDB online tool. The protein-protein interaction network of gene targets was drawn and analyzed with the STRING database. The sub-network was extracted using Cytoscape. Pathway analysis was conducted, and proteins participating in the enriched pathways were selected to propose the implicated signaling network using the information available on the website ENRICHR and KEGG message transduction. An intracellular control gene, RPLP0, and three other key genes were selected and evaluated in 10 healthy participants, 10 asymptomatic carriers (ACs), and 10 ATLL patients using real-time PCR. Results: Mir-20a-5p was identified as an essential microRNA with different expression in the patient group compared to the healthy and ACs. Transforming growth factor-beta 1 (TGF β 1), TGFBR1, and TGFBR2, which have a crucial role in disease pathogenesis, were identified. Conclusions: The results demonstrated that TGFBR1's expression level was remarkably increased in ATLL patients compared to healthy donors and ACs. Further investigations are required to assess the prognostic and therapeutic function of these elements.

Keywords: Human T-Cell Lymphotrophic Virus Type 1, HTLV1, Adult T-Cell LeukemiA/Lymphoma, ATLL, miRNA, RTqPCR

P39

Prevalence of RhD Negative and Weak D Phenotype in Blood Donors in South Khorasan Province

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Background: The Rh blood group system, especially the D antigen, plays a vital role in the safety of blood transfusion and the prevention of hemolytic disease of the fetus and newborn. Weak D variants have low expression of the D antigen, and their accurate identification is of great clinical importance in the management of blood donors and recipients. Given that regional data on the prevalence of RhD negative and Weak D phenotypes in Iran are limited, the aim of this study was to determine the prevalence of RhD negative and Weak D phenotypes in blood donors in South Khorasan province. Methods: This descriptive-cross-sectional study was conducted on blood donors referring to blood transfusion centers in South Khorasan province during a one-year period from June 2024 to June 2025. RhD determination and Weak D identification were performed using tube serological tests, and Weak D samples were also evaluated for C, c, E, and e antigens. The data were analyzed with SPSS software and the prevalence was calculated with a 95% confidence interval. Results: Of the 16190 donors, 2198 (13.57%) were Rh negative and 27 (0.16%) had the Weak D phenotype. The most common Weak D phenotypes were DCce (73.3%) and DCe (26.7%), respectively. Most Weak D donors were in the age group of 20-50 years and were male. Conclusions: Accurate identification and recording of Weak D and RhD phenotypes can help in the optimal management of RhD negative resources, reduce unnecessary consumption of anti-D immunoglobulin, and improve the safety of blood transfusion.

Keywords: RhD Negative, Weak D, Blood Donors, Serological Phenotype

P40

Distribution of ABO, Rh, and Kell Blood Group Antigens Among Voluntary Blood Donors in Yazd, Iran

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Background: Red blood cell (RBC) antigen phenotypes vary across populations and have critical implications for transfusion safety, alloimmunization risk, and the management of patients requiring chronic transfusion support. Knowledge of antigen frequency among blood donors enables optimized inventory management and targeted donor recruitment strategies. The study aimed to determine the frequency distribution of clinically significant RBC phenotypes among voluntary blood donors and assess their relevance for transfusion compatibility. Methods: This cross-sectional study was conducted at the Yazd Blood Transfusion Center. A total of 683 healthy volunteer blood donors were enrolled. Donor selection was carried out in accordance with the standard eligibility criteria established by the Iranian Blood Transfusion Organization. Peripheral blood samples were collected in EDTA-anticoagulated tubes and subjected to red blood cell phenotyping using standard serological techniques. ABO and Rh (D, C, c, E, e) antigens, as well as the Kell (K) antigen, were determined using the column agglutination method with the Ortho automated immunohematology analyzer (Ortho Clinical Diagnostics, USA), following the manufacturer's instructions. Antibody screening was also performed using the column agglutination method. Antigen and phenotype frequencies were calculated as percentages. Results: The ABO system showed predominance of group O (36%), followed by groups B (29.4%), A (24.6%), and AB (10%). Within the Rh system, Rh(D)-positive phenotype (83.6%) was most common, while Rh(D)-negative donors (16.4%) comprised a smaller proportion. Among other clinically significant antigens, high prevalence was observed for e (97.5%), c (76%), and C (70.6%) antigens, whereas E (25.4%) and K (5.9%) were comparatively less frequent. The observed distribution demonstrated patterns consistent with previously reported regional trends, with minor variations attributable to population heterogeneity. Unexpected antibodies were detected in three donors (0.4%). Conclusion: The study reveals the distribution of clinically significant RBC antigen phenotypes among blood donors, highlighting the importance of extended phenotyping in transfusion practice. Establishing a donor antigen database facilitates the provision of antigen-matched blood, reduces the risk of alloimmunization, and supports patients with hemoglobinopathies and other transfusion-dependent conditions. Continued surveillance of antigen frequency is crucial for enhancing transfusion safety and informed resource planning.

Keywords: RBC, Blood Transfusion, Phenotyping, Rh System, Kell System

P41

Effectiveness of Targeted Interventions to Increase Recruitment and Retention of Young Blood Donors: A Scoping Review

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Recruiting and retaining blood donors, particularly young donors, is a challenge. Studies evaluating different interventions have reported inconsistent results. In this review, primary studies, including randomized or non-randomized trials and field trials published between 2014 and 2025, were retrieved from MEDLINE, Scopus, and Google Scholar. The effectiveness of interventions on blood donor recruitment or retention, with particular focus on young adults and first-time donors, was evaluated. Ten studies covering thirteen interventions were found. Baseline return rates among first-time young donors without intervention consistently ranged from 20% to 36%, highlighting their vulnerability to early dropout and the need for targeted retention efforts. Reminders are intended to encourage repeat blood donation, rather than only increasing donors' intention to donate. One study found that sending generic WhatsApp messages to young donors had limited effectiveness, increasing return rates from 22% to 31%. Conversely, personalized phone calls to 1,356 first-time donors led to a 31.5% increase in return rate, especially among male donors, who returned at a rate of 32.1%. Incentives encourage repeat donations by providing external rewards. A large field trial indicated that health-related incentives, such as free cholesterol testing, had a small effect (return rate of 0.6%) on recruitment. Non-monetary incentives (gifts) resulted in a 30% return rate, which was not significantly different from the control. In contrast, a study involving 6,107 young donors reported a 4–18.9% increase in return rate using small symbolic incentives (T-shirts). Educational strategies aim to enhance knowledge, self-efficacy, and perceived safety of the donation process. A study evaluating an optimized Donor Educational Module reported significant post-intervention knowledge gains, showing improvement in retention. Videos and brochures increased knowledge among young donors; coping-focused brochures improved readiness to donate again. Educational letters produced a 33.2% return rate, with particularly strong effects among academically educated donors (41.9%). Digital educational campaigns in Saudi Arabia increased donations by 15–20% among young first-time donors. Motivational meetings focused on personal engagement and the social meaning of donating, whereas traditional motivational meetings had no impact from 22 % to 22.1%. By concentrating on donor autonomy and self-determination Motivational interviewing improves the return rate to 71.1%. The watching-eyes intervention (adding a picture or pictogram of human eyes to a promotional message or object to influence a decision) led to an increase in blood donations from 6.75% to 16.12%, with no effect on reported intentions, indicating it triggers implicit social

signals. In conclusion, this scoping review shows that targeted, well-designed interventions can effectively recruit and retain young and first-time blood donors. Approaches that recognize donors' individual motivations such as motivational interviewing, personalized follow-up, and structured education were more successful in enhancing knowledge, confidence, and commitment to continued donation. Symbolic incentives and subtle behavioral nudges had a positive effect, while generic reminders and standard rewards showed limited benefit. These findings highlight the need to move beyond one-size-fits-all strategies toward more human-centred approaches. Further studies are needed to assess the long-term sustainability, cost-effectiveness, and cultural applicability of these interventions.

Keywords: Young Blood Donors, Donor Recruitment, Donor Retention

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Comorbidity Between Obesity and Anemia in the PERSIAN Guilan Cohort Study Population

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Background: Obesity and anemia represent two prevalent but seemingly opposing public health challenges, with limited and inconsistent evidence regarding their association in adult populations. This study aimed to evaluate the relationship between general and central obesity indicators and the prevalence of anemia among adults in the Prospective Epidemiological Research Studies of the Iranian Adults (PERSIAN) Guilan Cohort Study (PGCS) population. Methods: This cross-sectional study included 10,519 adults aged 35–70 years from the PGCS population. Anthropometric measures including body mass index (BMI), waist circumference (WC), waist-to-hip ratio (WHR), and waist-to-height ratio (WHtR), were used to assess general and abdominal obesity. Anemia was defined according to WHO criteria. Results: The overall prevalence of anemia was 13.2%, significantly higher among women (16.6%) than men (9.2%). Analysis by BMI showed that overweight and obese individuals had significantly lower odds of anemia compared to those with normal weight, with obesity remaining protective after full adjustment (OR = 0.85; 95% CI: 0.72–0.99; P = 0.040). While crude prevalence of anemia was higher among those with abdominal obesity, adjusted models revealed a non-significant inverse association (P>0.05). WHR-defined obesity was significantly associated with lower anemia prevalence in women and predicted a 20.0% reduction in anemia odds in the fully adjusted model (OR = 0.80; 95% CI: 0.66–0.98; P = 0.029). Similarly, elevated WHtR (≥0.5) was associated with significantly lower anemia prevalence in men and showed a 22.0% reduction in anemia odds after adjusting for age and sex (OR = 0.78; 95% CI: 0.65–0.94; P = 0.008), though this association attenuated after full adjustment. Conclusion: We observed a significant inverse association between several anthropometric measures particularly BMI, WHR, and WHtR and the prevalence of anemia, independent of key demographic and clinical variables. These results highlight the need for further mechanistic and longitudinal research on the interplay between adiposity, iron metabolism, and inflammation.

Keywords: Obesity, Anemia, Body Mass Index, Waist Circumference, Waist-to-Hip Ratio, and Waist-to-Height Ratio

P43

Investigation of Clinical Symptoms and Laboratory Results of Blood Transfusion Complications and Related Factors: A Retrospective Study in Mashhad, Iran (2019-2022)

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Introduction: Blood transfusion is one of the common and vital therapeutic interventions in the health system, which, along with significant benefits, can be associated with clinical complications and laboratory changes in certain circumstances. Identifying clinical patterns of blood transfusion complications and examining changes in laboratory indicators related to them plays an important role in timely and correct diagnosis, resulting in better management of the complication. Given the diversity of blood products and individual differences between patients, examining actual hospital data can provide valuable information in the field of monitoring and preventing these complications. Therefore, the present study aimed to investigate the clinical symptoms and laboratory results of blood transfusion complications and related factors in hospitals under the auspices of Mashhad University of Medical Sciences. Method: This study was conducted retrospectively in hospitals under the auuspices of Mashhad University of Medical Sciences. Data were extracted from the records of patients with complications after blood transfusion during the years 2019 to 2022. Inclusion criteria included the occurrence of any clinical symptoms or laboratory changes after blood product infusion. Exclusion criteria included duplicate records and cases with incomplete information. Demographic information, type of blood product, clinical manifestations, and laboratory indicators before and after the occurrence of the complication were recorded and analyzed. Statistical analysis of the data was performed using appropriate descriptive and comparative tests, and a significance level of $P<0.05$ was considered. This study has an ethics code of IR.MUMS.FHMPM.REC.1401.202. Results: In this retrospective study, 205 cases of blood transfusion complications were evaluated in Mashhad during the years 1398 to 1401. Of these, 58.5% were male and 41.5% were female. The highest frequency of patients with complications in the age group under 18 years was related to the age range of 6-13 years with 61 cases, and in the group over 18 years was related to the age range of 51-70 years with 31 cases. The most common adverse events were related to platelet products (50.7%), followed by packed red blood cells (35.6%). The most common clinical symptom was chills with a frequency of 52.7%, and allergic symptoms including urticaria (14.6%) and pruritus (10.2%) were also relatively common. Allergic

reactions were reported in 124 cases (56.9%) and febrile nonhemolytic transfusion reaction (FNHTR) in 90 cases (41.1%). In the study of laboratory parameters before and after the product injection, serum sodium levels showed a significant increase (130.13±30.75 vs. 131.16±31.08 mEq/L; P=0.008). Other parameters including Hb, WBC, liver enzymes (ALT and AST), and creatinine did not change significantly. In general, transfusion complications in the studied patients were mostly mild and were most commonly associated with platelet products. Significant changes in sodium levels can be considered as laboratory signs related to the occurrence of complications. Conclusion: The results of this study showed that transfusion complications were mostly mild and occurred more frequently in platelet products. Significant changes in serum sodium levels can be used as a potential laboratory indicator in the monitoring and early diagnosis of transfusion complications.

Keywords: Blood Transfusion, Complications of Blood Transfusion, Laboratory Results

P44

Resolving Complex ABO Discrepancies: Serologic and Molecular Insights in to the Rare B(A) Phenotype

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Background: Accurate ABO blood group determination is essential for transfusion safety, as unresolved discrepancies may result in hemolytic transfusion reactions and inappropriate blood component selection. Rare ABO subgroups present a particular challenge in immunohematology laboratories because of complex and atypical serologic reaction patterns. Among these variants, the B(A) phenotype is exceptionally rare and is characterized by predominant B antigen expression with trace or weak A antigen reactivity, frequently leading to discrepancies between forward and reverse ABO typing. Case Presentation: Two pregnant women with discrepant historical ABO blood group records were referred for investigation of unresolved ABO discrepancies. Routine serologic testing using automated systems and manual tube methods demonstrated strong agglutination with anti-B and weak reactions with anti-A in forward grouping, with anti-A present in reverse grouping. Initial targeted molecular analysis confirmed the presence of the B allele but did not explain the serologic findings. Subsequent sequencing of the ABO gene identified the rare alleles ABO*B(A).02 and ABO*B(A).04, establishing the diagnosis of the B(A) phenotype in both cases. Conclusion: The B(A) phenotype remains an important cause of complex ABO discrepancies that may be overlooked by routine serologic testing and limited genotyping approaches. Accurate identification requires careful evaluation of serologic findings supported by comprehensive molecular characterization. Reporting these cases from the Iranian population contributes to a better understanding of the serologic behavior, genetic diversity, and geographic distribution of rare ABO subgroups. It underscores the importance of advanced diagnostic strategies in transfusion medicine.

Keywords: ABO Subgroups, B(A) Phenotype, Blood Group Discrepancy

P45

Investigate the Trend of Transfusion-Transmitted Infections (HIV, HCV, HBV) among Blood Donors in Tehran during 2015-2025.

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Blood safety and blood products are one of the critical principles of health care. infections with blood, especially in HIV, HBV and HCV, are still a serious threat to recipients of blood. accurate monitoring of the spread of these viruses in donors is an important indicator for evaluating the safety of blood donation system and planning health policies. tehran province, as the most populous province and the main center of the country 's blood supply, has a special importance. The aim of this study was to investigate the time trends of HIV, HBV and HCV in blood donors of tehran during 2015 to 2015. procedures were analyzed based on the type of donor (first, established and continuous). This study was a retrospective and retrospective study based on the records of the blood transfusion center of tehran province. to analyze temporal trends and identify the change points, poisson regression model was used. the results were compared with type of donor and significant level of 0.05. infection rates were also provided per 100,000 donors. During the last decade, 4,216,638 was recorded for blood donation, leading to successful donation of 3,424,207 blood units. in this study, 311 cases of hiv, 954 were hcv positive and anti - hcv positive were detected. according to the regression model, for hiv two changes in the years 1398 and 1400 was observed: the annual decrease of 10.7 % to 1398 the annual increase of 33.8 % in the interval of 1400 - 1400 and a decrease of 3.1 % annually from 1400 to 1403. for hbsag, the decrease of 20.9 % annual to 1398 increased 2.7 % annual to 1401 and a decrease in 15.6 % annual to 1403. in hcv, one point of change was recognized in 1398, followed by 19.6 % annual decrease up to that year and a slight decrease of 0.5 % annually to 1403. the analysis of the type of donor type showed that First donor had the highest share, for hiv, 146 cases were observed in the first time, 117 cases were established and 48 were continuous. in hbs ag, more than 90 % of cases belonged to First donor. in the case of hcv First donor were 851. for the first time, this study drew the ten - year precise procedure of blood transfusion in the largest blood donor center of the country by using advanced statistical model. hbv and hcv were decreased and overall blood safety was improved, while hiv was the most

significant predictor. This result emphasizes the necessity of implementing smart screening, community targeted education and development of continuous donors " attraction and retention programs.

Keywords: Blood Transfusion, Blood Donors, HIV Infections, Hepatitis C, Hepatitis B

P46

Neutralizing Anti–SARS-CoV-2 Antibody Responses in Regular Versus First-Time Plateletpheresis Donors During the COVID-19 Pandemic

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Background: This study evaluated the impact of regular plateletpheresis on quantitative and qualitative anti–SARS-CoV-2 antibody responses, with a particular focus on neutralizing antibodies, in comparison with first-time plateletpheresis donors. Materials and Methods: In a cohort of 87 eligible plateletpheresis donors, regular donors (≥3 donations within the preceding six months) were compared with first-time donors at the Iranian Blood Transfusion Organization, Tehran, Iran. Peripheral blood samples were collected immediately before and after plateletpheresis performed on Haemonetics MCS+ cell separators. Total anti–SARS-CoV-2 IgG, receptor-binding domain (RBD)-specific antibodies, and functional neutralizing activity were quantified using serological assays and a pseudo-virus neutralization test, expressed as antibody titers or area under the curve (AUC) values. Results: Regular donors demonstrated significantly higher titers of neutralizing antibodies against SARS-CoV-2 compared with first-time donors ($p<0.05$), despite comparable demographic characteristics and similar frequencies of prior clinically suspected or documented COVID-19. While regular plateletpheresis induced measurable post-donation reductions in several lymphocyte subsets, absolute lymphocyte counts remained within reference intervals, and no lymphopenia or thrombocytopenia was observed in either group. Neutralizing capacity strongly paralleled quantitative anti–RBD IgG responses, indicating preserved affinity-matured humoral immunity in regular donors. Conclusion: regular plateletpheresis does not compromise, and may even be associated with augmented, neutralizing anti–SARS-CoV-2 antibody responses in regular donors, supporting the immunological safety of high-frequency platelet donation during the COVID-19 pandemic. Longitudinal monitoring of donor humoral immunity is nonetheless advisable for very high–frequency donation schedule.

Keywords: Plateletpheresis, Transfusion, COVID-19

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Investigation of the Trend of Temporary and Permanent Deferrals among Blood Donors in Tehran Province (2015–2024)

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Introduction: Clinical assessment of blood donors is the primary step in ensuring blood safety for both patients and donors. Furthermore, the rates of temporary and permanent deferrals have a direct impact on blood inventory levels. Therefore, investigating the rates of permanent and temporary deferrals among donors and analyzing their trends is a critical issue in the fields of health management and blood supply. This study aims to determine the annual rates of temporary and permanent deferrals in Tehran province over the period from 2015 to 2024. Methods: In this retrospective descriptive study, the frequency of temporary and permanent blood donor deferrals across all blood transfusion centers in Tehran province was extracted from the Negareh system for the period spanning 2015 to 2025. To analyze the trends of temporary and permanent deferrals, a piecewise Poisson regression model was utilized. The Akaike Information Criterion (AIC) and the grid search method were employed to identify the number and timing of change points. All statistical analyses were performed using R software, version 4.4.1. Results: During the study period, a total of 4,216,638 blood donation visits were recorded. Of these, 575,234 cases (13.6%) were associated with temporary deferral, and 118,472 cases (2.8%) with permanent deferral. The analysis of the study period revealed that the trend of temporary deferrals changed in the years 2017 and 2022. Specifically, a decrease of 2.9% was observed from 2015 to 2016. This trend was increasing from 2017 to 2022, showing a growth of 3.2% (considering the occurrence of the COVID-19 pandemic from 2019 to 2021). In the period from 2022 to 2024, a decrease of 17.9% was again recorded. The distribution of donor types (first-time, lapsed, regular) with temporary deferral is presented in the chart below: During the study period, it was observed that the trend of permanent deferrals changed in the years 2017 and 2018. Specifically, a 50.7% increase was observed from 2015 to 2017; however, in the period from 2017 to 2018, the rate of permanent deferral decreased by 14.2%. Subsequently, in the period from 2018 to 2024, an average annual decrease of 2.8% in the rate of permanent deferral was recorded. The distribution of donor types (first-time, lapsed, regular) with permanent deferral is presented in the chart below: Conclusion: The ten-year review of blood donor deferral trends in Tehran province demonstrated that the pattern of deferrals was not uniform over time and underwent distinct structural changes. The higher proportion of temporary deferrals and the concentration of cases among first-time donors indicate that the observed changes are largely influenced by screening patterns and donor demographic characteristics, particularly donation history and health

status. These results highlight the importance of continuous monitoring of deferral indicators and special attention to screening processes and the management of new donors.

Keywords: Blood Donors, Blood Donation, Deferral from Blood Donation

P48

Evaluation of a Rapid Approach to Resolve Cold Agglutinin Interference in CBC Testing

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Introduction: Cold Agglutinin Disease (CAD) is a rare form of autoimmune hemolytic anemia, primarily mediated by IgM antibodies. These antibodies bind to antigens on the red blood cell membrane (mainly I/i) at temperatures below their thermal threshold, activating the classical complement pathway and causing red blood cell agglutination. This phenomenon is recognized as a persistent and significant artifact in the accuracy of Complete Blood Count (CBC) results and can lead to spurious results and subsequent clinical misdiagnosis. The standard traditional method to resolve this interference is pre-warming the blood sample at 37°C for 15–30 minutes. Although effective, its prolonged duration presents a significant challenge in the laboratory workflow and can lead to a considerable delay in Turnaround Time (TAT). The present study aims to review recent evidence supporting a rapid warming approach to overcome this challenge. Methods: A targeted search was conducted in PubMed for articles on Cold Agglutinin interference in CBC. An original study evaluating the 2-minute pre-warming method at 41°C on 32 clinical samples was selected as the primary source of evidence, and its findings were analyzed alongside other relevant literature. Results: The evidence review confirmed the classic interference pattern, which includes a falsely low Red Blood Cell count (RBC), a paradoxically elevated Mean Corpuscular Volume (MCV), and a strikingly implausible increase in Mean Corpuscular Hemoglobin Concentration (MCHC), typically exceeding 36 g/dL. The key finding of this review is the validation of a novel rapid warming approach as a credible alternative to the traditional method. According to the pivotal study, pre-warming samples at 41°C for only 2 minutes completely reversed the agglutination and corrected the CBC results without damaging the cells. This new approach showed no statistically significant difference compared to the standard 37°C method, while reducing the waiting time by more than 90%. Discussion and Conclusion: Credible new evidence demonstrates that the rapid warming approach of 41°C for 2 minutes is a simple, safe, and significantly more efficient solution than the traditional method. This approach, requiring no specialized equipment, dramatically reduces the test processing time and directly contributes to improving operational efficiency and enhancing the quality of laboratory services.

Keywords: Cold Agglutinin, Quality Control, Hematology, Sample Warming, MCHC

P49

Comparison of the Efficacy of Ferric Carboxymaltose Versus Iron Sucrose in Correcting Iron Deficiency Anemia and Reducing Blood Transfusion in Patients Undergoing Cardiac Surgery

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Background: Preoperative anemia is common in cardiac surgery and increases allogeneic blood transfusion, morbidity, and mortality. This study compared the efficacy of ferric carboxymaltose (FCM) versus iron sucrose (IS) in correcting iron deficiency anemia (IDA) and reducing perioperative transfusion. Methods: Randomized open-label trial in 66 IDA patients (Hb<13/12 g/dL for men/women; ferritin<100 ng/mL or 100–299 with TSAT<20%) undergoing elective cardiac surgery. Patients received single-dose FCM (1000 mg, n=30) or multi-dose IS (n=32) 3–5 weeks preoperatively. Hemoglobin (Hb), ferritin, TIBC, reticulocyte count, and transfusion requirements (RBC, FFP, platelets) were measured before and after iron therapy, and 3–5 days post-surgery. Trial registered under IRCT20170705034908N3. Results: Baseline characteristics were similar. Preoperative ferritin increased significantly more with FCM than IS (592.6±206 vs. 390±186.5 ng/dL, p<0.05). Postoperative Hb dropped similarly (FCM: 9.6±1.1 vs. IS: 9.9±1.0 g/dL, p>0.05). Transfusion rates did not differ (RBC: FCM 90% vs. IS 76.9%; FFP: 13.3% vs. 15.4%; platelets: 6.7% vs. 8.4%; all p>0.05). ICU stay (3.1±0.9 vs. 3.3±1.1 days, p=0.6) and hospital stay (9.3±3.2 vs. 7.6±0.7 days, p=0.06) were comparable. Conclusion: FCM achieves superior iron repletion but does not improve postoperative Hb or reduce transfusion compared to IS in cardiac surgery patients. Surgical bleeding and bypass-related hemodilution likely override any transfusion-sparing effect. FCM offers the advantage of single-dose administration with good patient tolerance.

Keywords: Cardiac surgery, Iron Deficiency, Ferric Carboxymaltose, Blood Transfusion

Coagulation Disorders & Thrombosis

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Impact of TauroLock™-HEP500 Versus Unfractionated Heparin for Prevention of Catheter Complications in Children with Malignancy: a Prospective, Randomized, Controlled Study

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Background: and aims Central venous catheters (CVCs) are essential for drug delivery in pediatric oncology patients but are associated with complications such as infection and thrombosis. This study aimed to compare the effects of taurolidine–citrate and unfractionated heparin lock solutions on catheter function, infection and thrombosis rates, and inflammatory markers in children with malignancies. Methods In this randomized, controlled trial, 76 pediatric oncology patients were allocated to receive either TauroLock™-HEP500 (containing taurolidine, 4% citrate, and 500 IU/mL heparin) or standard unfractionated heparin as the catheter lock solution. Patients were followed for 6 months. Laboratory evaluations, including complete blood count (CBC), high-sensitivity C-reactive protein (hs-CRP), and interleukin-6 (IL-6), were performed at baseline, 1 month, and 6 months, or upon clinical suspicion of infection. Results At 6 months, hs-CRP levels were significantly lower in the taurolidine–citrate group (2.1 ± 0.2 vs. 5.5 ± 2.2, $p = 0.001$), as was total WBC count (3792.1 ± 325.3 vs. 4994.5 ± 462.1, $p = 0.028$). IL-6 levels showed no statistically significant difference (9.2 ± 1.9 vs. 14.0 ± 3.1, $p = 0.067$). The incidence of catheter-related infections (HR 3.55, 95% CI 0.68–18.4, $p = 0.460$) and thrombosis (HR 4.13, 95% CI 0.43–39.91, $p = 0.221$) did not differ significantly between groups. Conclusion Taurolidine–citrate exhibited a modest anti-inflammatory effect, reflected by reduced hs-CRP and WBC levels, without significant improvement in catheter-related complications or IL-6. The lack of major clinical benefit may relate to the heterogeneous and immunocompromised nature of pediatric oncology patients. Larger, adequately powered studies are warranted to clarify the long-term efficacy and safety of taurolidine–citrate in this population.

Keywords: Catheter dysfunction, CRBSI, Malignancy, Lock Therapy, Heparin, Taurolidine

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Evidence-based Correction of Coagulopathy as a Vital Pillar of Patient Blood Management in Critical Bleeding

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Background: Critical bleeding (CB) is defined as a rapid loss of blood volume that needs massive transfusion. This major hemorrhage combined with the physiological stress of massive transfusion, can start coagulopathy. Patient Blood Management (PBM) is an evidence-based procedure emphasizing that survival depends not only on transfusion but on early hemorrhage control, physiological stabilization, and targeted correction of coagulopathy. Despite advances in PBM literature for managing CB, mortality rates remain high (19.4%). To help reduce the gap between evidence and bedside practice, this study summarizes the key recommendations about preserving hemostasis in CBs. Methods Based on the latest search in PubMed, Scopus, and google scholar on 15 August 2025, two major hemorrhagic guidelines were founded. The 2024 guideline, which is an updated version of the 2011 edition, was included in our study. In this update, the data of all randomized clinical trials and cohort studies till 2023 was systematically reviewed and meta-analyzed. Results In patients with CB, a minimum of 1 unit of FFP with every 2 units of packed cells was suggested to reduce mortality rate. The early use (within 3 hours) of tranexamic acid as part of a PBM in CBs is recommended, though not for gastrointestinal CBs. The use of viscoelastic hemostatic assays may be beneficial to guide therapy in patients with CBs. However, Fibrinogen concentrate and recombinant activated factor VII are not recommended for general CB. They were just recommended in patients with congenital fibrinogen deficiency congenital FVII deficiency. Discussion Effective CB management requires a comprehensive PBM strategy through integrated use of blood components, early antifibrinolytics, and targeted therapies. While current evidence suggests potential benefit, limitations continue to restrict their use. High-quality multidisciplinary efforts are needed to stablish and perform these protocols based on Iranian blood transfusion politics in Iranian hospitals.

Keywords: Patient Blood Management, Critical Bleeding, Hemostasis, Major Hemorrhage

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A Comparative Study on the Effect of Temperature Changes on the Storage of Platelet Concentrates

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Introduction Platelets, as key elements of primary hemostasis, play a vital role in the blood coagulation process. Platelet transfusion is a well-established medical procedure widely used in healthcare settings to prevent or treat bleeding. The platelet concentrate (PC) storage condition is 22 ± 2°C under gentle agitation in a platelet incubator by continuous agitation and the use of gas-permeable bags and thus PCs can be stored for up to 5 days. Under this condition, platelet suffers from structural and functional changes, this can lead to reduced platelet survival and function, and is known as platelet storage lesion (PSL). Limitation on platelet storage time not only creates logistical challenges for blood transfusion centers but also leads to the wastage of significant quantities of this vital resource. In response to these challenges, researchers have developed alternative methods such as cold storage (1-6°C), lyophilization, and cryopreservation, each offering unique advantages and limitations aimed at increasing product shelf life and improving safety. The choice among these methods depends on the clinical conditions, available facilities, and the patient's therapeutic needs. Methodology This research is a narrative review article that was carried out through a systematic search in esteemed databases such as PubMed, Scopus, Web of Science, Google Scholar, and SID, with no time limitations up to December 2023. Specialized keywords such as "Platelet Storage Lesion," "Cold Storage Platelets," "Cryopreservation," and "Lyophilized Platelets" were searched in combination. The inclusion criteria were original research articles, reviews, and clinical trials related to platelet storage methods and storage-induced damage. From an initial 278 articles, after reviewing titles, abstracts, and full texts, ultimately 72 articles were selected for data extraction and writing this review article. Conclusion The results of this review suggest that storing platelets at room temperature, while enhancing in vivo survival, encounters significant issues such as Platelet Storage Lesion (PSL) and the potential for bacterial contamination, which restricts the product's shelf life to 5-7 days. In contrast, various alternative methods possess distinct advantages and disadvantages: cold storage (1-6°C) is linked to diminished metabolism, an extended shelf life of up to 14 days, and enhanced hemostatic function. However, the survival of platelets in circulation diminishes due to structural alterations and rapid clearance by macrophage. Lyophilization allows for extended storage at room temperature; however, it results in a

significantly reduced in vivo survival rate. On the other hand, Cryopreservation, despite requiring advanced equipment and DMSO, makes multi-year storage possible. The selection of the most effective method for platelet storage depends on clinical conditions and therapeutic priorities: in acute bleeding and critical conditions, cold or cryopreserved platelets with high hemostatic efficacy are preferred, whereas for prophylactic applications, room temperature platelets with longer survival are more suitable. Development of novel technologies and conducting further clinical trials seem essential for the optimization of these methods.

Keywords: Platelet, Platelet Temperature, Platelet Storage Lesion, PSL

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Assessment of Venous Thromboembolism Prevention Practices in Hospitals of Tehran: From Guidelines to Implementation

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Introduction: Venous thromboembolism (VTE) is a common and potentially life-threatening complication of hospitalized patients and can lead to serious outcomes such as death, long-term disability, and prolonged hospital stay. Although VTE is largely preventable, preventive measures are still not implemented in an integrated and systematic manner in many hospitals. Consistent use of validated risk assessment models (RAMs) and evidence-based thromboprophylaxis policies plays a key role in reducing the incidence of VTE and is recommended as a standard of clinical care. Despite the fact that the Iranian healthcare system has taken pioneering steps in issuing official VTE prevention guidelines for certain high-risk settings, such as orthopedic surgery and the antepartum and postpartum periods, the extent of real-world implementation, clinical adherence, and integration of these recommendations across hospitals in Tehran has not been systematically evaluated. Moreover, in other clinical wards with a considerable risk of VTE, it remains unclear whether routine risk assessment and thromboprophylaxis are performed. Where such measures are applied, it is uncertain whether they follow standardized, unified protocols based on established guidelines or rely mainly on individual physician decision-making without a structured framework. The aim of this study was to evaluate the real-world implementation of RAMs and thromboprophylaxis and to identify existing barriers in hospitals in Tehran, in order to inform strategies for improving and enhancing the quality of care in this field in Iran. Methods: This cross-sectional descriptive study was designed to assess the status of VTE risk assessment and thromboprophylaxis policies in hospitals in Tehran. Data were collected using a 15-item online questionnaire, which was distributed to all hospitals in Tehran through official correspondence with the treatment deputies of Tehran University of Medical Sciences, Iran University of Medical Sciences, and Shahid Beheshti University of Medical Sciences. Results: Out of 162 hospitals in Tehran, 80 questionnaires were returned, of which 64 were eligible for analysis. Key findings included: Venous thromboembolism risk assessment (RAMs): Seventy-six percent of respondents reported that VTE risk assessment models were available and in use in their hospital or clinical ward. However, implementation was heterogeneous: 48% reported the presence of formal, hospital-wide protocols; 30% indicated that RAMs were applied only in selected departments; and 22% reported discontinuation of risk assessment despite previous implementation.

Thromboprophylaxis:Although thromboprophylaxis was performed in 71% of hospitals, substantial variability in reference sources was observed. More than half of respondents (56.8%) relied on national Ministry of Health guidelines, 22.7% followed

physician-specific decision-making or locally defined protocols, and a smaller proportion referred to international guidelines such as those from the American College of Chest Physicians (ACCP). Conclusion: This study demonstrates that while VTE prevention measures are implemented in many hospitals in Tehran, particularly in high-risk wards, the lack of standardization and unified execution remains a significant challenge. Strengthening education, developing uniform national protocols, and enforcing effective monitoring policies may improve the effectiveness of VTE prevention programs at the hospital level.

Keywords: Venous Thromboembolism, Risk Assessment, Thromboprophylaxis, Implementation Barriers, Hospital Policy

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Investigation of the Relationship between the Expression of Pro-Apoptotic Genes (BAK, BAX) and the viability of Platelet Concentrate (PC) During Storage

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Introduction Blood platelets play a leading role in blood hemostasis and thrombosis. One of the most common blood components used is the platelet concentrate (PC), as it prevents bleeding in patients with thrombocytopenia. The PC storage condition is 22 ± 2°C under gentle agitation in a platelet incubator. Under this condition, platelet suffers from structural and functional damage, called platelet storage lesion (PSL), and diminish the durability of platelet. In this regard, platelet apoptosis is one of the most influential agents in PSL and can affect platelet quality during storage. Various pro-apoptotic genes in platelet, such as BAK and BAX are associated with apoptosis in PSL. Despite previous studies, the simultaneous relationship between BAK and BAX gene expression and platelet viability during storage remains unknown. For this reason, this study investigated the relationship between the expression of these genes and platelet survival during platelet concentrate storage. Material and Methods This experimental study was conducted on 10 PC prepared by the PRP method from healthy male donors. Sampling was performed on storage days, day 0 (the day of PC preparation), day 1, 3, 5, and day7.The expression of BAX and BAK genes was measured by Real-Time PCR. Platelet viability was assessed by MTT assay. Statistical analysis was performed using One-way Repeated Measures ANOVA, Friedman test, and Wilcoxon signed-rank test with Bonferroni adjustment as post hoc test. Results The results of this study showed that during seven days of PC storage, a significant decrease in platelet viability was observed based on the MTT assay ($P<0.001$).The mean MTT optical density decreased from 0.8 on day 0 to 0.7, 0.6, 0.5, and 0.3 on days 1, 3, 5, and 7, respectively, indicating a gradual decline in mitochondrial activity and platelet viability during the storage period. Simultaneously with the decrease in viability, the fold change of pro-apoptotic genes BAX significantly increased from 1.05 on day 1 to 2.6 on day 3, 4.05 on day 5 and 5.85 on day 7 compared to baseline (day 0), ($P<0.001$). Also, the fold change of BAK showed a significant increase from 1.06 on day 1 to 2.56 on day 3, 4.37 on day 5 and 7.67 on day 7 compared to baseline (day 0), ($P<0.001$). Conclusion The present study demonstrated that with increasing storage time of PC, the expression of pro-apoptotic genes BAX and BAK significantly increases, while platelet viability simultaneously decreases. This inverse relationship confirms the central role of the mitochondrial apoptosis pathway in PSL. Simultaneous measurement of these two parameters can serve as a tool for monitoring the quality of PC during storage.

Keywords: Platelet Concentrate, BAK, BAX, Apoptotic, Storage

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Investigation of the Relationship between the Expression of Pro-Inflammatory Cytokine Genes (TNF, IL-6, IL-8) and the Viability of Platelet Concentrate (PC) During Storage

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Introduction: Platelet concentrates (PCs) are used as one of the vital products in blood transfusion to prevent and treat bleeding in patients with thrombocytopenia or platelet function disorders. However, the limited shelf life of these products (usually 3 to 5 days at 20-24°C) is one of the main challenges of blood banks due to the risk of bacterial growth and the occurrence of platelet storage lesions (PSL) which can lead to reduce platelet viability. On the other hand, accumulation of pro-inflammatory mediators during PC storage is one of the main causes of PSL and associated with the occurrence of side effects in recipients, such as febrile non-hemolytic transfusion reactions (FNHTR). In addition, the accumulation of cytokines can accelerate platelet apoptosis. Therefore, in this study, we investigated the relationship between the expression of these cytokines and platelet survival during storage. Methods This experimental study was conducted on 10 PC prepared by the PRP method from healthy male donors. Sampling was performed on storage days 0, 1, 3, 5, and 7. The expression of IL-6, IL-8, and TNF-α gene was measured by Real-Time PCR. Platelet viability was assessed by MTT assay based on mitochondrial dehydrogenase enzyme activity. Repeated Measures ANOVA, Friedman test, and Wilcoxon signed-rank test with Bonferroni adjustment as post hoc test. Results The results of this study demonstrated a significant decrease in platelet viability during storage based on the MTT assay ($P<0.001$). The mean optical density decreased from 0.8 on day 0 to 0.7, 0.6, 0.5, and 0.3 on days 1, 3, 5, and 7, respectively, indicating a gradual decline in mitochondrial activity and platelet viability. Simultaneously with the decrease in viability, the fold change of IL-6 significantly increased from 0.97 on day 1 to 1.26 on day 3, 1.6 on day 5 and 6.7 on day 7 compared to baseline (day 0), ($P<0.001$). Also, the fold change of IL-8 showed a significant increase from 2.0 on day 1 to 3.9 on day 3, and 4.74 on day 7 compared to baseline (day 0), ($P<0.001$). TNF-α had a fold change increase from 1.02 on day 1 to 2.56 on day 3, 2.88 on day 5 and 4.78 on day 7 compared to day 0 (baseline) of PC storage. Conclusion This study showed that with increasing storage time of PC, platelet viability decreases and simultaneously the expression of pro-inflammatory cytokine genes, especially IL-6 and TNF-α, increases. This inverse relationship confirms

the role of inflammatory pathways in the pathogenesis of PSL. Monitoring the expression of these genes can serve as a marker for evaluating the quality of platelet concentrates and predicting inflammatory complications after PC transfusion.

Keywords: IL-1, IL-6, IL-8-platelet concentrate-storage

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Evaluation of Mitochondrial DNA Levels in Red Blood Cell Bags and Their Correlation with Expiration

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Introduction: Mitochondrial DNA (mtDNA) can be released extracellularly due to cellular stress or mitochondrial membrane damage, and possesses unique characteristics owing to its circularity, lack of histones, and resemblance to bacterial DNA. The levels of free mtDNA in Red Blood Cells (RBCs) bags can be affected by oxidative stress and metabolic changes during storage and may be considered as an indicator of blood product quality. This study investigated the relationship between mtDNA levels in RBCs bags and product expiration. Material and methods: Mitochondrial DNA (mtDNA) levels were quantified in 22 donated red blood cell (RBCs)units. DNA was extracted using silica columns, and the ND6 gene was targeted via real-time PCR with SYBR Green on a Rotor-Gene Q. A BMV probe served as a positive control, confirming amplification and assessing PCR efficiency. Primer efficiency was determined using a standard curve from serially diluted PCR products. Samples were run in duplicate. Statistical analysis, performed in R software, included Spearman's correlation coefficient and quantile regression. The method for calculating the number of amplified products by real-time PCR was as follows: ND6 gene size: 108 bp Gene Concentration: 28.4 ng/µl Molecular weight: 108 × 650 daltons/bp (g/mole) =70200 Moles/µl :28. 4×10-9 70200 =404 ×10 -15 Molecules/µl: 404×10-15 ×6.023 ×1023 =24.3 ×1010 Results Blood bags were stored for an average of 17.7±5.5 days (range: 5-25 days). RBCs bags exhibited mtDNA copy numbers ranging from 0.001 X105 to 92.900 X105 ng/µl, with a median of 3.526 X105 ng/µl. A significant correlation was observed between storage time and mtDNA levels (rho=0.42, p=0.049), with quantile regression indicating a median increase of 0.456 mtDNA copy units per day of storage. This study revealed a significant positive correlation between RBCS bags' storage time and free mitochondrial DNA (mtDNA) levels. Extended storage leads to a substantial increase in mtDNA copies, likely due to oxidative stress and mitochondrial damage. Therefore, mtDNA measurement in packed red blood cells could serve as a quantitative biomarker to assess product quality during shelf life of optimizing consumption time. Conclusion: There is a positive and significant correlation between the storage time of RBC bags and the amount of free mitochondrial DNA (mtDNA). As the storage time of the product increases, the number of mtDNA copies increases significantly.

Keywords: Mitochondrial DNA, Expiration, Red Blood Cell Bags

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Heparin-Induced Thrombocytopenia and its Correlation with Clinical Outcome in Patients Admitted to Hamedan Besat Hospital in 2023

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Background: Thrombocytopenia is common among ICU patients and may increase morbidity, mortality, transfusion requirements, and healthcare costs. Heparin-induced thrombocytopenia (HIT) is an immune-mediated adverse reaction to heparin, particularly unfractionated heparin, caused by antibodies against the heparin–platelet factor 4 (PF4) complex. Early recognition is critical due to its potential impact on clinical outcomes. Methods: In this cohort study, 200 ICU patients receiving heparin at Besat Hospital, Hamedan, were evaluated. Platelet counts were measured before and 72 hours after heparin administration. Anti–PF4/heparin antibodies were assessed, and demographic data, underlying conditions, ICU length of stay, and final outcomes were recorded. Data were analyzed using SPSS version 26. Results: Mean platelet counts decreased from $211\times10^3/\mu L$ to $190\times10^3/\mu L$ after 72 hours. HIT was diagnosed in 9 patients (4.5%). Overall mortality was 17.5%. No significant differences were observed between HIT-positive and HIT-negative groups regarding age, gender, ICU stay, admission cause, or baseline platelet count. However, mortality was significantly higher in patients with HIT (77.8% vs. 14.7%, $P<0.001$). Conclusion: HIT was significantly associated with increased mortality in ICU patients. Early detection and careful monitoring of thrombocytopenia following heparin administration may improve clinical management and patient outcomes.

Keywords: Heparin-Induced Thrombocytopenia, Platelet Count, ICU, Mortality

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Factor VII Padua Variant: A Comprehensive Systematic Review of Reported Cases, Diagnostic Approaches, Clinical Presentations, and Treatment Considerations

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Background: Factor VII (FVII) Padua represents an uncommon hereditary coagulation disorder attributable to a missense mutation in the F7 gene (Arg364Gln), which leads to variable FVII activity levels depending on the thromboplastin reagent employed during laboratory assessment. Despite its established association with a hypercoagulable state, substantial knowledge gaps persist regarding its diagnostic criteria, clinical spectrum, and worldwide prevalence patterns. Methods: In accordance with PRISMA recommendations, a comprehensive literature search was performed across PubMed, Scopus, and Web of Science databases up to February 2026 to retrieve publications documenting cases of FVII Padua. Relevant data encompassing patient demographics, laboratory parameters, and hemorrhagic or thromboembolic events were systematically extracted from all eligible sources. Results: A total of 36 publications encompassing 75 patients were included. The predominant countries of origin were Italy (22.6%), Iran (20.0%), the United States (16.0%), France (10.6%), and Brazil (9.3%). Patient ages spanned from 5 to 79 years, with a marginally greater proportion of female (36%) compared to male (30.7%) individuals. Notably prolonged prothrombin time (PT) alongside substantially diminished FVII activity when rabbit-brain thromboplastin reagents were used constituted the hallmark diagnostic profile, whereas human or recombinant thromboplastin sources yielded comparatively modest reductions. Approximately half of all patients (n = 28; 49%) remained clinically asymptomatic; nevertheless, severe hemorrhagic complications were documented in a subset, including postpartum hemorrhage (PPH) (n = 1; 1.7%) and gastrointestinal bleeding (GIB) (n = 3; ~5%). Thromboembolic complications were recorded in 6 of 13 patients (46%), encompassing deep vein thrombosis (DVT) in two individuals (33.3%) and pulmonary embolism (PE) in one patient (16.6%). Conclusions: The present review highlights the broad geographical distribution and considerable clinical heterogeneity characterizing FVII Padua, underscoring the critical importance of thromboplastin-specific diagnostic protocols and patient-tailored therapeutic strategies. Additional investigations are

warranted to bridge the current gaps in both diagnosis and clinical management of this condition.

Keywords: Factor VII Padua, Arg364Gln, FVII Deficiency, Rare Bleeding Disorders, Thrombosis

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Diagnostic Value of Normal or Near-Normal Factor VIII Levels in Excluding Bleeding Disorders

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Background: Factor VIII (FVIII) is an essential coagulation protein used for diagnosing bleeding disorders, particularly hemophilia A and von Willebrand disease (VWD). FVIII levels are commonly used to evaluate bleeding risk, with normal or near-normal levels often being interpreted as evidence against significant bleeding disorders (Mannucci & Tuddenham, 2001). However, FVIII levels are subject to numerous biological and environmental influences, such as hormonal fluctuations, pregnancy, stress, and inflammation, which can alter FVIII activity without indicating a true underlying bleeding disorder (Goudemand & Manco-Johnson, 2013). This systematic review examines the diagnostic utility of normal or near-normal FVIII levels in both men and women Methods: A comprehensive search was conducted in PubMed, Scopus, and Web of Science databases through December 2025. The following terms were used: “factor VIII,” “bleeding disorders,” “hemophilia A,” “von Willebrand disease,” “normal factor VIII,” and “diagnosis.” Inclusion criteria were clinical studies, cohort studies, and observational studies involving FVIII activity measurement in patients with bleeding symptoms. Studies focusing on severe hemophilia A or animal models were excluded. Data were extracted by two independent reviewers on FVIII levels, bleeding phenotype, and final diagnosis, with disagreements resolved through consensus (Liberati et al., 2009) Results: From the 37 eligible studies (covering over patients), normal or near-normal FVIII levels were found in approximately 60% of individuals with clinically significant bleeding symptoms. This was particularly common in women, as well as patients with mild hemophilia A and VWD. Despite FVIII levels being within normal reference ranges, a substantial proportion of these patients exhibited severe bleeding events (Goudemand & Manco-Johnson, 2013). FVIII activity was found to be influenced by pregnancy, estrogen therapy, and inflammatory conditions, often resulting in transiently elevated FVIII levels in otherwise healthy individuals (Peyvandi & Garagiola, 2016). Several studies showed a weak correlation between FVIII levels and bleeding severity, indicating that FVIII testing alone lacks diagnostic sensitivity. In particular, FVIII levels failed to distinguish between mild bleeding disorders and healthy individuals in many cases. (Goudemand & Manco-Johnson, 2013) Conclusion: Normal or near-normal FVIII levels are not sufficient to exclude bleeding disorders, particularly in individuals with mild bleeding symptoms. FVIII activity is influenced by various physiological and environmental factors, which

can result in misleadingly normal values. Relying solely on FVIII levels to rule out bleeding disorders may lead to diagnostic delay or misclassification. A comprehensive diagnostic approach, including detailed clinical history, repeat testing, and additional coagulation assays, is essential to accurately diagnose bleeding disorders in both women and men (Peyvandi & Garagiola, 2016).

Keywords: Factor VIII, Bleeding Disorders, Hemophilia A, von Willebrand Disease

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Hemophilia a and Mim8 in Prophylactic Treatment

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Background: Hemophilia A is a hereditary bleeding disorder caused by factor VIII deficiency, leading to spontaneous bleeding and progressive joint damage. Prophylactic treatment with recombinant factor VIII (rFVIII) remains the standard approach, but frequent infusions can reduce adherence and affect quality of life (Bennett et al., 2020). Mim8, a bispecific monoclonal antibody, is emerging as a promising alternative, mimicking factor VIII activity while potentially reducing injection frequency (White et al., 2023). Methods: This systematic review was conducted through a systematic literature search of PubMed, Scopus, and the Cochrane Library for studies published between 2015 and 2025, using keywords including “Hemophilia A,” “Mim8,” “prophylaxis,” and “factor VIII.” Clinical trials, meta-analyses, and systematic reviews evaluating prophylactic therapies for Hemophilia A were included. Key outcomes extracted included annual bleeding rate (ABR), infusion frequency, and safety profiles. Results: Nine studies met inclusion criteria. Clinical trials indicated that Mim8 effectively reduced ABR compared with conventional rFVIII therapy (median ABR: 1.5 vs 3.8 episodes/year) (Bennett et al., 2021; Peyvandi et al., 2023). Patients on Mim8 required fewer infusions per month (1–2 vs 2–3 with rFVIII), contributing to improved adherence and quality of life(Gonzalez et al., 2022). Safety analyses revealed a lower incidence of infusion-related reactions and inhibitor development in Mim8-treated patients. Meta-analyses support that Mim8 provides comparable or superior efficacy to standard prophylaxis while decreasing treatment burden (Zhang et al., 2024). Conclusion: Mim8 shows significant potential as a prophylactic therapy in Hemophilia A, offering effective bleed prevention with reduced infusion frequency. These features may enhance adherence and patient quality of life. Long-term studies are warranted to confirm safety and solidify Mim8’s role as a standard prophylactic option.

Keywords: Hemophilia A, Factor VIII, Bleeding disorders

Diagnostic Methods of Prevalent Parasitic Diseases in Iran

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Prevalence and Some Associated Risk Factors of Oral Cavity Protozoa Among Autoimmune Disease Patients with Oral Lesions in Kashan, Iran, 2023

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Objectives: Two oral cavity protozoa that are commonly detected in patients with different kinds of periodontal disorders are Entamoeba gingivalis and Trichomonas tenax. The potential role of these protozoa in dental caries and oral infectious diseases remains unknown. The present study aims to determine the prevalence of these protozoa and some associated risk factors among patients with autoimmune diseases and oral lesions. Methods: This study was randomly conducted on 122 patients who suffered from autoimmune diseases and oral lesions referring to dental clinic centers in Kashan, in the center of Iran. Two specimens were obtained from oral lesions and saliva for each patient. The samples were immediately examined under a light microscope using wet mount preparation and stained with Giemsa and trichrome. Furthermore, the samples were cultured in Robinson's and diphasic Locke-egg media. Results: T. tenax and E. gingivalis protozoa were found in 12 (9.8%) and 7 (5.7%) of patients, respectively. The highest prevalence rate of total infections was found among patients with lupus erythematosus (20%) and lichen planus (17.9%). The lowest rate belonged to patients with psoriasis (11.1%). There was no significant difference between infection rates and autoimmune diseases (P = 0.0946). In the multivariate model, the frequency of parasites was significantly associated with age (P = 0.0374), brushing teeth, and the presence of dental caries (P = 0.0001).

Keywords: Dental Caries, Entamoeba Gingivalis, Trichomonas Tenax, Autoimmune Disease, Iran

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Nanotechnology in Diagnosis of Cryptosporidiosis: Improving the Quality of Laboratory Services in Rural Communities in Iran

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Introduction: Cryptosporidiosis is a parasitic disease caused by Cryptosporidium parvum, and is one of the most common waterborne parasitic diseases, which often result in severe cases of diarrhoea, dehydration and even death especially in immunocompromised individuals, young children and livestock. This infection is a major problem especially in rural communities of Iran where people face challenges of having access to safe water and modern laboratory facilities. Traditional methods of diagnosis, which are predominantly founded on microscopy and immunological assays, have low sensitivity levels, long processing times, and require advanced instruments. The aim of the present study was to review the nanotechnology interventions, such as gold, silver, and zinc oxide nanoparticles, and nano-PCR and nanoscale biosensor approaches, to increase the accuracy of the cryptosporidiosis diagnosis and the quality of laboratory services in rural areas of Iran.Methods: This systematic review was done using the PRISMA guidelines. Scientific databases including PubMed, Scopus, Web of Science, Magiran, SID, ScienceDirect, and Google Scholar were searched for articles published between 2000 and 2025. The keywords used were Nanotechnology, Nanoparticles, Cryptosporidium parvum, Detection, Diagnosis, and Biosensors. A total of 45 articles were selected for analysis.Results: The data demonstrated that nano-PCR tests using the gold nanoparticles (AuNPs) attained a tenfold enhanced diagnostic sensitivity that was in a position to recognize target DNA sequences (such as the cgd1_330 gene) with an amount of 10^2 picograms of DNA, without any cross-reactivity with other species of Cryptosporidium. Electrochemical biosensors that utilized gold nanoparticles and aptamers revealed a detection limit of 40-100 oocysts per mm^2 in water and feces thus decreasing the assay time to less than 30 minutes. These technologies have the potential to reduce prices, increase the accuracy of diagnosis, and assist in disease control in the rural Iranian communities. In addition, recent studies have also emphasized the effectiveness of zinc oxide nanoparticles (ZnO NPs) in the lysis of oocysts and release of DNA that could be amplified through downstream PCR.Conclusion: Nanotechnology use in the diagnosis of cryptosporidiosis has significant potential to significantly enhance the quality of laboratory services in rural communities of Iran to provide low-cost, sensitive, and rapid

modes of testing. These innovations are not only capable of early detection, but also play a significant role in preventing waterborne outbreaks. Future research should focus on developing portable diagnostic kits to improve accessibility in remote regions.

Keywords: Nanotechnology, Nanoparticles, Cryptosporidium parvum, Detection, Diagnosis, Biosensors

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In Vitro Evaluation of Apigenin-Coated Silver Nanoparticles Against Trichomonas Vaginalis: A Potential Alternative to Metronidazole

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Bakground: Trichomonas vaginalis is a protozoan parasite responsible for trichomoniasis, a prevalent sexually transmitted infection. Metronidazole is the standard treatment; however, concerns regarding side effects and emerging resistance necessitate the exploration of alternative therapies. Methods: This study aimed to evaluate the antiparasitic activity of silver nanoparticles coated with apigenin (Api@AgNPs) against T. vaginalis trophozoites in vitro. The nanoparticles were synthesized via a green synthesis method and characterized using UV-Vis spectroscopy and transmission electron microscopy, confirming an average size of 38.3 nm with a quasi-spherical morphology. Trophozoites were exposed to varying concentrations of Api@AgNPs and metronidazole for 24 and 48 hours. Viability was assessed using Trypan blue staining, and CC_{50} values were determined by probit regression. Results: Api@AgNPs exhibited CC_{50} values of 111.211 µg/mL and 81.331 µg/mL at 24 and 48 hours, respectively, compared to 107.09 µg/mL and 76.542 µg/mL for metronidazole. Conclusion:These findings suggest that Api@AgNPs possess promising anti-trichomonal activity and may serve as a potential therapeutic agent alone or in combination with metronidazole, pending further in vivo validation.

Keywords: Apigenin-Coated Silver Nanoparticles, Trichomonas Vaginalis, Metronidazole, Nanomedicine, Antiparasitic Therapy

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Ectopic Demodicosis: Case Series

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Background: Demodex mites are dermoparasites of pilosebaceous and sebaceous glands, almost found on the face including cheeks, nose, chin, forehead, eyelashes, temples and balding scalp and less in other seborrheic regions. Demodex infestation usually remain asymptomatic in normal individuals, but may cause pathogenic symptoms when present in high densities and in immunocompromised patients. Methods: In this report 12 cases (6 male and 6 female) of ectopic demodicosis from Southwest Iran in 2024 are presented. The patients were referred to Iran Zamin Medical Diagnostic Laboratory for fungal examination (9 cases for dermatophytosis, 2 specimens were nasal discharge and 1 specimen was ear discharge. Results: Scraping from the skin lesions, slide preparation with 20% KOH and microscopic examination revealed just Demodex folliculorum in 5 cases, 1 case with intertriginous candidiasis, in 2 cases co- infection of demodicosis and dermaphytosis, in 1 case with otomycosis (Asperglosis), in 1 case with nasal discharge candidiasis and in 1 case of nasal discharge only Demodex folliculorum was revealed. The patients were referred to their physicians for appropriate treatment. Conclusion: Ectopic demodicosis should be considered during the examination of specimens.

Keywords: Demodicosis, Ectopic, Fungi

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Investigation of the Expression Levels of miR-155, miR-133a, and miR-146b in the Serum of Acute and Chronic Forms of Cutaneous Leishmaniasis

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Background Leishmaniasis is a vector-borne infectious disease caused by intracellular protozoan parasites of the genus Leishmania. MicroRNAs (miRNAs) can influence the progress and outcome of the disease. This study aimed to investigate the expression levels of miR-155, miR-133a, and miR-146b in the serum of acute and chronic forms of cutaneous leishmaniasis (CL) in Iran. Methods Samples were collected from 30 clinical cases of CL in Golestan province, who suffered from either acute or chronic forms of the disease, including 15 for each. Leishmania species were identified using PCR (kDNA gene). Total RNA was extracted from serum samples, complementary DNA (cDNA) was synthesized based on the loop technique, and the expression levels of miRNAs (miR-155, miR-133a, and miR-146b) were determined through quantitative real-time PCR analysis. Results Conventional PCR on kDNA confirmed the presence of L. major in 30 patients. Healing after one course of treatment and no response to treatment were considered as acute and chronic forms, respectively. Although there were no statistically significant changes, the expression of miR-133a and miR-155 was upregulated in patients with acute CL compared to those with chronic form, while miR-146b was downregulated in patients with acute CL. Conclusions In the current study, the expression changes of miR-155, miR-146b, and miR-133a in acute patients was compared to those patients with chronic CL. Although it was not significant, alterations in the expression levels of miRNAs were observed between acute and chronic forms of CL suggesting different pathogenesis of clinical forms.

Keywords: Cutaneous Leishmaniasis, miR-155, miR-133a, and miR-146b

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Modeling the Impact of Climate Change on Cutaneous Leishmaniasis using Artificial Neural Networks

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Background: Climate change plays an important role in the spread of vector-borne diseases, including cutaneous leishmaniasis (CL). This study aimed to investigate the effects of climate change on CL incidence in central Iran using artificial neural networks (ANNs). Methods: The Gamma model was applied to determine the minimum prediction error and the optimal lag time. Future climate conditions were simulated using general circulation models (GCMs) under the RCP2.6 and RCP8.5 scenarios. ANN modeling was then used to evaluate the impact of climatic variables on disease trends. Results: The findings showed that temperature and precipitation were the main factors influencing CL incidence, and a 100-day lag time provided the best predictive performance. ANN analysis identified maximum temperature and rainfall as the strongest predictors of disease outbreaks. Climate projections indicated that the study area will become warmer by 2050. Under the RCP8.5 scenario, CL cases are expected to increase, whereas the trend remains relatively stable under RCP2.6. Seasonal patterns of the disease are also predicted to remain unchanged. Conclusion: ANN modeling is an effective tool for predicting CL trends and identifying high-risk areas under climate change conditions. These findings can support public health planning and improve disease prevention and control strategies.

Keywords: Cutaneous Leishmaniasis, Climate Prediction, GCMs, RCP Scenarios, Iran

Diagnosis and Therapy Monitoring in Acute Hematopoietic Neoplasms

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Hematologic Malignancies and an Overview of Emerging Therapies for Hematologic Malignancies: a Systematic Review

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Hematologic malignancies remain a major therapeutic challenge due to disease heterogeneity, treatment resistance, and significant toxicity associated with conventional therapies. In recent years, rapid advances in molecular oncology and immunotherapy have led to the development of multiple emerging therapeutic strategies. This review synthesizes evidence on novel approaches, including targeted therapies such as BTK inhibitors (e.g., ibrutinib), BCL-2 inhibitors (e.g., venetoclax), FLT3 and JAK inhibitors, and next-generation monoclonal and bispecific antibodies that enhance immune-mediated cytotoxicity. In addition, gene- and cell-based modalities—including CAR T-cell therapy and CRISPR-mediated gene correction—have demonstrated promising efficacy, particularly in relapsed or refractory leukemia and lymphoma. Despite these advances, significant limitations remain, including treatment-related toxicities, mechanisms of resistance, high relapse rates after CART therapy, and substantial financial and accessibility barriers. Gaps in predictive biomarkers, optimal sequencing of therapies, and long-term safety also limit widespread implementation. Precision medicine approaches, driven by molecular diagnostics and genomic profiling, continue to refine individualized treatment strategies and hold potential to overcome current challenges. Overall, this review provides an updated and comprehensive evaluation of emerging therapeutic modalities in hematologic malignancies and outlines key areas where further research is critically needed.

Keywords: Hematologic Malignancies, Clinical Trial, Immunotherapies, Precision Medicine, Emerging Therapies

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The Role of Exosomal PD-L1 in AML: A Key Mediator of Immune Evasion and Novel Therapeutic Target

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Background: Immune checkpoint inhibitors (ICIs) have demonstrated limited efficacy as monotherapy in acute myeloid leukemia (AML). Accumulating evidence indicates that exosomal PD-L1 (ExoPD-L1) released by AML blasts plays a pivotal role in driving systemic immunosuppression and conferring therapeutic resistance. This review aims to elucidate the role of ExoPD-L1 as a critical barrier to effective immunotherapy in AML. Methods: This review synthesizes recent preclinical and clinical studies investigating the biological functions and clinical relevance of ExoPD-L1 in AML pathogenesis. Results: AML-derived exosomes are highly enriched with functional, membrane-bound PD-L1. Mechanistically, ExoPD-L1 potently suppresses innate anti-leukemic immunity by engaging PD-1 on natural killer (NK) cells, thereby reducing degranulation and interferon-gamma secretion, ultimately impairing cytotoxic function. Moreover, elevated circulating levels of ExoPD-L1 function as a systemic "decoy," sequestering therapeutic antibodies before they reach the tumor microenvironment and directly contributing to ICI resistance. Importantly, ExoPD-L1 has emerged as a robust negative prognostic biomarker, predicting poor survival independently of blast membrane PD-L1 expression. Preclinical evidence indicates that this resistance mechanism can be overcome through combination immunotherapy targeting co-inhibitory receptors such as TIM-3 and LAG-3, which are co-expressed on exhausted immune effector cells. Conclusion: ExoPD-L1 functions as an active mediator of immune evasion in AML, primarily by suppressing NK cell activity and conferring resistance to ICI therapy. Measurement of circulating ExoPD-L1 holds significant prognostic value. Future therapeutic strategies must target this pathway, likely through rational combination immunotherapies, to improve clinical outcomes in AML.

Keywords: AML, ICI, PD-L1, Exosome, ExoPD-L1

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Association of Telomere Biology Markers with Diagnosis and Prognosis in Acute Lymphoblastic Leukemia: A Systematic Review and Meta-Analysis

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Background: Acute Lymphoblastic Leukemia (ALL) is the most common malignancy in children and remains a major clinical challenge in adults and those with relapsed or refractory disease. Telomere biology, including telomere length (TL), telomerase activity (TA), and hTERT expression, has been implicated in cancer development and progression. However, the role of these markers in ALL diagnosis and prognosis remains inconsistent across studies, necessitating a comprehensive synthesis of existing evidence. Methods: A systematic review and meta-analysis was conducted following PRISMA 2020 guidelines. Electronic databases (PubMed, Scopus, Web of Science, Cochrane Library) were searched up to October 2025. Inclusion criteria were observational studies comparing telomere biology markers in ALL patients versus healthy controls or stratified by clinical outcomes. Data on telomere length, telomerase activity, and hTERT expression were pooled using random-effects models. Subgroup analyses by age (pediatric vs. adult) and heterogeneity were assessed using I^2 statistics. Results: Twenty studies were included. ALL patients showed significantly shorter telomeres compared to controls (SMD = −2.027; 95% CI −3.307 to −0.746; I^2 = 98.32%, $P < 0.001$), with consistent findings in both pediatric and adult populations. Telomerase activity and hTERT expression were also significantly elevated in ALL patients (SMD = 1.937; 95% CI 1.336 to 2.538 and 1.141; 95% CI 0.749 to 1.534, respectively). Subgroup analyses confirmed these associations across age groups. However, the prognostic significance of these markers was less clear. While some studies linked higher telomerase activity or hTERT expression to worse outcomes, others reported no significant association or even contradictory results. Heterogeneity was substantial, likely due to differences in study design, measurement methods, and patient characteristics. Conclusion: Telomere biology markers are significantly altered in ALL patients compared to healthy controls, suggesting their potential as diagnostic indicators. However, their prognostic value remains uncertain due to conflicting findings and methodological variability. Standardization of measurement techniques and larger, well-defined cohorts are needed to validate these markers for clinical use. Future research should also explore the interaction between telomere biology and other molecular pathways to improve risk stratification and treatment strategies in ALL.

Keywords: Acute Lymphoblastic Leukemia (ALL), Telomere Length, Telomerase Activity, hTERT Expression, Prognostic Biomarker

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Evaluating the Spectrum of Germline Predisposition in Acute Myeloid Leukemia: A Comprehensive Study of WHO/ELN Recommended Genes Using ClinVar Database

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Background: The latest WHO and ELN classifications of AML, recommend germline predisposition related genes to be sequenced in AML. Germline predispositions effect on disease occurrence, prognosis, treatment response, relapse, and allogeneic HSCTs. These variants are divided into benign, likely benign, VUS, likely pathogenic, pathogenic. Notably, these classifications lack the information about the prevalence of each type of variant in each recommended gene, and this should be considered that not all have pathogenic impacts. Methods: We assessed each classification recommended gene in the ClinVar database. The obtained data were sorted in a table to analyze the results more properly. Results: Generally, 160630 variants were recognized, divided in subgroups of Deletion, Duplication, Insertion, Indel, and SNPs. The SNPs variants, by having 120806 variants, are the most prevalent type. Among all variants, 38323 were Pathogenic/Likely Pathogenic variants(P/LP). Deletion and SNPs variants have the most P/LP variants (15162 and 9162, respectively). Among all Variants, 288 were P/LP variants related to AML, and SNPs variants, by having 96 P/LP variants related to AML, is the most prevalent. Among 55 genes recommended by WHO and ELN, GATA2, CEBPA, NPM1, and TP53 account for 178, 61, 13, and 9 of P/PL variants related to AML, respectively, which are 261 out of 288 P/LP variants related to AML. Conclusion: The more information about the possible gene variants, like knowing which genes are more likely to have the most pathogenic variants, could be beneficial for a better insight into what germline predispositions are more likely to impact on AML.

Keywords: Germline Predisposition, Sequencing, AML, WHO/ELN Classifications, Bioinformatics

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Targeted Screening of Germline Variants and Gene Expression Profiling in AML with t (8;21): A Novel Scoring System Approach to Overcome NGS Limitations

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Background: Although WHO and ELN guidelines recommend NGS for AML, cost and accessibility limitations hinder its widespread use. We established a cost-effective alternative integrating bioinformatics (using ClinVar/Franklin/VarSome databases) validated by TETRA-ARMS PCR technique to detect germline predispositions in a study identifying differentially expressed genes in AML with t (8;21). Methods: DEG, WGCNA, and Enrichment analyses by R software and GEO database were used to find differentially expressed genes, and validated via Real-Time PCR technique. By designing a scoring system, using ClinVar/Franklin/VarSome databases, we prioritized high-impact pathogenic variants of recommended genes in WHO and ELN classifications to be assessed specifically in our understudied patients, besides evaluating differentially expressed genes in AML with t (8;21). Results: Among 55 genes recommended by WHO and ELN, 160630 variants were recognized. Among all variants, 38323 were Pathogenic/Likely Pathogenic variants(P/LP), which 288 were P/LP variants related to AML, and SNP variants, by having 96 P/LP variants related to AML, is the most prevalent. Using our designed scoring system, based on ClinVar/Franklin/VarSome databases, the top 10 highly pathogenic variants belonging to GATA2, CEBPA, TP53, RUNX1, DDX41 genes were defined and were analyzed in our samples by TETRA-ARMS PCR to evaluate possible germline predisposition pathogenic effects on our patients. Concurrently, DEG and WGCNA analyses using GEO data identified FGL2, IRF8, S100A4, and VCAN overexpression, validated via Real-Time PCR in newly diagnosed t (8;21) patients. Conclusion: This approach facilitates the evaluation of possible presence and pathogenic effects of germline predisposition in patients where NGS is impractical, offering a viable, targeted diagnostic strategy.

Keywords: Germline Predisposition, NGS, AML, WHO/ELN Classifications, Bioinformatics

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The Role of Prognostic Exosomal miRNAs in Acute Myeloid Leukemia: Emerging Biomarkers for Early Detection and MRD Monitoring

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Background: Acute Myeloid Leukemia (AML) is a heterogeneous and aggressive form of blood cancer that is associated with unfavorable long-term outcomes. The 5-year overall survival rates are still low, at about 25-30%, according to estimates derived from 2019 Global Burden of Disease (GBD) statistics. Despite advancements in treatment, relapse rates are still high. These challenges highlight the importance of finding reliable prognostic biomarkers to enhance patient management. Exosomal MicroRNAs (miRNAs) may be recognized as promising minimally invasive prognostic biomarkers in AML. They are protected from degradation, remain stable in body fluids, and more accurately reflect disease biology compared to free-circulating miRNAs. The prognostic value of exosomal miRNAs in AML is examined in this narrative review, focusing on overall survival, treatment response, and MRD monitoring. Methods: In order to compile the most pertinent research on our subject, we searched PubMed, Web of Science, and Google Scholar for articles published between 2015 and 2025. The search strategy included combinations of the keywords “acute myeloid leukemia” (AML), “exosomal miRNAs,” “microRNAs,” “prognosis,” and “biomarkers.” The review focused on human studies investigating the association between exosomal miRNA expression and clinical outcomes in AML patients. Results: Studies show that exosomal miRNAs, including miR-21, miR-10b, miR-125b, and miR-155, are consistently related to adverse clinical outcomes in AML patients. Higher levels of these miRNAs have been linked to lower overall survival, increased relapse risk, and poorer disease-free survival. Also, they can offer a minimally invasive approach to prognostic assessment and disease monitoring because they are easily detectable in body fluids like serum and plasma. However, current evidence remains limited and needs further investigation. Conclusions: Exosomal miRNAs have the potential to serve as prognostic biomarkers in AML, which could aid in risk stratification and the monitoring of MRD. Additional comprehensive studies are required to demonstrate their prognostic and clinical value and to develop guidelines for their use. Future research could aid in the early detection, prediction of treatment responses, and personalized management for patients with AML.

Keywords: Acute Myeloid Leukemia, Exosomal miRNAs, Prognosis, Biomarkers, Overall Survival

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Association of BMI1 Gene rs1042059 and rs11591377 Polymorphisms with Leukemia: Diagnostic and Prognostic Implications

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Background: Hematologic malignancies, which arise from the unregulated proliferation of hematopoietic and lymphoid tissues, account for 6.5% of all cancers globally. A variety of risk factors, including genetic disorders and single nucleotide polymorphisms, contribute to the development of hematologic malignancies. BMI1 is a gene that plays a crucial role in the regulation of self-renewal and differentiation of hematopoietic stem cells. Methods: A total of 69 leukemia patients (comprising 45 with AML, 18 with ALL, and 6 with CML) were selected, along with 80 control samples. The frequencies of the rs1042059 and rs11591377 polymorphisms in the BMI1 gene were assessed using the Tetra-ARMS PCR technique. Results: A statistically significant difference in the prevalence of the rs1042059 and rs11591377 polymorphisms was noted between the patient and control groups (P=<0.001). The occurrence of GA genotypes for both polymorphisms was found to be higher in patients than in the control group. Furthermore, a significant difference was identified in the prevalence of rs11591377 genotypes among the AML, ALL, and CML groups (P=0.002); however, no significant difference was detected in the prevalence of rs1042059 genotypes among these groups (P=0.578). Conclusions: Given the notable reduction in the prevalence of allelic variants in the control group compared to the leukemia group, the association of BMI1 with leukemia should be regarded as a potential diagnostic and prognostic marker.

Keywords: BMI1, Leukemia, Polymorphisms, Hematologic Malignancies, Genotype

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Acute Myeloid Leukemia: Advances in Diagnostic and Monitoring Strategies

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Background: Acute myeloid leukemia (AML) is a hematologic malignancy characterized by diverse molecular and cytogenetic abnormalities. Limited early diagnostic tools and effective therapies contribute to poor clinical outcomes. While bone marrow biopsy remains the gold standard for AML diagnosis, it is invasive, painful, and has low sensitivity. Therefore, identifying robust diagnostic strategies to guide effective therapies is crucial for improving patient prognosis. Methods: A literature review was conducted using Google Scholar and PubMed with search terms including AML, measurable residual disease (MRD), next-generation sequencing (NGS), immunophenotyping, and microfluidic. Finally, 50 related articles were selected from studies of the last 5 years. Results: Accurate AML diagnosis requires a combination of molecular studies, cytogenetic analyses, and immunophenotyping. For example, because AML exhibits high clonal heterogeneity, NGS plays a crucial role in its diagnosis. Some of the most frequently mutated genes in AML include RUNX1, NRAS, and TP53. For patient monitoring and assessment of MRD, RT-PCR and multiparametric flow cytometry are commonly used. Multiparametric flow cytometry is widely employed to detect intracellular and surface markers such as CD13, CD33, and CD34. To improve MRD assessment, highly sensitive approaches such as digital PCR for absolute quantification and emerging microfluidic technologies represent promising advances in AML diagnosis and monitoring. Conclusion: Recent advances in understanding AML pathogenesis and technological development have introduced novel diagnostic and monitoring approaches. These approaches aim to improve sensitivity and specificity for early detection and relapse monitoring, although some require integration with additional confirmatory data to optimize clinical utility.

Keywords: AML Diagnosis, MRD Detection, Immunophenotyping, NGS, RT-PCR

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Beta-Catenin–Associated Transcriptional Signatures and Prognostic Hubs in Acute Myeloid Leukemia CD34⁺ Cells

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Background: Acute myeloid leukemia (AML) is a heterogeneous malignancy driven by impaired differentiation and uncontrolled proliferation of hematopoietic progenitors. Beta-catenin, a key mediator of Wnt signaling, is essential for stem cell maintenance and has been implicated in leukemic stem cell persistence and adverse prognosis. This study investigates beta-catenin-associated transcriptional alterations in AML CD34⁺ cells to identify differentially expressed genes (DEGs), dysregulated pathways, and prognostic hub genes. Methods: Gene expression data from the GSE245305 dataset were analyzed in AML CD34⁺ cells stratified by high versus low beta-catenin expression and compared with healthy CD34⁺ controls. DEGs were identified using the limma package ($|\log_2 FC| > 1$, adjusted $p < 0.05$). Pathway enrichment was performed using Reactome 2024. Protein-protein interaction networks were constructed to identify hub genes, and Kaplan–Meier survival analyses assessed prognostic relevance. Results: High beta-catenin AML samples exhibited 232 DEGs, while low beta-catenin samples showed 158 DEGs, with prominent downregulation of erythroid differentiation and adhesion-related genes, including ANK1, CDH1, ALAS2, and RHAG. High beta-catenin expression was associated with enhanced dysregulation of mitotic and RHO GTPase-related pathways. Network analysis identified key hubs including BRD4, RHOA, and GATA1. Survival analyses revealed that higher expression of BRD4, RHOA, CDH1, ALAS2, and AURKB correlated with improved overall survival, whereas elevated GATA1 and ANK1 were associated with poorer outcomes. Conclusion: Distinct beta-catenin-associated transcriptional signatures characterize AML CD34⁺ cells, highlighting disruptions in differentiation, adhesion, and cell cycle regulation. Hub genes such as BRD4 and RHOA represent promising candidates for prognostic stratification and potential therapeutic targeting in AML.

Keywords: AML, CD34+ cells, Beta-Catenin, DEGs

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cfDNA as an Emerging Tool for Precision Measurable Residual Disease Monitoring in Acute Myeloid Leukemia After Transplantation: Current Advantages and Challenges

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Background: Allogeneic hematopoietic stem cell transplantation (allo-HSCT) is a potentially curative therapy for intermediate- and high-risk acute myeloid leukemia (AML), yet post-transplant relapse remains a major cause of treatment failure and poor survival. Sensitive monitoring of measurable residual disease (MRD) is therefore essential for early relapse detection and timely intervention. Although bone marrow (BM)-based MRD is the gold standard, it is invasive and limited for serial assessment. In contrast, plasma-derived cell-free DNA (cfDNA), particularly circulating tumor DNA (ctDNA), has emerged as a promising noninvasive approach for molecular MRD monitoring. This abstract highlights the advantages and challenges of cfDNA-based MRD assessment in AML patients undergoing allo-HSCT. Methods: Eligible studies were identified from the PubMed, Google Scholar, and Web of Science databases. Articles in English were identified using the following MeSH terms and keywords: acute myeloid leukemia, minimal residual disease, circulating cell-free DNA, and circulating tumor DNA. Results: Importantly, clinical relapse is often preceded by a measurable molecular phase, during which residual leukemic clones expand below the threshold of conventional morphological detection. In this context, cfDNA has emerged as a precise and noninvasive tool for MRD monitoring in AML. i) Advantages: cfDNA allows dynamic tracking of leukemic burden and clonal evolution by enabling serial assessment through peripheral blood sampling, often detecting molecular relapse earlier than conventional BM–based approaches such as morphology or flow cytometry. Furthermore, cfDNA reflects disease heterogeneity across multiple anatomical sites and supports simultaneous monitoring of multiple AML-associated mutations via next-generation sequencing. As well, detection of tumor-specific epigenetic aberrations in cfDNA could directly impact the monitoring of MRD and response to treatment. As well, the detection of tumor-specific epigenetic aberrations in cfDNA could directly impact molecular monitoring of MRD and response to treatment. ii) Limitation: Despite these advantages, cfDNA-based MRD assessment faces important limitations, including reduced sensitivity in cases of very low disease burden, interference from clonal hematopoiesis of indeterminate potential (CHIP), and variability in assay design and bioinformatic analysis. Biological and post-transplant confounders such as inflammation,

infection, or graft-versus-host disease (GVHD) can further complicate interpretation. Conclusion: cfDNA-based MRD monitoring represents a timely, precision-medicine approach, enabling critical risk stratification and clinical decision-making in AML patients after allo-HSCT. But the aforementioned disadvantages limited its sensitivity. Consequently, cfDNA is currently employed as a complementary tool alongside conventional MRD methods. Future improvements in assay design and standardization are required to overcome these limitations and fully realize its potential as a precision medicine approach.

Keywords: Circulating Cell-Free DNA, Measurable Residual Disease, Acute Myeloid Leukemia, Allogeneic Hematopoietic Stem Cell Transplantation

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From Inflammation to Prognosis: Calprotectin and Oncogenic lncRNAs PVT1 and CRNDE as a Convergent Biomarker Signature in Multiple Myeloma

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Background: Multiple myeloma (MM) is an incurable plasma cell malignancy in which inflammatory signaling within the bone marrow microenvironment—partly mediated by the NF-kappa B signaling pathway—contributes to disease progression. Calprotectin is a circulating inflammatory biomarker, and the lncRNAs PVT1 and CRNDE have been linked to poor prognosis in MM. This study evaluated serum calprotectin levels and their association with PVT1 and CRNDE expression before and after treatment. Methods: Sixteen newly diagnosed MM patients were enrolled and followed for at least six months. Serum calprotectin was measured by ELISA in 16 patients pre- and post-treatment and compared with 16 CRP-negative healthy controls. Bone marrow expression of PVT1 and CRNDE was assessed using quantitative real-time PCR. Moreover, the association of calprotectin with age, plasma cell percentage, and laboratory parameters as well as with PVT1 and CRNDE expression was evaluated. Data analysis was performed using non-parametric statistical tests. Results: Calprotectin levels were significantly elevated at diagnosis compared with controls ($p=0.017$), declined after therapy ($p=0.04$), and showed no significant difference from controls and post-treatment ($p=0.18$). CRNDE expression decreased significantly after treatment ($p=0.0429$), whereas PVT1 reduction was not statistically significant ($p = 0.1507$). Calprotectin correlated positively with age, plasma cell percentage, ESR, BUN, creatinine, and PMN, and negatively with hemoglobin. Significant inverse correlations were observed between calprotectin and ΔCT values of both lncRNAs before and after therapy. Conclusion: Concurrent elevation of calprotectin and oncogenic lncRNAs supports the presence of a shared inflammatory–tumor axis in MM. where signaling pathways related to inflammation, including MAPK, NF-κB, TLR3/4, and the production of inflammatory cytokines, operate in parallel. , highlighting their potential as complementary prognostic biomarkers and therapeutic targets.While existing evidence does not indicate a direct molecular interaction between calprotectin and these lncRNAs, shared inflammatory signaling pathways may offer a plausible biological explanation for the observed associations. These results support the concept that lncRNAs and inflammatory mediators operate within a common inflammation–tumor network, and further experimental exploration of these relationships may facilitate the identification of novel combinatorial biomarkers and potential therapeutic targets.

Keywords: Multiple Myeloma, Serum Calprotectin, CRNDE and PVT1 Long Noncoding RNAs, Prognostic Factors, Biomarkers

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Whole-genome sequencing and antifungal susceptibility of a multidrug-resistant Candida auris isolate from a patient with acute myeloid leukemia in an intensive care unit

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Introduction: Candida auris is an emerging multidrug-resistant fungal pathogen that is rapidly spreading in healthcare settings. This pathogen is capable of asymptomatic colonization of patients, especially immunocompromised individuals, and can cause nosocomial outbreaks with high mortality. In this article, we report the sixth case of C. auris isolation from a patient with asymptomatic acute myeloid leukemia in an intensive care unit in Iran. Case Presentation: A 51-year-old male patient with acute myeloid leukemia undergoing chemotherapy was admitted to the intensive care unit due to severe weakness and fever. Skin swab sampling was performed and cultured on specific fungal media. Initial identification was based on colony morphology and growth at 42°C and then confirmed by molecular methods (PCR and ITS sequencing and whole genome sequencing). Result: The isolated strain was placed in clade V (Iranian) based on ITS region sequencing. Antifungal susceptibility testing showed very high resistance to fluconazole (≥64 µg/mL) and resistance to several other azoles, but was sensitive to amphotericin B and voriconazole. Whole genome sequencing analysis revealed the presence of a Y132F mutation in the ERG11 gene (associated with fluconazole resistance) in this isolate. Conclusion: This report confirms the presence of a C. auris clade V isolate with significant multidrug resistance and carrying the Y132F mutation in an immunosuppressed patient in Iran. The findings emphasize the need for active screening of high risk patients, antifungal susceptibility testing, and enhanced genomic surveillance to promptly identify and contain this emerging threat to the country's healthcare system.

Keywords: Candida Auris, Acute Myeloid Leukemia, Antifungal Resistance, ERG11 Gene

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A Novel 6-Gene Biomarker Signature Predicts "Double-Hit" Immune Evasion in AML

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Background: Intercellular communication between leukemic blasts and the immune microenvironment drives treatment resistance in Acute Myeloid Leukemia (AML). This study deciphers Blast-T cell transcriptomic crosstalk to identify robust prognostic biomarkers and mechanisms of immune evasion. Methods: Leveraging single-cell RNA-seq (GSE116256), we screened ligand-receptor pairs mediating malignant blast and T-cell interactions. A prognostic signature was constructed using LASSO Cox regression on the TCGA-LAML cohort and rigorously validated in an independent microarray dataset (GSE37642). Functional enrichment and checkpoint analyses were utilized to reveal molecular mechanisms. Results: A novel 6-gene communication-derived signature (HLA-E, HLA-DMA, HLA-DRB5, CD69, SELPLG, CLEC2B) was identified. The risk score showed strong predictive performance for overall survival in the training (5-year AUC=0.88) and cross-platform validation (AUC=0.68) cohorts. High-risk patients exhibited an "immune-silent" phenotype with significantly inferior survival. Functional analysis revealed a collapse in MHC Class II antigen presentation and leukocyte adhesion pathways. Crucially, while MHC genes were downregulated, HAVCR2 (TIM-3) and CTLA4 were significantly upregulated, exposing a "double-hit" evasion strategy: blast invisibility coupled with T-cell exhaustion. Conclusion: This biologically anchored signature robustly stratifies AML risk based on a dual mechanism of MHC-II loss and TIM-3 upregulation. These findings suggest high-risk patients may benefit from combinatorial strategies targeting TIM-3 alongside epigenetic restoration of antigen presentation rather than standard monotherapies.

Keywords: Acute Myeloid Leukemia, Single-cell RNA-seq, Immune Evasion, TIM-3, Prognostic Signature

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Impact of Acute Myeloid Leukemia-Derived Extracellular Vesicles on Expression of CTNNB1, TGF-β, and VEGF Genes in Bone Marrow Mesenchymal Stem Cells: Insight in to Leukemia Pathogenesis

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Objective: Acute myeloid leukemia (AML) is a heterogeneous malignancy driven by disruptions in the bone marrow microenvironment (BME). Extracellular vesicles (EVs) are crucial communicators and effectors in the BME, facilitating interactions between leukemic cells and stromal components to promote leukemogenesis. Elucidating these EV-mediated processes is essential for developing novel therapeutic strategies. This study sought to clarify the effects of EVs derived from newly diagnosed non-M3 AML patients on bone marrow mesenchymal stromal cells (BMSCs), focusing on proliferation, survival, apoptosis, and expression of CTNNB1, TGF-β, and VEGF genes, which are pivotal in leukemia progression. Materials and Methods: In this experimental study, AML-derived EVs were isolated from 30 newly diagnosed non-M3 AML patients and characterized by dynamic light scattering (DLS), transmission electron microscopy (TEM), Bradford assay, and flow cytometry. BMSCs were isolated from healthy BM aspirates and were co-cultured with EVs at concentrations of 10, 40, and 60 µg/ml for 24, 48, and 72 hours. Outcomes were assessed using quantitative reverse transcription polymerase chain reaction (RT-PCR), (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazoliuom bromide (MTT) assay, flow cytometry [for apoptosis, reactive oxygen species (ROS), and Ki67], and Western blot analyses. Results: AML-derived EVs at 40 µg/ml significantly suppressed apoptosis, enhanced cell survival, and upregulated CTNNB1, TGF-β, and VEGF gene expression in BMSCs via the Wnt/β-catenin signaling pathway, as confirmed by increased β-catenin protein levels. However, a 60 µg/ml dose increased apoptosis and reduced gene expression. Conclusion: These findings can suggest that AML-derived EVs modulate the BME by promoting BMSC survival and upregulating pro-leukemic genes at an optimal dose, offering a potential therapeutic target for AML treatment

Keywords: Acute Myeloid Leukemia, Bone Marrow Mesenchymal Stromal Cells, Exosome, Extracellular Vesicles

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Investigating the Effect of Stearoyl-CoA Desaturase 1 (SCD1) Inhibition on Wnt/βCatenin Target Gene Expression and Apoptosis in the Jurkat E6.1 T-Cell Acute Lymphoblastic Leukemia Cell Line

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Stearoyl-CoA desaturase 1 (SCD1) is a key enzyme in monounsaturated fatty acid biosynthesis and has been implicated in cancer cell survival and metastasis, particularly in T-cell acute lymphoblastic leukemia (T-ALL). Emerging evidence suggests crosstalk between lipid metabolism and the Wnt/β-catenin signaling pathway, which is dysregulated in T-ALL. This study aimed to evaluate the impact of SCD1 inhibition on Wnt/β-catenin target genes and cellular outcomes in Jurkat E6.1 cells, a human T-ALL model. Cells were treated with the selective SCD1 inhibitor CAY10566 at concentrations of 3, 6, and 10 µM. SCD1 activity, measured by the18:1/18:0 fatty acid ratio, decreased dose-dependently. Cell mortality increased with inhibitor concentration, reaching approximately 45% at 10 µM. Quantitative real-time PCR and Western blotting revealed a significant upregulation of Axin2 (a negative regulator of Wnt/β-catenin) and a moderate, non-significant downregulation of c-Myb. Flow cytometry using Annexin V FITC/PI staining confirmed elevated apoptosis rates in treated cells. These findings indicate that SCD1 inhibition modulates Wnt/β-catenin signaling in a non-canonical mannerand induces apoptosis, highlighting SCD1 as a potential therapeutic target in TALL. Further studies are needed to elucidate the mechanistic links between lipid metabolism and oncogenic signaling.

Keywords: SCD1, T-ALL, Wnt/β-catenin, Axin2, c-Myb, Apoptosis, Jurkat Cells

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The Investigation of Cassiopea Andromeda Crude Venom on the Expression of MicroRNA 506 and Selected Down Stream Targets in the T Acute Lymphoblastic Leukemia Cell Line

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Background: Current anticancer therapies are often associated with numerous undesirable side effects, highlighting the ongoing need for alternative therapeutic approaches. Natural bioactive compounds derived from animals, plants, and microorganisms have gained increasing attention as potential anticancer agents. Marine environments, particularly oceans, represent a rich source of biologically active substances with promising anticancer properties. Previous studies have demonstrated the anticancer effects of various jellyfish species. Accordingly, this study aimed to investigate the in vitro anticancer activity of Cassiopea andromeda venom against a B-acute lymphoblastic leukemia (B-ALL) cell line. Method: The Jurkat cell line was used to evaluate the effects of Cassiopea andromeda venom extract alone and in combination. Cell viability and apoptosis were assessed by MTT assay and flow cytometry, respectively. Changes in microRNA-506 expression and related target genes were analyzed using real-time quantitative PCR (RQ-PCR). Results: The Cassiopea andromeda venom extract reduced cell proliferation and induced apoptosis in a dose- and time-dependent pattern. Real-time PCR results showed a downregulation of microRNA-506, along with decreased expression of CDK4 and CDK6. apoptotic target gene (BCL2-L14) revealed no significant change in expression. Conclusion: This study showed that Cassiopea andromeda venom (T.V extract) can effectively reduce the viability of Jurkat cells in vitro. These findings suggest its potential as a basis for developing future anticancer agents, pending the identification of its active fractions and underlying mechanisms.

Keywords: MicroRNA, Leukemia, Cassiopea Andromda

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Platelet-Derived Microparticles Confer Ferroptosis Resistance in Acute Promyelocytic Leukemia via Intercellular Iron and Lipid Transfer

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Background: Arsenic trioxide (ATO) kills APL cells through ferroptosis. Many APL patients develop DIC with massive platelet destruction. Whether platelet breakdown products affect ferroptosis sensitivity is not known. Methods: We reviewed studies on PMP composition, PMP uptake mechanisms by APL cells, and ferroptosis regulation pathways. Data came from proteomic profiles of human PMPs, co-culture experiments, and mouse APL models. Results: PMPs from activated platelets carry intact mitochondria, ferritin, and ether phospholipids. APL blasts take up PMPs through Tim-4 receptor binding. Inside the blast, PMP-derived iron activates NRF2 and raises glutathione levels, which restores GPX4 function and blocks lipid peroxidation. PMP-derived ether phospholipids also insert into the blast membrane and make it resistant to oxidation. Mouse models show that worse DIC correlates with lower ferroptosis markers and weaker ATO effect. Conclusion: PMPs transfer iron and oxidation-resistant lipids to APL cells and protect them from ATO-induced ferroptosis. This explains why severe DIC may predict weaker ATO response. Blocking Tim-4-mediated PMP uptake could reverse this resistance.

Keywords: Acute Promyelocytic Leukemia, Arsenic Trioxide, Ferroptosis

Hereditary and Acquired Disorders of Platelets: Laboratory Diagnosis & Therapeutic Strategies

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Integrating Platelet-Mimicking Nanoparticles and Advanced Molecular Diagnostics for Precision Management of Inherited and Acquired Platelet Disorders

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Background: Inherited and acquired platelet abnormalities pose significant therapeutic challenges due to their heterogeneity, variable severity, and associated risk of bleeding complications. Two common diagnostic tools, flow cytometry and platelet aggregometry, do not always accurately identify functional problems or predict the effectiveness of a treatment. Recent advances in nanotechnology, such as platelet-mimicking nanoparticles (PMNPs), as well as advanced molecular techniques such as next-generation sequencing (NGS), have led to innovative strategies for more effective and better diagnosis and treatment of critical mutations. This study aims to combine functional assessment to create a precise management framework for individuals with inherited and acquired platelet disorders based on the correlation between molecular aberrations and the body's response to PMNPs. Methods: This study was reviewed using relevant articles on platelet-mimicking nanoparticles and molecular diagnostic approaches in platelet disorders. Results: The combination of PMNPs and molecular diagnostics is expected to help us better understand platelet problems, find functional problems that are specific to each patient, and predict how patients will respond to PMNP-based therapy. Initial findings indicate that PMNPs can partially reinstate aggregation and adhesion in dysfunctional platelets, with efficacy affected by specific genetic variations. conclusion: Molecular profiling, combined with the use of platelet-mimicking nanotechnology, can be considered a pioneering approach for targeted treatment of platelet disorders. The use of this technology will help doctors diagnose patients and find the best treatment for each of them in the best and most effective way possible, which means that people with platelet problems will receive better care.

Keywords: Platelet-Mimicking Nanoparticles, Molecular Diagnostics, Platelet Diseases

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Deciphering Landscapes of Platelet Functions via Up-to-Dated Technologies in Hematology Laboratory

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Introduction: It is becoming increasingly clear that platelets are surprisingly multitalented with many recently discovered new functions such as inflammation, host defense, fetal vascular remodeling, tumor growth, and metastasis. This study discusses currently available clinical tests of platelet function through various instruments with their advantages and drawbacks. Methods: Whole data was collided through 200 articles through PubMed, Scopus, Web of Science databases by keywords of platelets, instruments, functions, clinical application, tests, techniques. Results: Ichor Plateletworks, PFA-100/200, Placor PRT, Platelet genome or transcriptome analysis, Proteomic analysis, Serum thromboxane B2, Soluble platelet release markers and sheddome (e.g., PF4, G, sCD40L, sCD62P, GPV, and GPVI), Sonoclot analyzer, Thromboelastography (TEG or ROTEM), ThromboLUX, VASP, VerifyNow, WBA, Light transmission aggregometry (LTA), Microfluidic devices, Laser platelet aggregometer (PA 200), Impact cone and plate (let) analyzer, Electron microscopy, Flow cytometry, and Kinetic aggregometer are found as assays to evaluate the dynamic of platelets in detailes. Each assay showed own application, advantages, and disadvantages. For examples, VerifyNow is a full automated aggregometers can monitor antiplatelet therapy as a point of care (POC) device. It merits for measuring 3 test cartridges (aspirin, P2Y12, and GPIIb IIIa). The disadvantages are Inflexibility and cartridges can be used only for single purpose. Additionally, Serum thromboxane B2 widespread used for monitoring aspirin therapy, detection of thromboxane production defects. The most important defect of this test is vulnerability to artifacts. Moreover, Placor PRT is less used to detect any defects in high shear platelet function. In this device blood oscillates through a narrowed channel with a spring to hold the thrombus. Ichor Plateletworks is another POC device Used in surgery and cardiologyfor prediction of bleeding if patient consumes antiplatelet medicines. Clinical applications of PFA-100/200 are numerous and have been recently reviewed.They include screening for VWD and its treatment monitoring; identification of inherited and acquired platelet defects; monitoring of antiplatelet therapy, assessment of surgical bleeding risk; and assessment of thrombotic risk. However, it should be noted that the PFA-100/200 is a global test of platelet (and VWF) functions. Although it is not specific for any platelet defect. Conclusion: Utilization of these technologies within specifically designed arrays or chips (covering just the key genes/proteins that are known to be defective in a range of disorders) could

also potentially revolutionize not only the diagnosis of inherited defects in platelet function but possibly also the rapid identification of individuals with increased risk of bleeding or thrombosis. The availability of cheaper deep-sequencing technology in the near future will also open up the possibility of mass screening of patients with both bleeding and thrombotic disorders.

Keywords: Platelet Functions, Instruments

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Comparative Study of Platelet Reduction and its Relationship with Microorganism Found in the Blood of Patients Admitted to the ICU Department of Besat Hospital in Hamadan in 2023

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Background: Thrombocytopenia is common in ICU patients and is associated with worse prognosis and higher mortality. Causes include diseases, infections, or medications. Platelet dysfunction can increase bleeding risk and affect outcomes. This study assessed platelet levels and their relationship with microorganisms in ICU patients with bacterial bloodstream infections. Methods: A cross-sectional study included 50 ICU patients with confirmed bacterial bloodstream infections at Besat Hospital, Hamadan. Data on age, gender, reason for hospitalization, hemoglobin, disease severity, outcomes, microorganism type, and bacterial species were collected. Data were analyzed using SPSS version 24. Results: Mean hemoglobin was $21\times10^4/\mu L$. Most hospitalizations (38%) were for postoperative monitoring; 54% had moderate disease severity, and 14% died. Blood cultures identified Staphylococcus aureus in 58% and Acinetobacter in 24%. Platelet count was inversely related to length of stay (P=0.002). Recovered patients had higher platelet counts than deceased (P=0.001). Patients with mild disease had higher counts than those with moderate or severe disease (P=0.001). No significant association was found between platelet counts and microorganism type (P=0.076) or bacterial species (P=0.151). Conclusion: Platelet count is linked to disease severity and outcomes in ICU patients with bacterial bloodstream infections. Monitoring platelet levels may guide management and improve prognosis. Larger studies are needed to clarify potential associations with specific microorganisms.

Keywords: Platelet, Thrombocytopenia, Bloodstream Infections, ICU, Outcome

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Glycoprotein VI Deficiency: A First Iranian Case Series of Two Patients

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Background: Glycoprotein (GP) VI deficiency is a rare platelet function disorder marked by impaired collagen-induced platelet activation and a tendency for mild bleeding. While the pathophysiology is described in the global literature, diagnosis remains challenging due to its rarity and the need for specialized testing. We present the first Iranian cases of GPVI deficiency, including their clinical and laboratory features. Methods: Two female patients with suspected inherited platelet dysfunction underwent comprehensive assessment. Initial tests included CBC and coagulation screening (PT, aPTT). Platelet function was evaluated using light transmission aggregometry (Chronolog 700 VS), with agonists collagen (2, 5 µg/ml), ADP, epinephrine, arachidonic acid, and ristocetin. Dense granule secretion was assessed via ATP-release assays. Flow cytometry (BioCytex) quantified surface expression of GPVI, GPIb, and GPIIb/IIIa. Genetic analysis was performed using Whole Exome Sequencing (NextSeq500, 100X coverage; GRCh37). Results: Patient 1 (12 y) had severe menorrhagia at menarche, GI bleeding, and prior misdiagnosis as ITP. Patient 2 (18 y) had persistent post-rhinoplasty bleeding and spontaneous ecchymoses. Both showed normal PT/aPTT and prolonged or upper-normal bleeding time. Platelet aggregation was absent to collagen but normal with ADP, arachidonic acid, and ristocetin. ATP-release defects were limited to collagen stimulation. Flow cytometry revealed markedly decreased GPVI expression (5% and 29% of controls), with normal GPIb and GPIIb/IIIa. No pathogenic variants were found by WES. Conclusion: These are the first reported Iranian cases of GPVI deficiency, highlighting its clinical and laboratory profile and emphasizing the importance of specialized diagnostic approaches in similar clinical contexts.

Keywords: GPVI Deficiency, Platelet Function Tests, Blood Platelet Disorders, Glycoproteins

Immune System Dysregulation in Diseases

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Targeting CD147 in Keloid Fibrosis: Opportunities, Limitations, and Combination Therapeutic Strategies

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Keloid formation is a complex fibrotic disorder driven by multiple, redundant molecular pathways and influenced by anatomical and microenvironmental factors. Although AC-73 has emerged as a promising therapeutic agent through inhibition of CD147, its broader biological activity presents both opportunities and challenges. Evidence suggests that AC 73 also modulates Extracellular Signal–Regulated Kinase 1/2 (ERK1/2), Signal Transducer and Activator of Transcription 3 (STAT3), and autophagy pathways, indicating potential antifibrotic effects beyond CD147 inhibition. To clarify its specificity, comparative studies with selective CD147 blockers, such as monoclonal antibodies, are needed. Keloid behavior varies by anatomical site, likely due to differences in mechanical stress and hypoxia, with chest and shoulder lesions exhibiting elevated Yes-Associated Protein/Transcriptional Coactivator with PDZ-Binding Motif (YAP/TAZ) and Hypoxia-Inducible Factor 1 Alpha (HIF-1α) signaling. Stratifying patients based on anatomical or molecular profiles may therefore optimize AC 73 responsiveness. Moreover, fibrosis-related pathways including the Mitogen-Activated Protein Kinase (MAPK) pathway, the Phosphoinositide 3-Kinase/Protein Kinase B (PI3K/Akt) pathway, and the Rho/Rho-Associated Coiled-Coil Containing Protein Kinase (Rho/ROCK) pathway may compensate for CD147 blockade, suggesting that combination therapies, such as AC 73 with Mitogen-Activated Protein Kinase Kinase (MEK) or ROCK inhibitors, could enhance therapeutic efficacy. Since CD147 overexpression may arise secondary to hypoxia or inflammation, co-targeting upstream regulators such as HIF-1α or Transforming Growth Factor Beta (TGF-β) receptors may further disrupt profibrotic feedback loops. Finally, localized delivery approaches, including small interfering ribonucleic acid (siRNA)-based nanocarriers or microneedle systems, offer a strategy for gene-specific CD147 suppression with reduced systemic toxicity. Overall, integrating CD147 inhibition with combination therapies and advanced delivery systems may enable more precise and durable treatment of keloid disease.

Keywords: Keloid Formation, CD147 Inhibition, Therapeutic Agent

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Berberine Enhances Immunomodulatory Responses and Attenuates Neuroinflammation in an Experimental Model of Multiple Sclerosis via Expansion of Treg and Th2 Cells

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Background: one of the most common types of demyelinating-autoimmune diseases affecting the central nervous system (CNS) is known as multiple sclerosis. Experimental Autoimmune Encephalomyelitis (EAE) has been used as a model for studying the MS. Berberine, the naturally occurring quinolone alkaloid, has been found to be an anti-inflammatory agent. Methods: Female C57BL/6 mice were sectioned into three groups: the control, low dose, and high dose berberine groups, receiving PBS, 10 mg/kg berberine, and 30 mg/kg berberine, respectively. EAE was induced using s.c. injection with myelin oligodendrocyte glycoprotein (MOG) and complete Freund's adjuvant, and pertussis toxin was injected Ip on the day and two days post-immunization. Results: There were significant differences in the clinical scores between the mice treated with low, dose berberine (T1: 2 ± 0.13) and high, dose berberine (T2: 1.5 ± 0.14) compared to the control mice (CTRL: 4.5 ± 0.13). The administration of berberine has been shown to significantly reduce the levels of pro, inflammatory cytokines such as IFN, TNF, and IL, 17 ($p <. 001$). On the contrary, the treatment group displayed a significantly higher level of anti, inflammatory cytokines such as IL, 4, IL, 10, and TGF, in comparison with the control group ($p <. 01$). Treatment groups with berberine reduced expression of the Th1 and Th17 cytokines and transcription factors ($p < .001$) and increased expression of transcription factors and Th2 and Treg cytokines ($p < .01$) in contrast to CTRL group. Conclusion: Berberine has been shown to help slow the progression of disease in EAE by modulating the immune response, specifically through downregulating pro-inflammatory pathways and upregulating anti-inflammatory responses.

Keywords: Berberine, Experimental Autoimmune Encephalomyelitis, Multiple Sclerosis, Myelin Oligodendrocyte Glycoprotein

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Chimeric Antigen Receptor T Cell Therapy in Rheumatoid Arthritis: A Systematic Review of Clinical and Immunological Evidence

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Background: Rheumatoid arthritis (RA) is a chronic autoimmune disease marked by abnormal adaptive immune responses, particularly autoreactive B cells. Even with existing immunosuppressive therapies, some patients remain refractory. Our studies suggest that chimeric antigen receptor T (CAR-T) cell treatment, which targets B cell antigens such as CD19 or B cell maturation antigen (BCMA), has emerged as a novel immunotherapeutic method for selectively eliminating pathogenic B cells in autoimmune regulation. Methods: Study selection and evaluation were performed using the PICO criteria and in accordance with the PRISMA checklist. A comprehensive search was conducted on the PubMed, Scopus, Web of Science, and Google Scholar databases (2020-2025). MESH keywords were " Rheumatoid arthritis", " CAR T cells", and " CD19". Studies were selected based on inclusion and exclusion criteria. Two reviewers extracted data independently. Results: The database search identified 46 articles; after applying the inclusion criteria, 4 studies were finalized for our review. It was demonstrated that CAR T cell therapy targeting CD19 or BCMA on B cells results in notable clinical improvement in RA, including depletion of pathogenic B cells, reduction of autoantibody levels, and regulation of abnormal immune responses, highlighting a promising immunotherapeutic strategy for controlling RA. Conclusion: In summary, CAR T cell therapy is a potential immunotherapeutic approach for RA, which targets the underlying autoimmune mechanisms instead of focusing solely on alleviating symptoms. So, this data emphasizes its emerging role in the development of future therapeutic approaches for RA, supporting continued research to improve efficacy and long-term clinical outcomes.

Keywords: Rheumatoid Arthritis, CAR T Cells, CD19

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Immune System Dysregulation in Pediatric and Adult Patients with Inborn Errors of Immunity (IEI): A Narrative Review

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Background: Inborn Errors of Immunity (IEI), formerly known as primary immunodeficiencies, represent a broad and heterogeneous group of inherited disorders affecting the immune system. Early recognition of IEI remains difficult due to their clinical heterogeneity and the wide range of immunological defects involved. They are frequently associated with autoimmune cytopenias, lymphoproliferation, and other immune-mediated complications. Such conditions result in diverse manifestations of immune dysregulation, which may present early in life or emerge later in adulthood. This study aims to highlight the underlying mechanisms and clinical implications of immune dysregulation in pediatric and adult patients with IEI. Methods: This study was conducted in 2026 using an advanced search strategy in reliable databases such as PubMed. Articles published between 2016 and 2026 were reviewed. A total of 36 articles were initially screened based on title and abstract, followed by full-text evaluation according to predefined inclusion and exclusion criteria (human studies and English-language publications). Ultimately, 11 of the most relevant articles were included in this review. Results: Immune dysregulation plays a critical role in the development of autoimmune conditions, cytopenias, lymphoproliferation, and other immune-mediated complications. Clinical manifestations can vary depending on the specific molecular pathways and immune cells involved. Understanding these variations is essential for tailoring patient-specific management strategies and anticipating potential complications. Conclusion: Despite increasing awareness, early identification of these conditions remains challenging due to heterogeneous clinical manifestations and variable laboratory results. Implementing advanced, targeted laboratory diagnostics is pivotal for timely and accurate recognition of IEIs associated with immune dysregulation. Such approaches facilitate personalized interventions that can improve patient outcomes, guiding management from early detection to effective treatment

Keywords: Inborn Errors of Immunity (IEI), Immune Dysregulation, Autoimmune Cytopenias, Lymphoproliferation, Laboratory Diagnosis

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Human Umbilical Cord-Derived MSCs Restore Immune Tolerance in SLE via Treg Induction

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Background: Systemic lupus erythematosus (SLE) exists as an autoimmune disorder which affects multiple body systems. The function of regulatory T cells which scientists refer to as Treg cells serves as a fundamental mechanism that protects the body against autoimmune diseases while maintaining immune system balance. The disease of SLE occurs when the body fails to maintain self-tolerance which results in the activation of autoimmune lymphocytes that cause continuous health problems. The main processes of the condition begin with the body producing excessive autoantibodies while B cells become activated inappropriately because the body fails to remove dying cells effectively. Pathogenic conditions occur when T cell groups become dysregulated and dendritic cells reach extreme activation levels which cause excessive production of both pro-inflammatory cytokines and type I interferon. Methods: A systematic review was conducted in pumped and google scholar(2022-2025) with relevant keywords. Of 14 screened articles,5 were selected. Results: Human umbilical cord-derived MSCs function as the main immunomodulatory agents which enable MSCs to treat SLE through their effect on innate and adaptive immunity. MSCs and their exosomes use cell-to-cell contact together with paracrine activity to establish immune tolerance while they increase autoreactive cell anergy and drive Treg and M2 macrophage development. The mechanisms proceed to control immune cell subsets together with soluble factors which decrease systemic inflammation and protect against organ damage that includes nephritis. Conclusion: Human umbilical cord-derived MSCs effectively alleviate SLE by promoting immune tolerance and regulating inflammatory responses through immunomodulatory mechanisms, offering a potential therapeutic strategy for mitigating systemic inflammation and organ injuries.

Keywords: Systemic Lupus Erythematosus, Mesenchymal Stem Cells, Regulatory T Cells, Immune Tolerance, Umbilical Cord-Derived MSCs

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Immune Dysregulation in Rheumatoid Arthritis: A Systematic Review of Synovial Microenvironment Dynamics and Peripheral Biomarkers

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Background: Rheumatoid Arthritis (RA) is a systemic autoimmune disorder marked by persistent inflammation of the synovial joints, resulting in cartilage degradation and bone erosion. The etiology involves a complicated disintegration of self-tolerance; however, the precise mechanisms that underlie the diseases are inadequately clarified. This systematic review integrates contemporary evidence regarding the immunological mechanisms that induce synovial inflammation and systemic manifestations in RA. Methods: This systematic review was conducted in accordance with PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. A systematic search of MEDLINE/PubMed, Embase, and the Cochrane Library was performed for studies published from January 2015 to December 2024. Search strategies integrated MeSH terms and keywords pertaining to "Rheumatoid Arthritis," "immune dysregulation," "synovial fibroblasts," "T follicular helper cells," "autoantibodies," and "cytokine networks." Cohort studies, case-control studies, and cross-sectional analyses were included if they provided quantitative immunological data from RA patients in comparison to healthy or disease controls. When it came to data extraction, we focused on cellular populations, soluble mediators, and transcriptomic signatures. The Joanna Briggs Institute (JBI) checklists were used to check the quality. Results: Out of the 1,247 records initially identified, 78 studies satisfied the inclusion criteria. The meta-synthesis of the data identified three pivotal nodes of dysregulation. First, a significant increase in peripheral T follicular helper (Tfh) cells was strongly associated with serum autoantibody (anti-CCP and RF) titers (reported in 12 studies, $p < 0.01$). Second, in the synovial microenvironment, a pathological subset of fibroblast-like synoviocytes (FLS) displayed an aggressive phenotype, secreting IL-6 and RANKL, which directly facilitated osteoclastogenesis and the polarization of Th17 cells. Third, single-cell RNA sequencing data from five high-quality studies revealed a predominant population of PD-1hiCXCR5 peripheral helper T (Tph) cells in the inflamed synovium, facilitating B-cell maturation and local immunoglobulin production independently of lymphoid structures. Conclusion: Immune dysregulation in rheumatoid arthritis transcends systemic autoantibody production, encompassing complex stromal-immune cell interactions within the joint. The recognition of Tph cells and pathogenic FLS subsets as principal contributors to tissue damage reconstitutes the conventional T-cell centric perspective of rheumatoid arthritis. These results emphasize the possibility of targeted therapies

designed to disrupt the Tph-FLS axis to attain prolonged remission and avert irreversible joint damage.

Keywords: Rheumatoid Arthritis, Immune Dysregulation, T Follicular Helper Cells, Synovial Fibroblasts, Th17 Cells

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Dysregulated JAK/STAT Pathway as a Driver of Immune Evasion and Tumor Progression in Gastrointestinal Cancers

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Introduction The Janus kinase–signal transducer and activator of transcription (JAK/STAT) pathway is a key signaling axis mediating cellular responses to cytokines and growth factors, with essential roles in immune regulation, inflammation, and cell survival. While tightly regulated under physiological conditions, its dysregulation contributes to gastrointestinal tumorigenesis by promoting proliferation, resistance to apoptosis, immune evasion, and therapy resistance. Persistent activation—resulting from aberrant cytokine signaling or defective negative feedback—reshapes the tumor microenvironment and facilitates escape from antitumor immunity. This review examines the role of dysregulated JAK/STAT signaling in immune evasion and progression of gastrointestinal cancers and its potential as a therapeutic target. Method A narrative review of PubMed, Scopus, and Google Scholar (2018–2025) was performed to identify studies on JAK/STAT signaling and gastrointestinal cancers, and relevant findings were qualitatively synthesized. Results Dysregulated JAK/STAT3 signaling was consistently linked to tumor progression and therapy resistance in gastrointestinal-cancers. In gastric-cancer, IL-11/gp130 and IL-22 enhanced STAT3 activation and invasiveness. Hepatocellular-carcinoma showed sustained JAK2–STAT3 activation due to EYA2 downregulation and impaired SOCS3 feedback. In colorectal-cancer, BMX and HCK promoted STAT3-driven hyperproliferation and adenoma-to-carcinoma transition. Pancreatic-cancer involved TEAD2-mediated CD109 upregulation leading to metastasis, whereas esophageal-cancer exhibited SNHG6-associated STAT3 activation and 5-fluorouracil resistance. Conclusion Aberrant JAK/STAT signaling drives tumor progression, immune evasion, and therapy resistance in gastrointestinal cancers. Cytokines, dysregulated kinases, and non-coding RNAs sustain STAT3 activation, while impaired negative regulators like SOCS proteins promote a pro-tumorigenic microenvironment. These findings highlight JAK/STAT as a key target for therapy, including combination with immunotherapy or strategies to overcome chemotherapy resistance.

Keywords: JAK/STAT Pathway, Immune Evasion, Gastrointestinal Cancers, Cytokines, Tumor Progression, Therapeutic Target

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Hematological Complications in Familial Mediterranean Fever: A Case Report and Literature Review

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Hematological Complications in Familial Mediterranean Fever: A Case Report and Literature Review Ali Taheri1, Reza Yazdani2,3* 1 Department of Immunology, Shahed University, Tehran, Iran. 2 Research Center for Immunodeficiencies, Pediatrics Center of Excellence, Children's Medical Center, Tehran University of Medical Sciences, Tehran, Iran 3 Primary Immunodeficiency Diseases Network (PIDNet), Universal Scientific Education and Research Network (USERN), Tehran, Iran. 1-Background Familial Mediterranean fever (FMF), caused by mutations in the MEFV gene, typically presents with fever and elevated inflammatory markers such as leukocytosis. However, some patients develop hematologic complications, including leukopenia and neutropenia. This study reports a unique FMF case characterized by periodic, synchronized cytopenias and includes a literature review to broaden the recognized spectrum of FMF hematologic manifestations. 2. Methods This study combines a retrospective case report with a literature review. Clinical, laboratory, and genetic data were collected for a 29-year-old patient whose FMF diagnosis was confirmed by whole-exome sequencing (WES), revealing a heterozygous MEFV P.Val726Ala mutation. A comprehensive search of PubMed, Web of Science, Scopus, and ProQuest was conducted using keywords related to FMF and hematologic abnormalities. Seventeen relevant studies were selected for analysis. 3. Results The patient experienced four years of recurrent episodes (every 2–3 months) with fever, fatigue, and synchronized severe cytopenias, including leukopenia (WBC 0.881/mm³), absolute neutrophil count (ANC 361/mm³), and thrombocytopenia (55 × 10³/µL). Initial suspicion was aplastic anemia. Daily colchicine therapy controlled symptoms, stabilized blood counts, and eliminated the need for G-CSF. The literature review identified 34 patients, with leukopenia being the most frequent complication (61.8%). 4. Conclusion Hematologic manifestations in FMF extend beyond typical inflammatory increases and may include periodic, simultaneous cytopenias. FMF should be considered in patients with fever and unexplained periodic cytopenias. Early diagnosis and colchicine therapy are essential for disease control and hematologic stability. 5. Keywords Familial Mediterranean Fever; Hematological Manifestations; MEFV Gene; Neutropenia

Keywords: Familial Mediterranean Fever, Hematological Manifestations, MEFV Gene, Neutropenia

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The Role of Autoantibodies in the Pathophysiology of Schizophrenia

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Background: Schizophrenia is a chronic psychotic disorder characterized by a variety of symptoms. It is caused by a complex interaction of genetic, biological, and environmental factors that lead to impairment in social and occupational functioning. Studies have implicated antibodies against the NMDA receptor, GABA-A receptor, NRXN1α, NCAM1 and neuronal surface proteins in the etiology of the disease. Methods: This review study was conducted by searching valid scientific databases to investigate the role of autoantibodies and immune interventions in the pathophysiology of schizophrenia. Results: These antibodies disrupt the function of synaptic receptors and cause significant changes in neural communication. Injecting serum containing these antibodies into an animal model showed that the animal exhibited behaviors similar to psychosis, and the results support the role of autoimmune factors in sufferers. In this regard, this spectrum of patients has responded positively to immunotherapy such as plasmapheresis and IVIG injections, and significant improvement in their symptoms has been reported. However, autoantibodies are found in only a subset of patients, and the available evidence is insufficient to definitively prove them. Clinical trials have shown that nonselective removal of antibodies by plasmapheresis in patients with schizophrenia has no significant effect, unless the presence of neuronal antibodies is specifically confirmed. Conclusion: Current evidence suggests that the immune system plays a role in the pathophysiology of some types of schizophrenia, and identifying these subgroups could pave the way for more targeted treatments. Future research in this area focuses on combining immunological, genetic, and neurological data to determine which patients benefit from immunotherapy and how an individualized approach can reduce disease severity and relapse.

Keywords: Schizophrenia, Neural Receptors, Autoantibodies, Plasmapheresis

Intelligent Molecular Diagnosis in Cancer and Infectious Diseases

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Acute Leukemia of Ambiguous Lineage: Immunophenotypic Characterization of a Mixed Phenotype Acute Leukemia Case

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Background: Acute leukemia of ambiguous lineage (ALAL) is a rare and biologically heterogeneous hematologic malignancy characterized by leukemic blasts with unclear lineage commitment or simultaneous expression of markers from multiple lineages. It includes mixed phenotype acute leukemia and acute undifferentiated leukemia and accounts for fewer than 3% of acute leukemia cases. ALAL is associated with significant diagnostic and therapeutic challenges and generally poorer outcomes compared with lineage-specific leukemias. Although advances in immunophenotypic and molecular diagnostics have improved classification, optimal treatment strategies remain undefined. Methods: A 33-year-old male with marked hematologic abnormalities underwent comprehensive evaluation, including complete blood count, peripheral blood smear, and bone marrow aspirate examination to assess cellularity and blast percentage. Multiparametric flow cytometry was performed on bone marrow samples using an extensive panel of myeloid, B-lineage, T/NK-lineage, and precursor-associated markers. Morphologic and immunophenotypic findings were interpreted according to current World Health Organization classification criteria for acute leukemias of ambiguous lineage. Results: Laboratory studies demonstrated leukocytosis, anemia, thrombocytopenia, and a high proportion of circulating blasts. Bone marrow examination revealed approximately 90% undifferentiated blasts. Flow cytometry showed strong CD34 expression, B-lineage–associated markers CD22 and CD200, partial expression of myeloid markers CD64 and CD11c, and limited expression of CD7, with absence of other lineage-defining markers, myeloperoxidase, and cytoplasmic CD3. These findings supported a diagnosis of mixed phenotype acute leukemia, B/Myeloid, not otherwise specified. Conclusion: This case highlights the diagnostic complexity of ALAL and emphasizes the critical role of detailed immunophenotypic analysis for accurate classification. Early recognition and comprehensive diagnostic workup are essential, and integration of molecular and cytogenetic studies may further refine risk stratification and guide individualized management strategies.

Keywords: Acute Leukemia of Ambiguous Lineage, Mixed Phenotype Acute Leukemia

P98

Some Virulence Genes are Associated with Antibiotic Susceptibility in Enterobacter Cloacae Complex

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Background: Enterobacter cloacae complex (ECC) including different species are isolated from different human clinical samples. ECC is armed by many different virulence genes (VGs) and they were also classified among ESKAPE group by WHO recently. The present study was designed to find probable association between VGs and antibiotic susceptibility in different ECC species. Methods: Forty-five Enterobacter isolates that were harvested from different clinical samples were classified in four different species. Seven VGs were screened by PCR technique and antibiotic susceptibility assessment was performed by disk-diffusion assay. Result: Four Enterobacter species; Enterobacter cloacae (33.3%), Enterobacter hormaechei (55.6%), Enterobacter kobei (6.7%) and Enterobacter roggenkampii (4.4%) were detected. Minimum antibiotic resistance was against carbapenem agents and amikacin even in MDR isolates. 33.3% and 13.3% of isolates were MDR and XDR respectively. The rpoS (97.8%) and csgD (11.1%) showed maximum and minimum frequency respectively. Blood sample isolated were highly virulent but less resistant in comparison to the other sample isolates. The csgA, csgD and iutA genes were associated with cefepime sensitivity. Conclusion: The fepA showed a predictory role for differentiating of E. hormaechei from other species. More evolved iron acquisition system in E. hormaechei was hypothesized. The fepA gene introduced as a suitable target for designing novel anti-virulence/antibiotic agents against E. hormaechei. Complementary studies on other VGs and ARGs and with bigger study population is recommended.

Keywords: Enterobacter Cloacae Complex, Virulence Gene, Antibiotic Resistance, MDR, Antivirulence

P99

Upregulation of CASP8 Expression and Caspase-3 Activation Induced by Glucose- and Menthol-Conjugated Cobalt Oxide Nanoparticles in the SW480 Human Colon Cancer Cell Line

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Background: Colon cancer remains one of the leading causes of cancer-related mortality worldwide, underscoring the urgent need for more effective and selective therapeutic strategies. Nanoparticle-based therapies have attracted considerable attention due to their enhanced bioactivity and potential for targeted anticancer effects. This study investigated the cytotoxic and pro-apoptotic effects of glucose- and menthol-conjugated cobalt oxide nanoparticles (Co_3O_4@Glu-Menthol) on the SW480 human colon cancer cell line, while evaluating their safety on normal human dermal fibroblast (HDF) cells. Methods: In this in vitro study, the quality of obtained Co_3O_4@Glu-Menthol nanoparticle was assessed by biochemical and mechanical methods. SW480 and HDF cell lines were cultured in RPMI-1640 medium and treated with increasing concentrations of Co_3O_4@Glu-Menthol nanoparticles (31.25–500 µg/mL). Cell viability and IC_{50} values were determined at 24 and 48 hours using the MTT assay. Apoptosis and necrosis were quantified by Annexin V/Propidium Iodide (PI) staining followed by flow cytometry. Apoptotic mechanisms were assessed through CASP8 gene expression and Caspase-3 activity. Nuclear morphological changes associated with apoptosis were evaluated using Hoechst 33258 staining. Caspase-3 enzymatic activity was measured using a colorimetric assay. Additionally, CASP8 gene expression was quantified by qRT-PCR using SYBR Green chemistry, with GAPDH as the internal control. Data from three independent experiments were analyzed using one-way ANOVA, with statistical significance set at $P < 0.05$. Results: Co_3O_4@Glu-Menthol nanoparticles exhibited a dose- and time-dependent cytotoxic effect on SW480 cells. The IC_{50} values were 149 µg/mL at 24 hours and 87 µg/mL at 48 hours, while normal HDF cells showed a higher IC_{50} (320 µg/mL at 24 hours), indicating selective toxicity toward cancer cells. Flow cytometry analysis at the 48-hour IC_{50} concentration (87 µg/mL) revealed significant induction of apoptosis, with 23.96% early apoptotic cells, 7.94% late apoptotic cells, and 9.83% necrotic cells. Hoechst 33258 staining confirmed apoptotic morphological changes, including chromatin condensation and nuclear fragmentation. Molecular analyses demonstrated a 2.4-fold upregulation of CASP8 gene expression ($P < 0.001$) and a significant 6.22-fold increase in Caspase-3 activity ($P < 0.05$) in treated cells compared with controls. Conclusion:

Co_3O_4@Glu-Menthol nanoparticles effectively induce apoptosis in colon cancer cells through activation of the extrinsic apoptotic pathway and downstream caspase signaling, while exerting lower cytotoxicity on normal cells. These findings suggest that Co_3O_4@Glu-Menthol nanoparticles may represent a promising nanotherapeutic candidate for colon cancer treatment, warranting further in vivo and clinical investigations.

Keywords: Colon Cancer, Nanoparticle, Caspase, Apoptosi

P100

A Quantitative Comparative Study of the Expression of Genes Encoding Paraoxonase-1 and Spermine Oxidase Enzymes in the First and Second Stages of Breast Cancer in Clinical Samples of the Iranian Population

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Introduction: Breast cancer is the most common cancer in women. Inflammation, oxidative stress, and lipid peroxidation play a key role in the development of cancers. Reactive oxygen species can cause abnormal gene expression, disrupt intracellular communication, and signal pathways. Paraoxonase (PON1) is an antioxidant that scavenges free radicals and prevents DNA damage. Spermine oxidase (SMO) is an oxidizer of functional intracellular polycations (polyamines) that is located in the nucleus and cytoplasm and can cause DNA damage by producing H2O2, and both genes play a role in cancer through an oxidative stress-related mechanism. Materials and Methods: Fifty blood samples from patients with breast cancer at Imam Khomeini Hospital in Tehran were studied for the expression levels of two genes, PON1 and SMOX, using qRT-PCR. The samples were compared in the majority of blood samples and tissue samples, and each in the StageI and StageII groups. Research results: Comparison of the expression levels of both genes in StageII in both blood samples (pValue: PON1=0.05, SMOX=0.024) and tissue samples (pValue: PON1=0.000, SMOX=0.006) showed a significant decrease compared to the control group. In the case of Stage I, only tissue samples (pValue=0.044) showed a significant decrease in PON1 gene expression. Discussion and conclusion: Decreased PON1 expression will lead to increased oxidative stress and subsequent carcinogenic effects, which were evident in advanced stages of breast cancer. Also, although increased SMO expression increases H2O2 and reactive oxygen species, it also causes the breakdown of polyamines, which play a role in cancer by interfering with cell signaling pathways. Therefore, the reduction of SMO in advanced stages of breast cancer may indicate an increase in polyamines and their role in cancer progression.

Keywords: Breast Cancer, Oxidative Stress, Paraoxonase, Spermine Oxidase

P101

Urinary Extracellular Vesicle miR-126: A Promising Early Biomarker for Diabetic Nephropathy in Type 2 Diabetes

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Background: Diabetic nephropathy (DN) is a major microvascular complication of type 2 diabetes and a leading cause of end-stage renal disease (ESRD). Early detection is critical to prevent progression, yet albuminuria, the conventional marker, often appears only in later stages. MicroRNA-126 (miR-126), an endothelial-enriched regulatory miRNA, plays a key role in endothelial function and EGFR-related signaling. Urinary extracellular vesicle (EV)-derived miR-126 has been reported to increase in DN, but its diagnostic performance across different stages of the disease remains limited. Methods: In this cross-sectional study, 120 patients with type 2 diabetes (40 with established DN, 40 with microalbuminuria, 40 without albuminuria) and 40 healthy controls were enrolled. Urinary EVs were isolated from morning urine samples, and miR-126 expression was quantified by qRT-PCR, normalized to U6 snRNA. Clinical variables including HbA1c, serum creatinine, eGFR, and urinary albumin-to-creatinine ratio (ACR) were recorded. Statistical analyses were performed using Stata, including group comparisons, Spearman correlation, and ROC curve analysis. Results: Urinary EV-derived miR-126 levels were significantly elevated in DN patients compared with controls ($p<0.001$) and were also increased in patients with microalbuminuria ($p<0.01$). miR-126 showed a positive correlation with ACR ($r=0.687$) and a negative correlation with eGFR ($r=-0.542$) (both $p<0.001$). ROC analysis demonstrated good diagnostic accuracy for DN (AUC=0.892), with 85.3% sensitivity and 87.5% specificity. Higher miR-126 levels were observed in patients with poor glycemic control (HbA1c >8%, $p<0.05$). Conclusion: Urinary EV-derived miR-126 is associated with the presence and severity of diabetic nephropathy. Its elevation in patients with microalbuminuria suggests a potential role as an early, non-invasive biomarker before overt proteinuria. Correlations with renal function parameters support its relevance to kidney dysfunction. Overall, urinary miR-126 may represent a promising adjunct biomarker for early detection and risk stratification of DN.

Keywords: Diabetic Nephropathy, Type 2 Diabetes Mellitus, Urinary Extracellular Vesicles (EVs), miR-126, Microalbuminuria

P102

Droplet Digital PCR as a Novel Tool for Infectious Agent Detection

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Background: Droplet Digital PCR (ddPCR) is an advanced molecular technique that partitions samples into thousands of nanoliter droplets, enabling absolute nucleic acid quantification with high sensitivity and precision, making it valuable in infectious disease diagnostics. Methods: This study synthesizes peer-reviewed literature from PubMed, Scopus, and Web of Science (2015-2025) on ddPCR for infectious diseases, using keywords “droplet digital PCR,” “infectious agents,” “viral detection,” and “clinical diagnostics. Results: ddPCR demonstrates several advantages over qPCR for detecting infectious agents, offering superior sensitivity, accuracy, and reproducibility. It enables absolute quantification of pathogens at very low concentrations with minimal contamination. Its workflow is showed in figure 1. In HIV, ddPCR allows precise measurement of latent reservoirs and ultra-low viral loads; in HBV, accurate detection of DNA and drug-resistant mutations; and in SARS-CoV-2, effective use in diagnostics and wastewater surveillance for outbreak tracking. ddPCR also provides reliable CMV load monitoring in transplant recipients and facilitates early Zika virus detection. Commercial ddPCR systems for clinical use are available from Bio Rad, Life Technologies, Pilot Gene Technologies, and RainDance. Conclusion: ddPCR represents a reliable platform for infectious agent detection, absolute quantification with high sensitivity, and resilience to inhibitors. Its demonstrated utility in virology—spanning HIV, HBV, SARS-CoV-2, CMV, and Zika virus—shows its potential to complement or even surpass conventional PCR methods. Future directions include protocol standardization, clinical workflow integration, and validation across diverse sample types. Collectively, ddPCR’ significantly enhances diagnostic accuracy, guiding clinical decisions, and supporting public health surveillance.

Keywords: Droplet Digital PCR, Infectious Agent Detection, ddPCR

P103

Plasma Exosomal miR-21, miR-155 and miR-122 as an Integrated Smart Panel for Non-Invasive Discrimination of Hepatocellular Carcinoma from Cirrhosis

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Background: Plasma derived exosomes in patients with hepatocellular carcinoma (HCC) exhibit a different miRNA expression pattern compared to patients with liver cirrhosis. This feature has made exosomes a promising choice as liquid biopsy biomarkers. Previous studies have shown that level of miR-21 in exosomes obtained from patients with HCC is elevated, while the miR-122 level has decreased compared to normal values. Furthermore, these two regulatory microRNAs have exhibited superior diagnostic performance compared to alpha-fetoprotein (AFP). Accordingly, developing a multi-miRNA panel holds promise for substantially improving diagnostic sensitivity and specificity in distinguishing HCC from cirrhosis. Methods: In our case–control study, 80 patients with imaging- and pathology-confirmed HCC, 80 patients with cirrhosis but no evidence of HCC, and 40 healthy controls were enrolled. Plasma-derived exosomes were isolated using a combined precipitation and ultracentrifugation method and subsequently characterized by the detection of exosomal markers CD63 and TSG101, along with nanoparticle tracking analysis (NTA). RT-qPCR was used to quantify exosomal miR-21, miR-155, and miR-122, with miR-16 as the internal reference. Data were analyzed using Student's t-test or Mann–Whitney U test for continuous variables and chi-square test for categorical variables. Univariate and multivariate logistic regression analyses were conducted, and diagnostic performance was evaluated using ROC curve analysis. Results are presented as AUC, sensitivity, specificity, and odds ratios with 95% confidence intervals. Statistical analyses were performed using Stata (v14.2). Results: Exosomal levels of miR-21 and miR-155 were significantly higher in patients with HCC, whereas miR-122 levels were significantly lower compared with both the cirrhosis and healthy control groups (all $p < 0.001$). For discriminating HCC from cirrhosis, the areas under the ROC curve (AUCs) were approximately 0.85 for miR-21, 0.80 for miR-155, and 0.83 for miR-122, with sensitivities of 70–80% and specificities of 75–85%. A combined diagnostic model incorporating all three miRNAs yielded an AUC of 0.92–0.95, with sensitivity of 85–90% and specificity of 88–92%, demonstrating markedly superior performance compared with AFP alone (AUC ≈ 0.75). Multivariate logistic regression analysis showed that all three miRNAs were independently associated with HCC after adjustment for age, sex, and AFP levels. Conclusion: This three-miRNA exosomal panel

shows strong potential as a noninvasive diagnostic biomarker for differentiating HCC from cirrhosis, outperforming AFP alone. Larger, multicenter validation studies are needed before clinical implementation for early HCC detection.

Keywords: Hepatocellular Carcinoma, Liver Cirrhosis, Exosomes, microRNA, Liquid Biopsy, Diagnostic Biomarkers, Alpha-Fetoprotein

P104

Aptamer-Functionalized Magnetic Beads for Selective Isolation of Circulating Tumor Cells in Lung Cancer

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Background: Lung cancer is still the major cause of cancer death in the world. Circulating Tumor Cells (CTCs) are an important biomarker for non-invasive liquid biopsy and have great potential for early diagnosis and disease monitoring. Nevertheless, because CTCs are rare in peripheral blood, very sensitive and specific enrichment methods are required. Methods: In this study, we designed and constructed a novel magnetic separation system using magnetic beads (Fe3O4) functionalized with specific DNA aptamers targeting EPCAM overexpressed on lung cancer cells. The magnetic beads were synthesized and characterized using TEM, DLS, and FTIR. The aptamers were covalently conjugated to the bead surface. The capture efficiency was evaluated using Lung Cancer Cell Line A549 spiked into healthy human blood. Results: Characterization results confirmed the successful synthesis of uniform magnetic nanobeads and stable aptamer conjugation. The platform demonstrated a capture efficiency of approximately 85%, and cell viability of 93%. Cell counting and viability assessment were performed using the trypan blue exclusion method, confirming reliable enumeration and preservation of cellular integrity. Conclusion: The constructed aptamer-based magnetic beads provide a rapid, specific, and cost-effective strategy for CTC isolation. This method holds great promise for clinical applications in lung cancer diagnosis and personalized therapy.

Keywords: Lung Cancer, Circulating Tumor Cells (Ctcs), Aptamer, Magnetic Beads, Cell Isolation, Liquid Biopsy

P105

Impact of Oxygen Tension on Stem Cell-Derived Extracellular Vesicles: A Systematic Review of Quantity, Cargo, and Angiogenic Pathway Modulation

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Background: Stem cells preconditioning under hypoxia frequently represents an area of great interest concerning improving the potential of the secreted extracellular vesicles (EVs). The systematic review aimed to understand how oxygen tension affects the biophysical properties of stem cell-derived EVs, as well as their content and angiogenic bioactivity. Methods: A literature search was conducted in MEDLINE, Embase, and Web of Science databases according to the PRISMA 2020 guidelines. Eligible studies were original articles that compared EVs derived from stem cells cultured under hypoxia (typically ≤5% O_2) with normoxia. Data from 45 included studies were combined in a narrative manner. Methodological quality was assessed using the SYRCLE risk tool. Results: Hypoxic preconditioning, often at 1–2% O_2 for 48 h, resulted in increased EV yield, while particle size remained largely stable (typically 30–200 nm). Hypoxia induced a profound enrichment of angiogenesis promoter molecules such as miRNAs (e.g., miR-126, miR-210-3p, miR-21-5p), mRNA, protein (e.g., VEGF, angiogenin, annexins), as well as regulatory circRNAs (e.g., circ-IGF1R). In vitro, hypoxia-induced EVs showed robust promotion of endothelial cell growth, migration, and tube formation. In vivo, EVs improved blood perfusion and capillary density (CD31+ vessels) in lower limb ischemia models of myocardial infarction and cutaneous wounds. These were mechanistically associated with activation of the HIF-1α, VEGF/PI3K/AKT, and ERK signaling pathways. Conclusion: Hypoxia increases the production capacity and the angiogenic potential of stem cells-derived EVs. This information increases the validity of performing hypoxic preconditioning as an important step in the standardized production of EVs. Keywords: Angiogenesis, Extracellular vesicles, Exosomes, Hypoxia preconditioning, Stem cells.

Keywords: Angiogenesis, Extracellular Vesicles, Exosomes, Hypoxia Preconditioning, Stem Cells

P106

Transcript-Dependent Post-Transcriptional Regulation of RHOA in Breast Cancer

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Background: RhoA is a small GTPase that plays a key role in cytoskeletal organization, cell migration, and signal transduction—processes frequently dysregulated in breast cancer progression and metastasis. Alternative splicing of RhoA generates transcripts with distinct untranslated regions (UTRs), which may influence gene expression regulation without altering protein structure. Understanding transcript-specific regulatory mechanisms may provide insight into RhoA-mediated functions in breast cancer. Methods: Protein structure prediction for RhoA isoform 2 (187 amino acids) was conducted using the Protein Homology/analogY Recognition Engine (Phyre2). RNA secondary structure folding energies of the 5′ and 3′ UTRs were analyzed for RhoA transcript 1 (ENST00000418115.6) and transcript 3 (ENST00000422781.6) using UCSC database data. Protein structures encoded by these transcripts (NP_001655.1 and NP_001300872.1) were compared using the NCBI database. The functional implications of UTR structural differences were interpreted in the context of known RhoA roles in breast cancer biology. Results: Structural modeling confirmed that RhoA isoform 2 maintains a conserved protein structure across transcripts. Analysis of the 5′ UTR revealed that transcript 1 exhibited a more negative folding energy (−52.90 kcal/mol) than transcript 3 (−49.00 kcal/mol), indicating greater structural stability that may impede ribosome scanning and reduce translation efficiency. In contrast, the less stable 5′ UTR of transcript 3 may support more efficient translation initiation. Analysis of the 3′ UTR showed that transcript 3 had a more negative folding energy (−319.50 kcal/mol) compared with transcript 1 (−267.00 kcal/mol), suggesting increased mRNA stability and enhanced interactions with regulatory proteins or microRNAs. These transcript-specific regulatory features may influence RhoA expression levels in breast cancer cells, potentially affecting tumor cell migration, invasion, and metastatic potential. Conclusion Although RhoA protein structure is conserved between transcripts, significant differences in UTR folding energy suggest transcript-dependent post-transcriptional regulation. In the context of breast cancer, transcript 3 may promote higher RhoA expression through enhanced translation efficiency and mRNA stability, potentially contributing to cancer cell motility and disease progression. These findings highlight the importance of alternative transcript regulation of RhoA as a potential mechanism influencing breast cancer behavior and warrant further functional validation.

Keywords: RhoA, Breast Cancer, Post-Transcriptional Regulation, Phyre2

P107

The IGF-1/IGF-1R Axis in Peripheral Blood Mononuclear Cells and Serum: Diagnostic, Prognostic, and Therapeutic Significance in Lung Cancer

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Background: Lung cancer remains one of the leading causes of cancer-related mortality worldwide. Identification of non-invasive biomarkers that reflect not only disease presence but also disease severity and treatment status is of significant clinical importance. The insulin-like growth factor (IGF) axis plays a critical role in cancer cell proliferation, survival, and tumor progression. Methods: This case–control study included 60 biological samples derived from 30 patients diagnosed with lung cancer—comprising both metastatic and non-metastatic cases—and 30 age- and sex-matched healthy controls.Patients were further stratified based on disease severity and treatment status. Peripheral blood mononuclear cells (PBMCs) were isolated, and the gene expression level of IGF-1 receptor (IGF-1R) was quantified using real-time PCR.Serum concentrations of insulin-like growth factor-1 (IGF-1) and its primary binding protein, IGFBP-3, were quantified using enzyme-linked immunosorbent assay (ELISA). Comparative statistical analyses were subsequently conducted to assess intergroup differences and to evaluate the diagnostic or prognostic potential of these IGF axis components as biomarkers. Results: IGF-1R gene expression in PBMCs was significantly higher in lung cancer patients compared with healthy controls. Increased IGF-1R expression was associated with higher disease severity and metastatic status. Moreover, differences in IGF-1R expression and serum levels of IGF-1 and IGFBP-3 were observed between treated and untreated patients, suggesting a potential relationship with treatment status. All evaluated components of the IGF axis demonstrated notable discriminatory power between patients and controls. Conclusion: These findings indicate that IGF-1R expression in PBMCs, together with serum IGF-1 and IGFBP-3 levels, may serve as non-invasive biomarkers for lung cancer diagnosis, disease severity assessment, and treatment-related monitoring. The IGF axis represents a promising target for liquid biopsy–based evaluation in lung cancer.

Keywords: Lung Cancer, PBMC, IGF_1, IGF_1R, IGFBP3, Biomarkers, Treatment Response

P108

BMI-1 Gene Expression in Patients with Acute and Chronic Myeloid Leukemia in the Northeast of Iran

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Background: The B-cell-specific Moloney murine leukemia virus integration site1 (BMI-1) is one of the famous members of the Polycomb ring finger group, which plays a crucial role in the gene transcription regulation through histone changes. Hence, it is believed to be necessary to further clarify the clinical effects of BMI-1. Method: This cross-sectional study was conducted on 70 acute myeloid leukemia (AML), 70 chronic myeloid leukemia (CML), and 20 healthy individuals, as the control group. We used real-time quantitative polymerase chain reaction in order to assess the BMI-1 level expression and its effect on prognosis in AML patients in the Molecular Pathology Research Center. Results: The results of the present work indicated that the BMI-1 overexpression was significantly higher in the AML and CML patients compared with that in the healthy controls ($P < 0.001$). Furthermore, a significant relationship was observed between the BMI-1 overexpression and poor prognosis in the AML patients (Hazard ratio=1.749, $P < 0.001$, 95% confidence interval = 1.31-2.32). Additionally, BMI- 1high was found in chronic and blastic phase in the CML patients ($P < 0.001$). Conclusion: We concluded that investigation of BMI-1 gene expression pattern will be conducive to the prognosis and treatment of myeloid leukemia.

Keywords: BMI-1 Gene, Acute Myeloid Leukemia, Chronic Myeloid Leukemia, Prognostic effect

P109

Diagnostic Performance of Multiplex PCR versus Culture for Rapid Identification of Common Gram-Negative Uropathogens in Urine Samples

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Background: Urinary tract infections (UTIs) are among the most common bacterial infections worldwide. Uropathogenic Escherichia coli is the most common Gram-negative causative bacterium, followed by Klebsiella pneumoniae and Proteus mirabilis. Rapid and accurate detection of causative pathogens is essential for appropriate therapy and infection control. This study aimed to evaluate the diagnostic performance of multiplex PCR for the detection of common Gram-negative uropathogens directly from urine samples. Methods: Four pairs of species-specific primers were applied in a multiplex PCR assay for the detection of Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Proteus mirabilis. The diagnostic performance of multiplex PCR was evaluated in comparison with urine culture as the gold standard, using samples obtained from 34 patients with UTI. Results: Out of 34 urine samples included in the comparative analysis, 19 (55.88%) were positive for the target Gram-negative bacteria by culture, while 15 (44.11%) were culture-negative or yielded other organisms. Multiplex PCR identified 15 Escherichia coli (44.11%), 11 Klebsiella pneumoniae (32.35%), 6 Pseudomonas aeruginosa (17.64%), and 2 Proteus mirabilis (5.88%). In comparison with culture, 15 samples were true positive and 7 were true negative. Four samples were false negative and eight were false positive. Accordingly, the sensitivity, specificity, positive predictive value, and negative predictive value of multiplex PCR were 78.94%, 46.71%, 65.25%, and 63.61%, respectively. Conclusion: Multiplex PCR demonstrated good sensitivity for the rapid detection of common Gram-negative uropathogens directly from urine samples. While specificity was moderate compared with culture, this method can complement conventional culture for early diagnosis and timely management of UTIs.

Keywords: Urinary Tract Infection, Multiplex PCR, Gram-Negative Bacteria, Uropathogens

P110

Evaluating the Local Gene and Protein Expression of Matrix Metalloproteinase-9 in Osteosarcoma Patients and its Association with Clinicopathologic Features

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Background: Osteosarcoma is the most frequent type of primary malignant bone tumors. This type of cancer is well known by its aggressive behavior regarding to the metastasis and developing secondary tumors. Considering poor prognosis and lack of specific approaches to early detection, assessment of molecular targets is necessary to clarify its underlying pathological mechanisms and providing biomarkers to more accurate diagnosis. Methods: The total number of 60 tissue samples (30 cancerous tissues, and 30 normal adjacent tissues) were assessed to determine local pattern of MMP-9 expression. Real-time PCR and immunohistochemistry were used to evaluate the mRNA and protein levels of MMP-9. t-test and Mann–Whitney U test were performed to clarify the differences between tumor tissues and their relevant controls. Additionally, the correlation of the MMP-9 expression with demographic features of patients were assessed. Also, the ROC curve and regression models were used to evaluate the MMP-9 diagnostic and predictive values. Results: Tumor tissues demonstrated significant increased of MMP-9 gene and protein expression compared to the paired non-cancerous tissues. Also, patients with more severe conditions, especially, metastatic tumors, had higher expression of MMP-9. Meanwhile, the expression pattern of MMP-9 was associated with tumor invasiveness and regression models indicated the value of MMP-9 expression in predicting clinicopathologic features, such as grade, chemotherapy status, Metastasis, and recurrence of tumor. In addition, the amount of MMP-9 expression significantly discriminated tumor tissues from normal adjacent tissues. Conclusion: Collectively, our data shed more light on the possible role of MMP-9 in mediating pathophysiologic mechanisms involving in progression of osteosarcoma. In addition, our study clarifies the diagnostic value and therapeutic potential of MMP-9 in detection and treatment of the patients.

Keywords: MMP-9, Osteosarcoma, High-Grade, Metastasis, Recurrence

P111

Downregulated Extracellular Matrix-Associated CILP and MFAP4 Genes Reveal Link to Prognostic Value in Colorectal Cancer

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Background: Colorectal cancer (CRC) is a leading cause of cancer mortality. The extracellular matrix (ECM) plays a critical role in tumor progression, and its associated genes may serve as prognostic biomarkers. This study investigated two ECM-related genes CILP and MFAP4 to evaluate their expression and clinical significance in CRC development. Methods: RNA-seq data from TCGA-COAD and microarray datasets (GSE23878, GSE89076) were analyzed to identify differentially expressed genes (DEGs). Experimental validation was performed using RT-qPCR on 20 paired CRC and adjacent non-cancerous tissues. Associations between gene expression, clinicopathological features, and overall survival were assessed. Results: Both RNA-seq and microarray analyses revealed significant downregulation of CILP and MFAP4 in CRC tissues compared to non-cancerous samples ($p < 0.05$). RT-qPCR confirmed lower expression levels in tumor tissues ($p < 0.0001$). Survival analysis showed non-significant trends toward poorer prognosis in patients with lower gene expression. Univariate Cox regression analysis revealed no significant association between age, sex, histologic grade, Clinical stage, and low expression of CILP and MFAP4 with overall survival in CRC patients ($P > 0.05$). To assess the independent prognostic value of CILP and MFAP4, we performed multivariate Cox proportional hazards regression, adjusting for age, gender, histological grade, and clinical stage. In the adjusted model, clinical stage remained a significant independent prognostic factor for the CILP ($p = 0.04$) and MFAP4 ($p = 0.04$) models, confirming its established strong association with survival. Conclusion: These findings demonstrated that CILP and MFAP4 function as potential tumor suppressors in CRC. Their significant downregulation in tumor tissues and associations with and clinical features highlighted their possible role in CRC pathogenesis, making them potential therapeutic targets.

Keywords: Colorectal Neoplasm, Extracellular Matrix, Prognosis

P112

Antisense Oligonucleotides: Targeting Oncogenic Long Non-Coding RNAs for Cancer Therapy

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Purpose: This narrative review aims to summarize current evidence on antisense oligonucleotide (ASO)-based strategies targeting oncogenic long non-coding RNAs (lncRNAs) and to evaluate their therapeutic potential in cancer initiation, progression, metastasis, and treatment resistance. Methods: A narrative review of preclinical studies was conducted, focusing on ASO-mediated silencing of cancer-associated lncRNAs, including MALAT1, PVT1, NEAT1, and other emerging lncRNAs, across multiple malignancies such as lung, breast, ovarian, gastrointestinal, and head-and-neck cancers. Advances in ASO chemical design and delivery strategies—including lipid and polymeric nanoparticles, ligand-directed conjugates, peptide-based carriers, and gymnotic uptake—were also examined. Results: Preclinical evidence consistently demonstrates that lncRNA-targeted ASOs efectively suppress tumor growth, invasion, metastasis, and chemoresistance while promoting apoptosis. Improvements in ASO chemical modifcations and delivery platforms have signifcantly enhanced ASO stability, biodistribution, and intracellular uptake, thereby improving therapeutic efcacy across diverse cancer models. Conclusion: Targeting oncogenic lncRNAs using ASO-based approaches represents a promising and rapidly evolving strategy in precision oncology. Although substantial progress has been achieved in ASO design and delivery, further optimization and well-structured clinical trials are required to facilitate the translation of these therapies into routine cancer treatment

Keywords: Antisense Oligonucleotides, Long Non-Coding RNAs, Oncogenic lncRNAs, Cancer Therapy, Precision Oncology, RNA-Based Therapeutics

P113

Improving the Quality of Molecular Diagnosis of Antibiotic Resistance Using Bacterial Membrane Vesicles, CRISPR, and Metagenomics

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Background: Antibiotic resistance (AMR) is recognized as one of the most serious global health threats. Rapid detection of resistant pathogens is the key to infection control. However, conventional diagnostic methods are often time-consuming and have limitations in sensitivity. Bacterial membrane vesicles (BMVs/EVs) have emerged as promising sources of resistance biomarkers. CRISPR-based diagnostics and metagenomics, as advanced detection technologies, enable direct and comprehensive identification of the resistance genes (resistome) without the need for culture, as well as rapid, sensitive, and specific detection. This study aims to propose a novel diagnostic framework based on the integration of BMVs/EVs, metagenomics, and CRISPR to improve the molecular diagnosis of AMR. Methods: This study was conducted as a comprehensive review with a systematic search in PubMed, Scopus, and ScienceDirect databases. Search keywords included "bacterial membrane vesicles", "antibiotic resistance", "molecular detection", "metagenomics", and "CRISPR". Articles published from 2020 to the present were reviewed. Key findings were extracted and presented as an integrated diagnostic framework. Results: Relevant studies demonstrated that BMVs/EVs serve as reservoirs of resistance biomarkers, containing β-lactamases, resistance genes, DNA, and RNA, while protecting their cargo against degradation by nucleases. Metagenomics enables complete resistome profiling without culture, and CRISPR (e.g., Cas12/Cas13) provides rapid confirmation of resistance genes such as blaNDM and mecA. In the "EV-CRISPR-Metagenomics" framework, bacterial extracellular vesicles are first isolated and enriched from clinical samples. Then, metagenomic sequencing of their cargo identifies all resistance genes, pathogen species, and virulence factors without culture. Finally, CRISPR-Cas systems are used for point-of-care confirmation of key resistance genes. Conclusion: This integrated approach, with high sensitivity (vesicle enrichment), comprehensive coverage (metagenomics), and rapid confirmation (CRISPR), reduces turnaround time from several days to a few hours and enables the design of point-of-care kits. Despite challenges such as standardization of vesicle isolation and the high cost of sequencing, this framework holds significant potential for the development of next-generation point-of-care diagnostic kits.

Keywords: Bacterial Membrane Vesicles, Antibiotic Resistance, Molecular Diagnosis, CRISPR, Metagenomics, Point-of-Care Diagnostics

P114

Study of the Prevalence of Human Papillomavirus in Samples of Symptomatic Patients Referred to Private Laboratories Affiliated with Mazandaran University of Medical Sciences in 2024-2025

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Background and Objectives: Human papilloma viruses (HPV) are the most common sexually transmitted viruses that comprise more than 230 types of viruses that cause cervical cancer, which is the fourth most common cancer in women. Materials and Methods: The study population included patients suspected of having HPV who referred to private and public laboratories in Mazandaran Province in 2024-2025. In this study, 12753 patients were sampled with the aim of determining the frequency in men and women and in 4 age groups and Types of high and low risk HPV genotypes and smear cytology have been performed and examined using the RT-PCR kit. Findings: In this study, out of a total of 12753 samples, 3636 cases (28.51%) were positive, of which 89.27% were women and 10.73% were men. most of the samples were related to the age group under 30 -40years old with a number of 5282 cases (41.42%) and above 50 years has the lowest number of 1045 cases (8.19%). The most frequency of high-risk genotypes were H16, H52, H56 and the most frequent of low-risk genotypes was L6, L11, L42. and the highest frequency among the high and low risk genotypes, respectively, the genotypes that were the most abundant include H16, L6, H52, H56,. In the cytology examination, 6.49% of the positive cases were HSIL, 10.26% LSIL and 28.77% were in Ascus form. Conclusion: With timely and faster diagnosis, especially high-risk genotypes, RT-PCR molecular methods can save the patient from death. HR HPV infection can cause cytological and histological changes that can be detected by Pap smear screening, colposcopy or biopsy.

Keywords: Human Papillomavirus (HPV), Genotype, High Risk, Low Risk, RT-PCR

P115

Extracellular Vesicle-Derived MicroRNAs as Emerging Biomarkers for Early Diagnosis and Risk Stratification of Sepsis: A Systematic Review

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Background: The heterogeneity of clinical presentation and the limited diagnostic performance of conventional biomarkers such as C-reactive protein (CRP) and procalcitonin (PCT) still represent a major clinical challenge in the early diagnosis of sepsis. Recently, extracellular vesicle (EV)-derived microRNAs (miRNAs) have been proposed as potential minimally invasive biomarkers because of their biological stability and involvement in immune and inflammatory signaling pathways related to sepsis. Methods: A preliminary systematic literature search was performed on PubMed, Scopus, Web of Science and supplementary Google Scholar to find studies on extracellular vesicle or exosome-derived miRNAs in patients with sepsis or septic shock. Eligible studies were human observational studies evaluating diagnostic or prognostic utility of EV-derived miRNAs. Relevant data on study population, EV isolation methods, miRNA profiling techniques and reported diagnostic outcomes were extracted and qualitatively synthesized. Initial searches identified approximately 80 potentially relevant records, of which almost 35 studies passed the initial eligibility criteria after title and abstract screening. Several EV-associated miRNAs, including miR-150, miR-223, miR-146a, miR-483-3p and let-7d-3p, showed promising diagnostic and prognostic potentials in patients with sepsis. Across the studies included, EVderived miRNAs were associated with disease severity, inflammatory response, organ dysfunction, and mortality related outcomes. Some studies have demonstrated better diagnostic performance than conventional inflammatory markers particularly in early stage sepsis and septic shock. However, a high methodological heterogeneity was observed for EV isolation protocols, sample sources and miRNA quantification techniques. Results: Initial searches identified approximately 80 potentially relevant records, of which almost 35 studies passed the initial eligibility criteria after title and abstract screening. Several EV-associated miRNAs, including miR-150, miR-223, miR-146a, miR-483-3p and let-7d-3p, showed promising diagnostic and prognostic potentials in patients with sepsis. Across the studies included, EVderived miRNAs were associated with disease severity, inflammatory response, organ dysfunction, and mortality-related outcomes. Some studies have demonstrated better diagnostic performance than conventional inflammatory markers, particularly in early stage sepsis and septic shock. However, a high methodological heterogeneity was observed for EV isolation protocols, sample sources and miRNA quantification techniques. Conclusion: Extracellular vesicle-derived miRNAs could be

potential biomarkers for early sepsis diagnosis and risk stratification. However, before routine clinical implementation, standardization of analytical methods and larger multicenter studies are required. Further systematic evaluation and quantitative synthesis may elucidate their clinical applicability in critical care settings.

Keywords: Sepsis, Extracellular Vesicles, Exosomes, microRNA, Biomarkers, Septic Shock, Diagnostic Accuracy

Laboratory Economics in Normal and Crisis Conditions

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P116

Walking Blood Bank System for Mass Casualty Management in War and Disasters

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Uncontrolled massive hemorrhage is the primary cause of potentially preventable battlefield deaths. More than 90% of casualties die before reaching the field hospital, making early blood transfusion in the field critical. On the other hand, there are some logistical limitations in both blood supply and transfusion equipment in combat zones. Therefore, military blood bank systems must ensure the availability of blood transfusion for combat injuries to mitigate the negative effect of postponed medical interventions. Since 2016, the Joint Trauma System guidelines have recommended the use of whole blood (WB) instead of component therapy. WB has many biological advantages by providing all the blood components in a single unit, which is important in logistically challenging situations. The term Walking Blood Bank (WBB) describes a rapid collection of whole blood from a pool of prescreened donors available "on call" for emergency use at the site of emergency need. WBB has been used successfully in military medical services in cases of depletion of inventories. In this protocol, a soldier donates blood into a transfer bag and then returns to the fight within about 10 minutes. Low titer group O whole blood is recommended for use in combat casualty care because it offers plasma, red cells and platelets in a balanced ratio in a logistically advantageous way. It can be transfused to anyone in need, regardless of their blood group. Potential risks for WBB are unsanitary field conditions, the impossibility of testing blood products, donors and unreliable donor information and adverse transfusion reactions. WBB system may provide rapid, safe, and adequate blood supply in the combat zone. However, more research is needed in this field.

Keywords: War, Disaster, Bleeding, Blood Bank

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The Role of Digital Financial Innovation in Enhancing Efficiency, Transparency, and Economic Sustainability in Medical Diagnostic Laboratories

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In recent years, digital transformation in healthcare has moved beyond clinical and diagnostic processes and has increasingly influenced the managerial, financial, and operational dimensions of healthcare organizations. Medical diagnostic laboratories, as one of the key components of the diagnosis and treatment chain, face several financial challenges, including rising costs of equipment and consumables, delayed reimbursement from insurance organizations, complex accounting procedures, limited financial transparency, and the growing need to improve patient satisfaction. In this context, digital financial innovation can be considered an effective approach to improving both the financial performance and operational efficiency of diagnostic laboratories. Digital financial innovation refers to the application of technology-based financial solutions such as electronic payments, digital wallets, electronic invoicing, intelligent accounting systems, financial data analytics, digital interaction with insurance providers, and health-oriented fintech platforms. The adoption of these tools in medical diagnostic laboratories can accelerate admission and payment processes, reduce human errors, improve the accuracy of transaction records, increase transparency in revenues and expenditures, and enhance cash flow management. Moreover, the digitalization of financial processes enables laboratory managers to monitor financial performance in real time, forecast financial needs, control unnecessary costs, and make more informed decisions based on reliable data. Another important area in which digital financial innovation can create significant value is the relationship between laboratories and insurance organizations. Electronic submission of documents, intelligent verification of claims, reduction of financial discrepancies, and shorter reimbursement cycles can contribute to more efficient cooperation between laboratories and payers. In addition, transparent billing, remote payment options, and easier access to financial information related to laboratory services can strengthen patient trust and improve the overall service experience. Despite these advantages, the implementation of digital financial innovation in medical diagnostic laboratories is not without challenges. Data security and confidentiality, initial implementation costs, lack of integrated infrastructure, resistance to organizational change, and regulatory uncertainties are among the major barriers to adoption. Therefore, the successful application of these innovations requires careful planning, staff training, the development of clear operational standards, and investment in secure and interoperable digital infrastructure. Overall, digital financial innovation can play a

strategic role in enhancing efficiency, transparency, and economic sustainability in medical diagnostic laboratories. By integrating financial technologies with laboratory management systems, these centers can improve their financial resilience, optimize administrative processes, and support the delivery of higher-quality diagnostic services in an increasingly digital healthcare environment.

Keywords: Digital Financial Innovation, Medical Diagnostic Laboratories, Health Fintech, Financial Management, Digital Transformation, Electronic Payment

Microbiomes and Their Impact on Health and Disease

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P118

The Role of HPV Infection in Shaping the Vaginal and Cervical Microbiome and Its Association with Clinical Outcomes

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Microbial communities, which coexist symbiotically with us, aid in metabolic processes, and bolster our immunological defenses against pathogens, are essential to the human defense system. With their interactions playing a crucial role in determining the health or disease condition, a varied bacterial community in the vagina helps to maintain dynamic homeostasis. The primary cause of cervical cancer is persistent, high-risk human papillomavirus (HPV) infections. Evidence is growing that the cervicovaginal microbiome is crucial in regulating HPV persistence and the development of cervical neoplasia. Although it is thought that more than 80% of sexually active women acquire this infection at least once in their lives, the majority of cervical HPV infections disappear on their own. However, in a small percentage of women, the virus remains in the cervix and causes dysplasia and cancer. The vaginal microbiome, specifically the shift from communities dominated by Lactobacillus crispatus to dysbiotic conditions high in Gardnerella, Fannyhessea, and Sneathia, has become a major regulator of HPV persistence, local inflammation, and epithelial alteration. In particular, commensal bacteria have a variety of immunoregulatory roles that can either boost or reduce anti-tumor responses. This study emphasizes the current understanding of how host factors influence the makeup of the vaginal microbiome, as well as how the vaginal microbiome plays a role in preserving homeostasis or promoting pathogenesis. A greater understanding of the relationship between the host and the vaginal microbiome may reveal new targets for the diagnosis, prognosis, or therapy of disorders associated with the microbiome.

Keywords: Cervicovaginal Microbiome, Human Papillomavirus (HPV), Cervical Cancer, Lactobacillus Dominance, Microbial Dysbiosis

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The Modulatory Role of Intestinal Helminths in the Composition and Diversity of the Human Gut Microbiome: Immunological and Therapeutic Implications

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Background: Intestinal helminths like the Trichuris trichura and Ascaris lumbricoides are known as harmful pathogens, but recent studies have highlighted their ability to regulate the microbiome of the human gut. Such modulations can expand the diversity of bacteria and optimize immune reactions, thus creating therapeutic opportunities to inflammatory diseases. This study evaluates how helminths can alter the microbiome composition and diversity of the gut, the immunological effects of the helminths and the therapeutic consequences. Methods: A systematic literature search has been conducted in PubMed, Scopus, Web of Science, and included ISI indexed articles on the period 2010-2025. Keywords used included helminths, gut microbiome, immune modulation, and therapeutic implication. Human and animal experiments of alpha and beta diversity, changes in bacteria, and immune response results were chosen. Results: Eighteen articles identified that helminth infections increase alpha and beta microbial diversity, enrich the commensal species of Lactobacillus and Bifidobacterium, and alleviate dysbiosis. The evidence indicates that the presence of helminths is associated with enhanced microbial diversity, which is mediated by the release of anti-inflammatory cytokines (IL-10) and activation of regulatory T cells, which facilitate type 2 immunity. Such changes can provide immunity to inflammatory bowel disease (IBD), allergies, and autoimmune disorders. Helminth interventions have demonstrated preclinical success in animal models as well as in preliminary clinical studies in relieving IBD symptoms; however, the effect of helminth interventions differs based on the intensity of infection and the species of helminths. Conclusion: Helminths have a modulatory effect on the microbiome, and they have a therapeutic potential in immunoregulatory disorders.

Keywords: Helminths, Gut Microbiome, Immune Modulation, Therapeutic Implications

P120

Investigation of the Drug Sensitivity of Candida Species Isolated from the Mouth to Hydroalcoholic Extracts of Medicinal Plants Rosemary and Milk Thistle Compared to Common Antifungal Drugs in In Vitro Conditions in the Year 2025-2026

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Background: Oral candidiasis is a common fungal infection of the oral mucosa, primarily caused by Candida species. These fungi are part of the normal oral flora but may become pathogenic in conditions such as immunosuppression or the use of immunosuppressive drugs. Conventional antifungal agents like nystatin and fluconazole are effective; however, increasing drug resistance has prompted interest in medicinal plants with antifungal properties as natural alternatives. Rosmarinus officinalis (rosemary) and Silybum marianum (milk thistle) have reported antimicrobial effects. Limited research in Iran exists regarding their activity against oral Candida isolates, motivating this study to investigate the antifungal effects of hydroalcoholic extracts of rosemary and milk thistle under laboratory conditions. Methods: This experimental study was descriptive-analytical and fundamental-applied, conducted ethically using samples from a previous study at Poursina Neurology Clinic, Rasht, and the Serology Laboratory, Tehran University of Medical Sciences. Samples were re-examined with 10% potassium hydroxide for initial identification, then cultured on Sabouraud dextrose agar with chloramphenicol to isolate fungi. Species differentiation was performed using Candida chromagar and cornmeal agar, and Candida albicans was confirmed by chromagar colony color and chlamydoconidia formation. Susceptibility of isolates to fluconazole and nystatin (64 µg/mL) and hydroalcoholic extracts of rosemary and milk thistle (500 mg/mL) was assessed using the CLSI/NCCLS M27-A3 microbroth dilution method. Candida krusei ATCC 6258 was used for quality control. Hydroalcoholic extracts were prepared by soaking authenticated plant material. Fungal suspensions were adjusted to McFarland 0.5 (~10^6 cells/mL). Minimum inhibitory concentrations (MICs) and minimum fungicidal concentrations (MFCs) were determined. All experiments were performed in triplicate, and mean values were reported. Results: Among 76 Alzheimer's patients (40 females, 36 males), 48 fungal-positive isolates were obtained, of which 45 were Candida species: 37 C. albicans, 5 C. glabrata, 2 C. parapsilosis, and 1 C. krusei. C. albicans was the predominant species and underwent drug susceptibility testing. Both fluconazole and nystatin showed significant inhibitory activity. MIC ranges for fluconazole were 0.125–64 µg/mL (MIC50=2, MIC90=64), while for nystatin, 0.5–4 µg/mL (MIC50=1, MIC90=2), indicating stronger activity for nystatin. Among plant extracts, rosemary showed MIC 0.244–62.5 mg/mL, and milk thistle 0.244–31.25 mg/mL; MIC50 for both was 3.906 mg/mL and MIC90 15.625 mg/mL. Both extracts exhibited antifungal activity,

with milk thistle demonstrating the strongest effect among herbal extracts. Conclusion: Candida isolates from the studied Alzheimer's patients remained susceptible to standard antifungal drugs. Hydroalcoholic extracts of rosemary and milk thistle demonstrated antifungal activity, with milk thistle showing the most potent effect, suggesting their potential as natural adjunctive therapies against oral candidiasis.

Keywords: Drug Sensitivity, Candida Species, Medicinal Plants, Antifungal Drugs, In Vitro Conditions

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Shadows of Resistance in Colorectal Cancer: Clinical Impact of Carbapenem- and Metronidazole-Related Determinants in Bacteroides Fragilis

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Background: Bacteroides fragilis is a key anaerobic pathogen in colorectal cancer (CRC) patients, yet routine anaerobic antimicrobial susceptibility testing (AST) is rarely performed in clinical laboratories. We aimed to evaluate phenotypic resistance and critical genetic determinants with direct implications for empirical therapy and laboratory stewardship in CRC patients compared with healthy individuals. Methods: In a 12-month case–control study, 60 stool isolates of B. fragilis from histologically confirmed, non-metastatic CRC patients and 60 from age- and sex-matched healthy controls were analyzed. AST for 10 agents, including carbapenems and metronidazole, was performed by broth microdilution following CLSI M11-Ed11. Polymerase chain reaction was used to detect nim, cfiA, cepA, and bft genes, and genotype–phenotype correlations were assessed using standard statistical tests. Results: CRC isolates showed higher resistance to meropenem (25.9% vs 19.2%, p=0.045) and moxifloxacin (23.1% vs 17.0%, p=0.049), with overall high clindamycin resistance (≈77%) in both groups. Phenotypic metronidazole resistance remained low (3.5%), but the nim gene was exclusively detected in CRC isolates (8.3% vs 0%, p=0.027), indicating a silent reservoir for future resistance under drug pressure. The cfiA carbapenemase gene was more prevalent in CRC patients (25.0% vs 13.3%, p=0.048), while cepA was ubiquitous and bft carriage was significantly higher in CRC isolates (93.3% vs 78.3%, p=0.025). Conclusion: CRC-associated B. fragilis isolates exhibit a more alarming resistance and virulence profile, combining nim-mediated metronidazole resistance potential with enriched cfiA-positive strains and high bft prevalence. Implementing routine anaerobic AST and targeted PCR screening for nim and cfiA in CRC patients can enhance laboratory quality, optimize empirical regimens, and prevent treatment failure in this high-risk group.

Keywords: Bacteroides Fragilis, Colorectal Cancer, Antimicrobial Resistance, Nim Gene, cfiA

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The Correlation Between Cervical Intraepithelial Neoplasia and Sexually Transmitted Infections

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Background: Cervical intraepithelial neoplasia (CIN) is a precursor lesion for cervical cancer, with human papillomavirus (HPV) being the major cause. Co-infection with other sexually transmitted infections (STIs) may affect cervical inflammation, HPV persistence, and CIN development. This study aimed to evaluate the correlation between CIN grade and STIs. Methods: In this study, we recruited 41 women between the ages of 18 and 50 who were undergoing colposcopy for abnormal cervical screening results or positive HPV testing. Cervical specimens were tested for ten STIs by PCR-based flow-hybridization assays. Colposcopy and histopathology results were recorded. Fisher's exact test, Spearman correlation, and logistic regression were used for data analysis. Results: The study population had a mean age of 34.1 ± 7.4 years, with a prevalence of 80% for high-risk HPV. Among the 36 patients with available histopathology results, a weak positive correlation was found between CIN grade and STIs; however, this was not statistically significant ($r = 0.192$, $p = 0.261$). Ureaplasma parvum and Mycoplasma genitalium were the two STIs with the highest prevalence among study patients. There was no significant correlation between CIN grade and other factors, including age, marital status, and sexual activity. Conclusion: Although a positive correlation was observed, no significant relationship was found between CIN grade and STIs in our study population. This study provides important information on STIs and CIN grade among Iranian women and emphasizes the need for further studies in this regard. Keywords: Human Papillomavirus Viruses, Cervical Intraepithelial Neoplasia, Sexually Transmitted Diseases, Ureaplasma, Mycoplasma genitalium

Keywords: Human Papillomavirus Viruses, Cervical Intraepithelial Neoplasia, Sexually Transmitted Diseases, Ureaplasma, Mycoplasma genitalium

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Gut Microbiome Profiling Guiding a Precision Approach for Acute Graft-Versus-Host Disease Prediction

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Background: In the context of allogeneic hematopoietic stem cell transplantation (allo-HSCT), the pre-transplant conditioning regimen increases intestinal permeability and microbial translocation from the lumen to the lamina propria, as evidenced by gut microbiome (GM) dysbiosis. These phenomena activate antigen presentation to alloreactive T cells, modulate innate and adaptive immune responses, and alter microbiota-derived immunomodulatory metabolite profiles, thereby driving the development of acute graft-versus-host disease (aGVHD). In this conference abstract, we focus on GM profiling as a tool for predicting aGVHD, highlighting its potential as a precision and personalized approach Methods: Eligible studies were identified from the PubMed, Google Scholar, and Web of Science databases. Articles in English were identified using the following MeSH terms and keywords: gut microbiome, dysbiosis, acute graft-versus-host disease, and prediction. Results: A comprehensive literature search indicated that age-related and person-specific alterations in GM diversity and abundance before and after transplantation are significantly associated with the development of aGVHD. In this line, longitudinal analysis of patients' samples by 16S rRNA sequencing and shotgun sequencing revealed patients with aGVHD had a significant reduction in short-chain fatty acid (SCFA)-producing bacteria such as Faecalibacterium, Blautia, Ruminococcaceae, Bacteroides, and Clostridia, which have a protective role in maintaining intestinal mucosal integrity and modulating immunity; in contrast, opportunistic species such as Enterococcus, Escherichia-Shigella increased, which can promote inflammation and T cell hyperactivation by releasing lipopolysaccharide. Meanwhile, liquid/gas chromatography-mass spectrometry showed decreases in protective metabolites, such as butyrate, acetate, propionate, and indole derivatives, while increases in metabolic pathways related to bile acids and glycolysis/pyruvate, indicating profound functional alterations in the microbiome-immune axis. These results suggest that a combined profile of species and metabolites could serve as a predictive biomarker for aGVHD and enhance therapeutic strategies based on microbiome and metabolome modification. Conclusion: GM diversity, a decrease in commensal and beneficial strict anaerobes, and overgrowth of pathobionts,

together with alterations in the spectrum of bacterial metabolites, predisposed patients to aGVHD. Given that interindividual differences in GM profiles greatly exceed intraindividual changes over time, microbiome profiling can establish a personalized microbiome fingerprint for each patient for aGVHD prediction. Future studies should focus on standardizing laboratory methods for GM assessment and on improving individualized microbiome-based predictive models to guide precision preventive and therapeutic strategies for aGVHD.

Keywords: Gut Microbiome, Acute Graft-Versus-Host Disease, Prediction, Precision Medicine

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Link Between Helicobacter pylori Infection and Colorectal Polyps: Implications for Screening in Northern Iran

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Background: Helicobacter pylori (H. pylori) is a common gastrointestinal pathogen implicated in gastric malignancies, and emerging evidence suggests a potential link to colorectal neoplasia. However, the association between H. pylori infection and colorectal polyps remains controversial. This study aimed to investigate the relationship between H. pylori infection and colorectal polyps in a Middle Eastern population with high background prevalence of both conditions. Methods: In this hospital-based cross-sectional analytical study, 382 adults undergoing both upper endoscopy and colonoscopy at Razi Hospital in Rasht, Iran, were enrolled over a one-year period. H. pylori infection was detected via histopathological examination of gastric biopsies. Colorectal polyps were identified during colonoscopy and confirmed by histological evaluation. Demographic, clinical, and lifestyle data were collected. Logistic regression analyses were performed to assess the association between H. pylori infection and colorectal polyps, adjusting for age, sex, and other confounders. Results: The mean age of participants was 56.93 ± 13.51years with aged 18 years and older. The overall prevalence of H. pylori infection and colorectal polyps was 48.4% and 33.0%, respectively. No significant association was observed between H. pylori infection and colorectal polyps in unadjusted (OR=1.10; 95% CI: 0.72–1.68; P=0.667) or adjusted models (adjusted OR=1.19; 95% CI: 0.76–1.87; P=0.435). Polyp prevalence increased significantly with age (P for trend = 0.049) but did not differ by sex or H. pylori status. Conclusion: This study found no significant association between H. pylori infection and colorectal polyps. These results underscore the need for further prospective and mechanistic research across diverse populations to clarify this relationship.

Keywords: Helicobacter Pylori, Colorectal Polyps, Colonoscopies, Colorectal Neoplasia

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Evolution of Microbiota Analysis Approaches in Obesity from 16S rRNA to Machine Learning: A Narrative Review

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Background and aim Shifts in body weight have been associated with compositional changes in the gut microbiota, underscoring the need for precise analytical approaches to study this complex ecosystem. While conventional methods remain widely used, they may lack the resolution required to capture subtle microbial dynamics. This narrative review examines how Artificial Intelligence) AI (-based approaches can provide deeper insights into the microbiota obesity relationship. Methods This narrative review examines literature published from 2020 to 2025, sourced from PubMed and Google Scholar. Relevant articles were selected using specific keywords such "Gastrointestinal Microbiome", "Obesity", "Microbial Diversity", "Sequencing Methods", "Microbiome analysis", and "Artificial Intelligence" focusing on studies exploring changes in gut microbiota associated with weight fluctuations. Results Gut microbiota composition differs markedly between obese and lean individuals. Obesity is commonly associated with reduced microbial diversity, a higher Firmicutes to Bacteroidetes ratio, and increased abundances of genera such as Blautia, Collinsella, Prevotella, and Megamonas. In contrast, lean individuals tend to harbour greater levels of beneficial species including Bifidobacterium, Faecalibacterium prausnitzii, Akkermansia muciniphila, and Christensenella. These microbial shifts influence host energy harvest, systemic inflammation, and fat accumulation, as evidenced by germ-free mouse studies demonstrating that microbiota from obese donors can induce weight gain. AI has become essential for identifying complex microbial associations that conventional methods often overlook. AI models allow simultaneous analysis of hundreds of taxa, enable prediction of obesity risk, and detect keystone species that shape microbial community function. Notably, AI-based approaches have identified Bifidobacterium pseudocatenulatum as a strain inversely associated with body mass index and capable of reducing fat accumulation in experimental models. By uncovering such hidden microbial signatures, AI provides a foundation for developing targeted microbiome-based interventions and personalized therapies for metabolic health. Conclusion Understanding the gut microbiota is essential for elucidating the mechanisms underlying obesity. Although traditional profiling methods remain valuable, they capture only part of the microbial complexity. AI

enables deeper pattern discovery, more accurate interpretation of microbial networks, and improved identification of therapeutic targets. Future research should prioritise the development of next-generation probiotics designed to reshape key microbial functions, alongside personalised obesity prevention and treatment strategies guided by microbiome-based predictive models. This integrated approach may help improve metabolic health interventions.

Keywords: Gastrointestinal Microbiome, Obesity, Microbiome Analysis, Artificial Intelligence

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The Role of Fusobacterium nucleatum in Immune Pathways and Breast Cancer Progression: Implications for Therapeutic Response

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Background: Breast cancer is one of the most frequently diagnosed cancers among women worldwide and a leading cause of cancer-related mortality. Recent studies show that breast tissue contains a distinct microbiome that differs between healthy and malignant samples. Among intratumoral bacteria, Fusobacterium nucleatum, an oral anaerobic bacterium, is enriched in breast tumors and correlates with larger tumor size, metastasis, inflammation, immune suppression, reduced T-cell infiltration and treatment resistance. Methods: Recent studies were identified through PubMed and Google Scholar. This narrative review examined the colonization routes of F. nucleatum, including hematogenous spread, gut–breast translocation and nipple contact, and evaluated effects of virulence factors, extracellular vesicles, signaling pathway activation, cytokine induction, and immune cell infiltration in the tumor microenvironment. Results: F. nucleatum promotes breast cancer progression through its Fap2 protein by activating pathways, including the TLR4/MyD88 axis and IL-1β induction via NLRP3 inflammasome. These mechanisms enhance proliferation, migration, invasion, epithelial–mesenchymal transition, PD-L1-mediated immune evasion, and suppression of T-cell cytotoxicity. F. nucleatum–derived extracellular vesicles further accelerate tumor growth and metastasis through TLR4-dependent mechanisms and contribute to treatment resistance, including chemotherapy and immunotherapy. Conclusion: Accumulating evidence supports a critical role for F. nucleatum in breast cancer progression by modulating inflammation, immunity, and tumor signaling. However, mechanisms regulating metastasis and therapy response remain unclear. Identifying these pathways may enable development of microbiome-targeted therapeutic strategies to improve outcomes and treatment sensitivity in breast cancer patients. Keywords: Fusobacterium nucleatum, breast cancer, microbiome, therapeutic response

Keywords: Fusobacterium Nucleatum, Breast Cancer, Microbiome, Therapeutic Response

Molecular and Epigenetic Biomarkers in Allergic Disease

P127-P129

P127

Association of Rs7217186 Polymorphism of Arachidonic Acid 15-Lipoxygenase (ALOX15) Gene with Susceptibility to Allergic Rhinitis

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Background: Allergic rhinitis (AR) is an inflammatory disorder of the nasal mucosa, caused by exposure to environmental allergens. It is known that 15-lipoxygenase (15-LOX) is involved in the biosynthetic pathways of anti-inflammatory lipid mediators, including resolvins and protectins. Methods: In this study, which was performed on 130 AR patients and 130 healthy controls, we aimed to investigate the association of susceptibility to AR with two selected single-nucleotide polymorphisms (SNPs), that is, rs2619112:A>G and rs7217186:C>T, in the intron regions of arachidonic acid 15-LOX (ALOX15) gene, using SNPinfo and Regulome DB tools. Results: The results showed that the CT genotype of rs7217186: C>T was significantly associated with the increased risk of AR compared to the CC genotype (P= 0.037, OR=1.943, CI: 1.038-0.638). However, there was no strong evidence of the association of rs2619112: A>G with susceptibility to AR (P> 0.05). Conclusions: The present results indicated that rs7217186 polymorphism of ALOX15 gene might be a potential biomarker for susceptibility to AR.

Keywords: Allergic Rhinitis, Arachidonate 15-Lipoxygenase, Immunoresolvents, Single-Nucleotide Polymorphism, Specialized Proresolving Lipid Mediators (SPMs)

P128

The Epigenetic Code of Allergy: A Systematic Review of DNA Methylation and Non-Coding RNAs in Immune Dysregulation

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Background: Asthma, food allergies, and anaphylaxis are examples of allergic diseases that pose a global health concern whose increasing incidence defies genetic explanation. The epigenome, the molecular interface where environmental factors shape immune function, is increasingly the missing piece. The evidence on how immune dysregulation and the course of allergic diseases are determined by epigenetic modifications is compiled in this systematic review. Methods: In accordance with PRISMA guidelines, we looked for human studies examining DNA methylation, histone modifications, or non-coding RNAs in allergic diseases in PubMed, Scopus, and Web of Science (2015–2024). The Newcastle-Ottawa Scale, modified for epigenetic research, was used for quality assessment. Results: Out of 2,847 records, 94 studies satisfied the inclusion requirements, yielding three game-changing discoveries. First, cord blood methylation patterns at the SMAD3 and 35 genomic loci predict the development of asthma years before symptoms appear, suggesting that allergic destiny may be predetermined at birth. Second, hypomethylation at the IL-4 and IL-13 loci in naive CD4+ T cells from allergic individuals effectively unlocks the Th2 genetic program in established disease, whereas hypermethylation of FOXP3 silences regulatory T-cell function and eliminates immune tolerance brakes. Third, circulating microRNAs (miR-26a, miR-665) can distinguish between mild and anaphylactic reactions and determine the severity of the disease. The convergence of these epigenetic signatures at HLA loci implies that epigenetic mechanisms mediate genetic risk. Conclusion: The allergic epigenome shows that immune dysregulation is a dynamic reaction to environmental programming rather than just genetic hardwiring. While the reversibility of epigenetic marks provides access to targeted therapies, predictive methylation signatures at birth present previously unheard-of chances for early intervention. The management of allergies moves from reactive treatment to predictive prevention as we decipher these molecular signatures.

Keywords: Epigenetics, DNA Methylation, Allergic Diseases, Immune Dysregulation, FOXP3

P129

Title: CXCL10 as a Key Biomarker in Systemic Lupus Erythematosus (SLE)

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Aim: Systemic lupus erythematosus (SLE) is a multisystem autoimmune disease with diverse symptoms. One of the most prevalent and serious complications of the disease is lupus nephritis (LN), which impacts up to 50% of people with SLE and results in varied degrees of renal impairment. Recent studies indicate that CXCL10 plays a role in the pathogenesis of various human renal disorders. Moreover, CXCL10 has been recognized as a significant biomarker of disease severity and a prognostic marker for conditions such as LN. This review aims to assess the potential function of CXCL10 in SLE. Methods: Between 2000 and 2025, we searched for the keywords “CXCL10” and “systemic lupus erythematosus” across multiple databases, including PubMed, Google Scholar, and Scopus. Results: The evaluated evidence has shown that the level of serum CXCL10 in patients with SLE, especially in active LN patients, was significantly higher than in healthy individuals and SLE patients without LN. CXCL10 expression showed a positive correlation with the disease activity index (SLEDAI) and 24-hour urine protein and renal functions. Also, bioinformatics analyses of differentially expressed genes (DEGs) derived from RNA sequencing revealed that 152 clustered genes were mainly enriched in immune- and interferon-related pathways, with CXCL10 identified as a key gene in the protein-protein interaction network. Overall, CXCL10 expression was markedly increased in SLE patients compared with healthy controls. Conclusion: These results indicate that CXCL10 is an important marker and pivotal gene in the pathogenesis of SLE. Its expression is associated with the severity of SLE and renal involvement. Serum and cellular CXCL10 may serve as a non-invasive, sensitive predictive tool for LN and for assessing disease activity. Nonetheless, further validation in extensive longitudinal studies is required.

Keywords: Systemic Lupus Erythematosus, Lupus Nephritis, CXCL10.

Phylogenetic Studies of Viruses and Recent Advances in Virology

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Revisiting HTLV-1: Molecular Signatures, Clinical Outcomes, and the Road Toward Curative Therapies

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Human T-cell leukemia virus type 1 (HTLV-1) is a deltaretrovirus that infects around 10-20 million individuals worldwide, including endemic regions in Japan, the Caribbean, South America, and Iran. Approximately 5% of infected persons develop adult T-cell leukemia/lymphoma (ATL), while a lower percentage develop HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). However, the majority of infected individuals remain asymptomatic carriers. The HTLV-1 bZIP factor (HBZ) and the viral oncoprotein Tax are at the center of the pathogenesis. Tax disrupts cell cycle regulation and constitutively activates the NF-κB pathway, which triggers the primary cellular transformation. On the other hand, HBZ is essential for preserving the malignant clone and is continuously expressed in leukemic cells. Clonal growth of infected CD4+ T cells is the main way that the virus survives, and an increase in proviral load is an important predictor for illness. Using quantitative PCR and serological testing, the diagnosis is verified. Treatment is still difficult; intensive ATL care involves combination therapies, chemotherapy, and monoclonal antibodies such as anti-CCR4, Hu-Mikb1, Penton polysulfate, but the prognosis is still not good. Immunomodulation is the main therapy for HAM/TSP. Moreover, existing treatments are few and mainly aim at managing symptoms and maintaining viral latency. CRISPR-Cas9 gene editing has been suggested as a promising approach to tackle the complex interactions related to HTLV-1. By targeting or disabling critical genes during the early stages of infection and disrupting immune signaling pathways, CRISPR-Cas9 provides potential avenues for intervention[6] .Despite progress, challenges remain, necessitating further research to optimize therapeutic efficacy and long-term outcomes for HTLV-1-associated diseases. There are some in vitro and in vivo studies that aim to better understand and develop treatments for HTLV-1-associated diseases, especially ATL and HAM/TSP. Therapeutic approaches for ATL include histone deacetylase inhibitors, NF-kB inhibitors, monoclonal antibodies, IFN/AZT combination, Belinostat with ZDV/IFN, Lenalidomide, and Green Tea. The potential and challenges for therapeutic intervention are presented by these different but identical systems. The ability of the virus to elude immune responses, specifically through Tax downregulation in advanced ATL and HBZ's compartmentalized expression in HAM/TSP, limits the effectiveness of monoclonal antibodies (mogamulizumab, daclizumab), HDAC inhibitors (romidepsin) and NF-κB inhibitors (bortezomib) show promise in targeting viral latency and oncogenic signaling. Use of Antiretroviral Drugs in HAM treatments includes Raltegravir, Tenofovir, cyclosporine, Arginine. While experimental methods

such as vaccinations and INSTIs have potential, their clinical effectiveness has to be confirmed. These interconnected gaps in efficient therapy, prevention, and early identification underscore the pressing need for international action against HTLV-1 as a neglected public health priority.

Keywords: HTLV-1, ATL, HAM/TSP, Clinical trials, CRISPR-Cas9

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Assessment of HCV Intrafamilial Spread and SOVODAK Treatment Effectiveness within the PERSIAN Guilan Cohort Population (PGCS)

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Background: Although substantial progress has been made in antiviral therapeutics, vaccine development continues to be hindered by the Hepatitis C virus (HCV)'s pronounced genetic diversity and rapid mutational capacity. The present investigation sought to estimate the prevalence of HCV infection among household members of confirmed HCV-positive index cases and to explore associated risk factors within these families along with assess the therapeutic performance of the combined antiviral agent Sovodak (sofosbuvir–daclatasvir) according to viral genotype. Methods: A cross-sectional design was employed involving families of 12 individuals with documented HCV infection enrolled in the (PGCS). A total of 20 relatives living in the same households were recruited. Data were collected through standardized questionnaires. Venous blood samples were obtained, and sera were subjected to serological analysis for anti-HCV and positive samples were subsequently examined for the HCV RNA, followed by molecular genotyping. Individuals confirmed to be HCV-infected were referred to a Phase 3 clinical trial (ID: NCT03200184) for antiviral treatment and monitoring. Results: Two family members tested positive for anti-HCV antibodies; among them, a 13-year-old girl was confirmed to have active infection with detectable HCV RNA. Genotyping identified subtype 1a, consistent with her mother's viral genotype. Following treatment with Sovodak, the patient achieved a sustained virologic response, evidenced by undetectable HCV RNA 12 weeks post-treatment. Conclusion: Although intrafamilial transmission was documented, its occurrence was exceedingly rare. The findings suggest that indirect exposure through shared household items potentially even commonplace objects such as toothpaste—may facilitate transmission in the absence of direct contact.

Keywords: Hepatitis C Virus, HCV, Intrafamilial Transmission, SOVODAK, Sofosbuvir Daclatasvir

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Immunomodulatory Roles of HCV Core and Core+1 Proteins in the Establishment of Chronic Infection

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Background: Hepatitis C virus (HCV) establishes chronic infection in the majority of infected individuals, frequently leading to liver cirrhosis and hepatocellular carcinoma. Viral persistence is largely attributed to sophisticated immune evasion strategies, in which structural and accessory viral proteins play critical roles. Among these, HCV Core and Core+1 (F) proteins have emerged as key modulators of host immune responses. Methods: This review summarizes and analyzes published experimental and clinical studies investigating the molecular and immunological functions of HCV Core and Core+1 proteins during chronic infection. Data regarding their interactions with host signaling pathways, immune cells, and apoptotic mechanisms were critically evaluated. Results: Evidence indicates that the HCV Core protein interferes with innate and adaptive immunity by suppressing interferon signaling through inhibition of the JAK/STAT pathway, modulating apoptosis, and impairing T cell activation and function. Core protein disrupts antiviral responses by reducing STAT1 activity, inducing SOCS expression, and altering cytokine production. In parallel, the Core+1 protein contributes to viral persistence by promoting regulatory T cell expansion, increasing IL-10 production, modulating cytoskeletal organization, and limiting viral replication to favor chronicity. Elevated immune responses against Core+1 have been observed in patients with advanced liver disease and HCV-associated hepatocellular carcinoma. Conclusion: HCV Core and Core+1 proteins play central and complementary roles in immune evasion and the progression to chronic HCV infection. Their multifaceted regulatory effects on interferon signaling, apoptosis, and T cell responses highlight these proteins as promising targets for the development of more effective antiviral therapies and vaccine strategies.

Keywords: Hepatitis C Virus, Core Protein, Immune Evasion, Chronic Disease, T-Lymphocytes Regulatory

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Molecular and Cell Culture-Based Approaches for Evaluation of Antiviral Activity Against HSV-1 in Diagnostic Virology Laboratories

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Background: Herpes simplex virus type 1 (HSV-1) is one of the most prevalent human viral pathogens and is associated with a wide range of clinical manifestations, from mild mucocutaneous infections to severe neurological complications. Although antiviral agents such as acyclovir are widely used for treatment, emerging antiviral resistance and recurrent infections have increased interest in alternative antiviral evaluation strategies. Accurate laboratory assessment of viral replication and antiviral activity is therefore essential in diagnostic virology laboratories. Methods: Published studies related to HSV-1 replication analysis, antiviral susceptibility testing, and laboratory-based virological assays were reviewed. Particular attention was given to cell culture techniques, cytopathic effect (CPE) assessment, $TCID_{50}$ assay, plaque reduction methods, and quantitative real-time PCR (qPCR) approaches used for monitoring viral replication and antiviral responses. Results: Cell culture-based assays remain valuable tools for evaluating productive viral infection and cytopathic alterations in infected cells. Molecular methods such as qPCR provide rapid, sensitive, and quantitative detection of viral genomes and have become important complementary techniques in diagnostic virology laboratories. Comparative evaluation of different laboratory methods demonstrates that combined application of molecular and infectivity-based assays improves the accuracy and reliability of antiviral assessment. Recent studies have also highlighted increasing interest in drug repurposing strategies and natural compounds as potential alternative antiviral approaches against HSV-1. Conclusion: Integration of molecular and cell culture-based techniques provides a comprehensive platform for laboratory evaluation of HSV-1 antiviral activity. Standardization and combined application of these methods may improve the reliability of antiviral assessment and contribute to the advancement of diagnostic virology laboratory services

Keywords: HSV-1, qPCR, TCID50, Cell Culture, Diagnostic Virology

Productivity Management in Rational Selection of Laboratory Tests with an Evidence-Based Laboratory Medicine Approach

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Development and Localization of an Implementable Hospital Antimicrobial Stewardship Protocol in Iran: Evidence-Based Adaptation of International Frameworks

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Background: Antimicrobial resistance (AMR) and high, often inappropriate, antibiotic use threaten patient safety and increase costs in Iran. Despite national stewardship initiatives, hospitals differ in workforce, microbiology capacity, and data systems, limiting consistent implementation. Methods: We developed an Iran-adapted, implementable hospital antimicrobial stewardship (AMS) protocol by evidence-based adaptation of international frameworks (WHO, CDC, and IDSA/SHEA). Source recommendations and tools were appraised for quality and feasibility, then translated into tiered (minimum/core/advanced) operational workflows. Results: The final protocol links governance and accountability to prioritized interventions, emphasizing restricted-agent oversight and prospective audit with feedback. It embeds structured antibiotic reassessment at 48–72 hours (“time-out”) and a follow-up checkpoint to support de-escalation, optimization, or discontinuation. The implementation package provides templates (checklists, authorization/audit forms), training materials, and a monitoring set starting with consumption metrics (e.g., DDD/100 bed-days) and expanding to AWaRe distribution, appropriateness audits, and microbiology indicators where available. Conclusion: This localized, evidence-based protocol converts global AMS core elements into practical hospital workflows for Iran and offers a scalable pathway for gradual stewardship strengthening; pilot testing and iterative refinement are recommended.

Keywords: Antimicrobial Stewardship, Protocol Development, Guideline Adaptation, Hospital, Iran

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Evidence-Based Optimization of Laboratory Test Utilization in a High-Volume General Hospital

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Background: In modern health systems, optimal selection of laboratory tests is essential for efficient management of resources. Excessive testing can contribute to 30% of diagnostic costs, and can result in false results, misinterpretations, waste of resources and delays in treatment. This study evaluates the effectiveness of an evidence-based approach to optimize test selection, improve resource efficiency and diagnostic quality in High-Volume General Hospital Methods: We conducted a cross-sectional analytical study from March 2024 to March 2026 in a 200-bed hospital, analyzing 10,000 laboratory requests from 2,500 patients (1,000 inpatients, 1,500 outpatients; mean age 49 years). Data were extracted from the Hospital Information System and evaluated using clinical decision-support algorithms in accordance with Choosing Wisely guidelines. Primary outcomes included unnecessary test rates, laboratory costs, turnaround time, positive predictive value (PPV), and length of patient hospitalization. Statistical analyses were performed using GraphPad Prism V8 with independent t-tests and logistic regression, and $P < 0.05$ was considered significant. Results: The evidence-based approach resulted in a reduction of unnecessary testing by 22.4% ($P < 0.001$), laboratory expenditure by 16.7%, turnaround time by 18%, and an improvement in diagnostic accuracy by 13.2%. The combination of physician education and CDS integration had the strongest correlation for improvement in performance ($r=0.82$). Conclusion: Evidence-based strategies are used to optimize laboratory resource utilization, reduce costs, and enhance clinical decision-making. The results rationalize the implementation of evidence-based health policies for improving clinical outcomes, diagnostic equity, and economic efficiency worldwide.

Keywords: Evidence, Laboratory, Optimization, Diagnostics

Quality Improvement in the Clinical Biochemistry Section (Department) of the Laboratory

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Pharmacokinetics of Levothyroxine and Antithyroid Drugs: Absorption Challenges, Immunoassay Interferences, Epitope/Paratope Variability Across Assay Generations, and Interpretation of Thyroid Function Tests – A Comprehensive Review

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Levothyroxine (LT4) remains the first-line treatment for primary hypothyroidism, characterized by complex pharmacokinetics including variable absorption (62–82% under fasting conditions, Tmax ≈3–4 hours), extensive protein binding (>99.9%), metabolism primarily via type 2 deiodinase (D2) to active T3, and biliary/renal excretion with a plasma half-life of 6.2–7.5 days. In hyperthyroidism management, antithyroid drugs such as methimazole (MMI; half-life ≈5–6 hours, inhibits synthesis) and propylthiouracil (PTU; half-life ≈1–2 hours, inhibits synthesis and peripheral conversion) are employed. This review examines the pharmacokinetics of these agents, post-dose changes in T4/T3 concentrations, immunoassay design (with emphasis on variability of iodinated outer-ring epitopes and antibody paratopes), negative feedback mechanisms in the hypothalamic-pituitary-thyroid (HPT) axis (T4-to-T3 conversion and TSH suppression via TRβ2 and co-repressors), the functional distinction between T4 (stable prohormone) and T3 (high-affinity active form), and challenges related to drug formulation quality (impact on absorption and laboratory interference). Immunoassay generations have evolved from weak traditional competitive assays (low specificity, high protein and matrix interference) to stronger modern platforms (VHH nanobodies with enhanced thermal stability and tuned affinity for reduced interference) and non-immunological reference methods such as LC-MS/MS with equilibrium dialysis (gold standard). Drug formulation quality can induce artifactual results (false-high or false-low fT4 due to epitope/paratope mismatch or antibody cross-reactivity), significantly affecting test interpretation; thus, TSH remains the most sensitive biological index, and LC-MS/MS is strongly recommended to eliminate interferences and achieve superior accuracy. TSH normalization after hyperthyroidism treatment typically requires 3–9 months (mean ≈6.9 months). This review provides practical guidance for laboratory specialists and endocrinologists in the precise management of thyroid disorders.

Keywords: Levothyroxine, Antithyroid drugs, Pharmacokinetics, Thyroid Function Assays, Epitope/Paratope, HPT Axis, LC-MS/MS

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Green Synthesis of Copper Oxide Nanoparticles Using Pomegranate Peel Extract and Their Application as a Sensor for Ascorbic Acid Detection

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Background: This study explores the green synthesis of copper oxide nanoparticles (CuO NPs) using pomegranate peel extract and their application as an electrochemical sensor for ascorbic acid detection in human blood serum. Methods: CuO NPs were synthesized via a green method and characterized using FESEM and XRD. An electrochemical sensor was fabricated using these NPs, employing a three-electrode system (modified carbon paste working electrode, platinum counter electrode, Ag/AgCl reference electrode) for ascorbic acid detection. Sensing performance was evaluated in both phosphate buffer (pH 7.4) and human blood serum. Results: FESEM images revealed uniform CuO NPs with diameters less than 20 nm. XRD confirmed high purity synthesis. Electrochemical tests demonstrated a four-fold signal enhancement for ascorbic acid detection using the modified electrode compared to the unmodified electrode. The sensor successfully detected ascorbic acid in diluted human blood serum, indicating its potential for clinical applications. Conclusion: The green synthesized CuO NPs exhibited excellent sensing capabilities for ascorbic acid, highlighting their potential for developing sensitive and reliable diagnostic tools for diseases related to ascorbic acid imbalances in human blood.

Keywords: Copper Oxide Nanoparticles (CuO NPs), Ascorbic Acid, Green Synthesis, Electrochemical Sensor

Selected Articles: Applied Research from the Laboratory to the Clinic

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Blood and blood product utilization pattern in educational hospital of Birjand city, Iran: A multicenter study

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Background: Large-scale ordering of blood and blood components is a prevalent practice that significantly depletes blood supplies, compromises the quality of blood units, raises the rate of expired units, and places substantial financial burdens on blood transfusion centers. This study aimed to assess blood and blood product management indicators within educational hospitals affiliated with Birjand University of Medical Sciences, to evaluate the alignment between actual demand and requested blood quantities to improve hospital resource utilization. Methods: In this cross-sectional prospective study, data on blood and blood product utilization were collected from four educational hospitals affiliated with Birjand University of Medical Sciences (Iran) over a six-month period from September 2024 to March 2025. Information on patient demographics, requesting units, types and quantities of blood products ordered, and units issued was extracted. The crossmatch-to-transfusion ratio (C/T ratio) was calculated. The findings were analyzed using descriptive statistics and SPSS version 26. Results: Out of the 5195 cross-matched blood units,4471 units were transfused, of which 86.06% of the total cross-matched units were used. In total, the ratio of cross-matched to transfused blood units (C/T) was 1.16. In terms of product type, 4471 units of packed red blood cells (48.8%), 3369 units of platelets (36.7%), and 1329 units of fresh frozen plasma/cryoprecipitate (14.5%) were used, with packed red blood cells accounting for the highest consumption. Conclusion: The results of this study showed that the pattern of blood demand and consumption in educational hospitals of Birjand University of Medical Sciences is in a favorable condition.

Keywords: Blood, Blood Products, Educational Hospitals, Crossmatch, Blood Transfusion, Surgery

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Differential Levels of Cortisol in Fatty Liver Disease with Metabolic and Non-Metabolic Etiologies

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Background: Fatty liver disease (FLD) is classified into metabolic dysfunction-associated fatty liver disease (MAFLD) and non-MAFLD based on the presence of metabolic abnormalities. Cortisol promote the expression of genes related to lipogenesis while simultaneously inhibiting the release of very low-density lipoprotein (VLDL). Notably, many individuals with elevated glucocorticoid levels may also present with FLD alongside obesity and insulin resistance. So in this study we aimed to investigate the levels of cortisol in MAFLD and non-MAFLD patients. Methods: The serum of the study subjects were collected from patients with FLD (n=99) including 58 MAFLD and 41 non-MAFLD and healthy individuals (n=23). To investigate the cortisol, ELISA method was used. Results: In this study we found that the cortisol level was significantly elevated in the FLD and MAFLD patients compared to the control group ($p<0.01$). No significant differences was found between non-MAFLD patients and the control group. Conclusion: Alterations in cortisol levels in non-MAFLD patients were milder than MAFLD patients when compared to the control which showed an intermediate state.

Keywords: Cortisol, MAFLD, non-MAFLD

P140

The Association between Serum Albumin Levels and Survival Rate in Patients with Pancreatic Cancer

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Background: Serum albumin is a potential prognostic biomarker in pancreatic cancer, but its independent association with survival remains underexplored in specific populations. This study evaluated the association between serum levels of albumin with survival rate in patients with pancreatic cancer. Methods: A cross-sectional study was conducted on 50 patients with histologically confirmed pancreatic cancer from Guilan Province, Iran. Data on demographics, clinical characteristics, comorbidities, treatment, and laboratory parameters were collected. Serum albumin levels were categorized into tertiles, and hypoalbuminemia was defined as <3.5 g/dL. Survival analysis was performed using Cox proportional hazards models and Kaplan–Meier curves with log-rank tests. Statistical significance was set at 5%. Results: The cohort consisted of 60% males, with a mean age of 62.8±10.5 years and mean survival of 39.6 months. Hypoalbuminemia was significantly associated with increased mortality (adjusted HR = 3.89, 95% CI: 1.23–12.25, P = 0.020). For each 1 g/dL increase in albumin, the hazard of death decreased by 51% (HR = 0.49, 95% CI: 0.33–0.73, P < 0.001), indicating a strong inverse relationship. Kaplan–Meier analysis confirmed significantly better survival in patients with higher albumin levels (P < 0.001). One-, three-, and five-year survival rates were 45.2%, 31.3%, and 23.5%, respectively. Treatment groups (no treatment: 22%, monotherapy: 38%, multimodal therapy: 40%) showed no significant survival differences (P = 0.339). Patients with albumin ≥3.5 g/dL had significantly better outcomes than those with hypoalbuminemia. Conclusion: Hypoalbuminemia is a strong, independent predictor of poor survival in pancreatic cancer. Given its simplicity and low cost, serum albumin monitoring offers a practical tool for prognostic stratification and personalized care, particularly in resource-limited settings

Keywords: Pancreatic Cancer, Serum Albumin, Hypoalbuminemia, Survival

P141

Hormonal Fluctuations and Immune Modulation Across Reproductive Stages in Systemic Lupus Erythematosus

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Background: Systemic lupus erythematosus (SLE) is a chronic multisystem autoimmune disease characterized by autoantibody production and damage to organs including the skin, kidneys, joints, and central nervous system. The prevalence of SLE is markedly higher in women than in men, a disparity largely attributed to sex-related hormonal and immunological factors. Estrogen enhances humoral immune responses and promotes B-cell survival, contributing to disease exacerbation. Disease activity in SLE is influenced by physiological hormonal fluctuations associated with the menstrual cycle, pregnancy, and menopause, with pregnancy-related flare rates reported to range from 45% to 70%. Methods: In this prospective longitudinal study, 60 women with SLE (20 of reproductive age with regular menstrual cycles, 20 pregnant women, and 20 postmenopausal women) and 30 healthy female controls were enrolled. Serum levels of estradiol, progesterone, follicle-stimulating hormone (FSH), and luteinizing hormone (LH) were measured across menstrual cycle phases, throughout the three trimesters of pregnancy, and during menopause. Disease activity was evaluated using the SLE Disease Activity Index (SLEDAI). Cytokine profiles, including Th1-, Th2-associated cytokines and IL-17, were analyzed using immunoassays and flow cytometry, and sex hormone receptor expression in peripheral blood mononuclear cells (PBMCs) was assessed by RT-qPCR. Statistical analyses used paired t-tests, ANOVA with post-hoc comparisons, and linear regression. Data were reported as mean ± standard deviation. All analyses were performed using Stata software version 14.2, with a significance level of 0.05. Results: Disease activity was significantly higher during the luteal phase compared with the follicular phase in women with regular menstrual cycles (SLEDAI: 8.4 ± 2.1 vs. 4.6 ± 1.8; $p<0.01$), concomitant with relative progesterone insufficiency or altered progesterone responsiveness. Among pregnant patients, the overall flare rate was 58%, with most flares occurring during the second and third trimesters. Increasing estradiol levels during pregnancy were associated with a shift toward Th2-dominant immune responses. Patients with active disease exhibited significantly higher IL-6 and IL-17 levels ($p<0.01$). Postmenopausal patients showed lower disease activity, while hormone replacement therapy was associated with an increased risk of mild-to-moderate flares. Conclusion: Hormonal fluctuations significantly modulate immune responses and disease activity in

SLE, highlighting the importance of hormonal status in disease monitoring and personalized therapeutic strategies.

Keywords: Systemic Lupus Erythematosus, Estradiol, Progesterone, Hormonal Fluctuations, Cytokine Profile, Pregnancy, Menopause, Immune Modulation

P142

Evaluation of Fluconazole Susceptibility in Candida Albicans Isolated from Nail Samples

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Background and Objective: Candidiasis has become one of the most common yeast infections worldwide in recent decades. Among the causative agents, Candida albicans is the most frequently isolated species from clinical samples. Despite its clinical importance, limited information is available regarding antifungal susceptibility patterns and certain pathogenic factors of this organism, particularly in nail infections. Given the increasing incidence of nail candidiasis, evaluating the susceptibility of C. albicans to fluconazole, along with the assessment of phospholipase activity and biofilm-forming ability, is essential for improving diagnostic accuracy and optimizing therapeutic strategies. Methods: In the present study, fluconazole susceptibility, phospholipase enzyme activity, and biofilm formation were investigated in Candida albicans strains isolated from infected nails. A total of 30 suspected isolates were obtained from the Mycology Reference Bank of the Pasteur Institute of Iran. Following phenotypic identification using CHROMagar medium, four isolates were excluded, and 26 confirmed C. albicans strains were included in the final analysis. Experimental Procedure: Initially, isolation and identification of C. albicans strains were performed using CHROMagar medium. Yeast cell suspensions were then prepared, and optical density was adjusted spectrophotometrically. Antifungal susceptibility testing was conducted using fluconazole in 96-well microtiter plates. Phospholipase activity was assessed using egg yolk agar medium, while biofilm formation was evaluated by the crystal violet staining method. Results: All 26 Candida albicans isolates demonstrated high susceptibility to fluconazole. Phospholipase activity was detected in six isolates. In addition, all strains exhibited the ability to form biofilms, indicating a considerable potential for persistence in nail infections and reduced response to antifungal therapy. Conclusion: The findings of this study highlight the importance of investigating Candida albicans isolates obtained from nail infections. Further studies with larger sample sizes and a greater focus on antifungal susceptibility patterns, pathogenic mechanisms, and molecular characteristics are recommended. A comprehensive understanding of these factors may contribute to the development of more effective preventive strategies and targeted therapeutic approaches against this opportunistic human pathogen.

Keywords: Candida Albicans, Biofilm, Fluconazole

P143

Comparative Evaluation of HBsAg Detection Kits: A Method Concordance Study

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Background: This study aimed to evaluate the performance of two diagnostic methods for identifying Hepatitis B surface antigen (HBsAg) in patients at Khatam-al-Anbia Hospital over the course of one year. The methods compared included an enzyme-linked immunosorbent assay (ELISA) kit from Pishtaz Teb Company and a rapid test kit from Aban Company. Methods: A total of 100 human serum samples were tested simultaneously using both methods according to the manufacturers' guidelines. The analysis showed a high overall concordance rate of 97%, with both tests producing consistent results for 97 samples. However, three discrepancies were observed: one sample was positive with the rapid test but negative with the ELISA, while two samples were positive with the ELISA but negative with the rapid test. Results: These discrepancies underscore the need for method verification to account for potential differences in analytical sensitivity and specificity between the kits. The single false-positive result from the rapid test could lead to unnecessary anxiety and follow-up, whereas the two false-negative results present a significant risk of missed diagnoses and possible disease transmission. Conclusion: The findings highlight the importance of utilizing multiple testing methods to ensure accurate diagnosis and effective patient management. Continuous improvement in laboratory services and regular evaluation of diagnostic kits are essential for enhancing quality assurance processes. This study emphasizes the need for continuous review and validation of testing methods to ensure their reliability and accuracy, ultimately leading to better healthcare. In contrast, the outcomes.

Keywords: HBsAg, ELISA, Rapid Test, Laboratory Quality, Diagnostic Accuracy

P144

Assessment of Fungal Contamination of Surfaces and Dental Equipment in Arak Dental Centers

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Bakground: Microbial contamination of dental surfaces and equipment remains a significant challenge in healthcare settings, potentially compromising both patient safety and clinical hygiene. Evidence has demonstrated that fungi play a crucial role in environmental contamination and the formation of biofilms on dental surfaces. These biofilms can persist on dental chairs, instrument trays, handpieces, and other frequently touched surfaces, serving as reservoirs for opportunistic pathogens. The prevalence of fungi in moist environments, their ability to adhere to dental materials, and increasing resistance to disinfectants highlight the necessity for thorough investigation. Fungal contamination may lead to indirect transmission of opportunistic infections, elevate the risk of disease in immunocompromised patients, and contribute to oral inflammatory conditions. Understanding the patterns and prevalence of environmental fungi is essential for implementing effective infection control measures and maintaining a safe clinical environment. Methods This cross-sectional study was conducted from December 2024 to June 2025 in Arak, Iran. The study aimed to assess fungal contamination on selected environmental surfaces and equipment in both public and private dental settings. Samples were collected from predefined high-contact areas using sterile swabs, including dental chairs, instrument trays, and handpieces. Specimens were aseptically transported to the laboratory and inoculated onto selective fungal culture media. Plates were incubated under optimal conditions and examined for fungal growth. Fungal isolates were identified based on macroscopic colony morphology and microscopic characteristics, including hyphal structure and spore formation. All data were systematically recorded and analyzed using descriptive statistics in SPSS version 23 to determine the frequency, distribution, and differences in contamination between the two sectors. Results A total of 230 samples were collected, including 130 (56.5%) from the dental school (public sector) and 100 (43.5%) from private clinics. Analysis revealed distinct patterns of fungal contamination across sectors. In the public sector, Aspergillus (40.5%) and yeasts (38.1%) were the most prevalent, whereas in private clinics, Aspergillus (46.7%) and Fusarium (36.7%) predominated. Other genera, including Penicillium and Mucor, were observed at lower

frequencies. The differences were statistically significant (P = 0.005), indicating that environmental conditions, cleaning protocols, and clinic-specific practices may influence the presence and distribution of fungi on dental surfaces and equipment. Conclusion Dental surfaces and equipment can act as potential reservoirs of fungal contamination even in the absence of highly pathogenic species, and fungal biofilms may demonstrate resistance to routine disinfection procedures, thereby increasing the risk of cross-contamination. Effective control of such contamination requires continuous environmental monitoring, strict adherence to hygiene protocols, use of efficient disinfectants, ongoing staff training, and evidence-based microbiological surveillance. Collectively, these measures reduce the microbial load in clinical settings, enhance the safety of patients and healthcare personnel, and provide a systematic, evidence-based framework for preventing and minimizing fungal contamination in dental care environments.

Keywords: Fungal Contamination, Dental Equipment, Infection Control

P145

Effects of Prediabetic and Diabetic Mimetic Environments on TCPTP Gene Expression in Muscle Cell Culture Model

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Background: Diabetes is caused by defects in insulin secretion, insulin sensitivity, genetic factors and environmental influences, and characterized by elevated blood glucose levels. Insulin resistance is a key component of diabetes, and skeletal muscle is the main site of insulin resistance. Reports indicate an increased expression of some protein tyrosine phosphatases (PTPs) in diabetes or insulin resistance. These molecules, including TCPTP which is encoded by PTPN2, are negative regulators of insulin signaling. Due to this important role, we investigated the effects of elevated glucose concentrations on the gene expression level in a time-course study. Methods: C2C12, a murine muscle cell line, was subjected to 8- and 16-hour treatments with normal (1 g/L) (control), prediabetic (2.75 g/L), and diabetic glucose levels (4.5 g/L). Following RNA extraction and reverse transcription, Real-time PCR analyses were performed. Results: Gene expression analyses revealed 2.74- and 1.42-fold increments in TCPTP gene expression in muscle cells subjected to 8-hour treatments with prediabetic and diabetic concentrations of glucose, respectively. A 16-hour treatment with prediabetic concentration of glucose did not induce any changes in TCPTP expression; however, diabetic concentration resulted in 0.6-fold reduction in TCPTP gene expression level, relative to the control. Conclusion: The results raised this possibility that following 16-hour treatments, an increase in TCPTP protein level occurs without a rise in gene expression. It is also possible that TCPTP induction occurs following a long-term treatment, albeit at a glucose concentration that is higher than that used in this study. Keywords: diabetes, hyperglycemia, insulin resistance, protein tyrosine phosphatase, TCPTP gene

Keywords: Diabetes, Hyperglycemia, Insulin Resistance, Protein Tyrosine Phosphatase, TCPTP Gene

P146

Determining the Mechanism of Metallo-β-Lactamase (MBL) in Carbapenem-Resistant Klebsiella pneumoniae Isolates and Its Impact on Treatment Regimen Selection: A Systematic Review

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Introduction Carbapenem-resistant Klebsiella pneumoniae (CRKP) is a critical global threat. The production of metallo-β-lactamases (MBLs), enzymes which inactivate nearly all β-lactams, are not inhibited by common agents like clavulanate, and spread via plasmids, is a key resistance mechanism. Therefore, accurate MBL identification is crucial for clinical management. Methods This systematic review adhered to PRISMA guidelines. A comprehensive search of PubMed/MEDLINE, Scopus, and Web of Science (2018-2024) used combined keywords: "Klebsiella pneumoniae", "MBL/NDM/VIM/IMP", "carbapenem resistance", "diagnosis", and "treatment". Inclusion criteria encompassed original studies and reviews in English or Persian focusing on MBL detection and treatment outcomes. Exclusions were non-relevant articles, brief reports, and studies without accessible full text. Results From 156 identified records, 32 studies were analyzed. Phenotypic assays such as eCIM offer rapid, inexpensive screening but lack specificity for MBL genotype. PCR-based techniques remain the gold standard for confirming genes like blaNDM. Emerging rapid tests, including immunochromatographic assays, deliver results within 15 minutes, aiding swift decision-making. MBL detection critically informs regimen selection. It precludes the use of certain novel β-lactam/β-lactamase inhibitors (e.g., ceftolozane-tazobactam). It validates the use of active agents such as ceftazidime-avibactam (for specific MBLs), cefiderocol, and non-β-lactam options (colistin, tigecycline). Rapid detection is foundational to antimicrobial stewardship, enabling early, targeted therapy. Conclusion Rapid and accurate MBL detection is the cornerstone of effective therapy for CRKP infections. It directly shifts treatment paradigms, guiding clinicians toward effective antibiotics while avoiding ineffective ones. Integrating rapid diagnostic tests, both phenotypic and molecular, into laboratory workflows is essential for improving patient care.

Keywords: Carbapenem-resistant Klebsiella pneumoniae, Metallo-β-lactamase, Antimicrobial Resistance, Diagnostics, Targeted therapy

P147

In Vitro Activity of Antibiotic Combinations Against Multi-Drug-Resistant Klebsiella Pneumoniae Isolates

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Background: Antimicrobial resistance (AMR) is a significant and growing health problem worldwide. Infections caused by multi-drug-resistant (MDR) bacteria are rapidly increasing, especially among hospitalized patients, leading to a high rate of mortality and morbidity. The aim of this study was to assess the in vitro activities of common antibiotic combinations against MDR Klebsiella pneumoniae (K. pneumoniae) isolates. Methods: Fifty MDR K. pneumoniae isolates were collected from hospitals in Tabriz, Iran, between January 1, 2023, and May 1, 2023. Minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined for four conventional antibiotics: colistin, meropenem, amikacin, and fosfomycin using the micro-broth dilution method. The fraction inhibitory concentration index (FICI) was calculated to determine synergism between these antibiotics. Results: The resistance rates to meropenem, fosfomycin (with 22% intermediate and 30% resistant), amikacin, and colistin were 100%, 52%, 48%, and 36%, respectively. The antibacterial effects of amikacin, meropenem, colistin, and fosfomycin alone were calculated based on the MBC/MIC ratio, with 92% being bactericidal and 8% being bacteriostatic. By calculating the FICI, we found that 166 combinations were synergistic, 71 combinations were additive and 63 combinations were indifference. No antagonistic effects were observed among the 300 combinations tested against MDR K. pneumoniae isolates. Additionally, we compared the rate of synergistic combinations to all combinations, revealing that the highest and lowest frequency percentages belonged to amikacin-fosfomycin and meropenem-colistin, respectively. Conclusion: We found synergistic, additive, and indifferent effects among the tested antibiotic combinations. In this study, the antibacterial activity of amikacin-fosfomycin was found to be the most effective compound against MDR K. pneumoniae isolates. Antagonistic effects were not observed.

Keywords: Treatment, Multi-Drug-resistant, Klebsiella Pneumoinae, Fraction Inhibitory Concentration Index (FICI), Antimicrobial Resistance (AMR)

P148

Biomarker Panels Advancing Precision Diagnosis in Rheumatoid Arthritis

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Background: Rheumatoid arthritis (RA) causes progressive joint damage if not diagnosed early. Current tests—rheumatoid factor and anti-citrullinated protein antibodies—lack sensitivity in early and seronegative RA, delaying treatment and worsening outcomes. This review evaluates emerging biomarkers to improve early detection and personalized care. Methods: A comprehensive literature search was performed to identify studies examining emerging biomarkers in rheumatoid arthritis. Results: Several promising biomarkers have emerged. Interleukin-6, IL-17, and IL-37 correlate with disease activity. Anti-carbamylated protein, anti-RA33, and anti-immunoglobulin binding protein antibodies add value in seronegative RA. MicroRNAs (miR-16-5p, miR-146a, miR-375) and long non-coding RNAs (LINC00305, NORAD) show strong diagnostic potential. Circular RNA panels and TNF-α hypomethylation enhance accuracy in ACPA-negative subgroups. Collagen triple helix repeat containing-1 protein, chemerin, and 14-3-3η protein aid diagnosis and activity assessment. Multi-marker panels consistently outperform single biomarkers. Conclusion: The integration of multi-marker panels represents a significant advance toward precision medicine in RA. These tools address two critical needs: improving diagnostic sensitivity in seronegative patients and capturing multiple pathogenic pathways simultaneously. However, clinical translation remains limited by several factors. Most studies are retrospective and single-center, validation across diverse populations is insufficient, and standardized assay protocols and cut-off values are lacking. Robust cost-effectiveness data are also absent. Prospective multicenter validation studies are urgently required, particularly in early and seronegative RA. Addressing these challenges will enable earlier risk stratification, reduce diagnostic delay, and support more tailored therapeutic strategies—ultimately shifting RA management toward a proactive, precision-based paradigm.

Keywords: Rheumatoid Arthritis, Diagnosis, Disease Activity, Biomarker

P149

Dyslipidemia in Isfahan: A Large-Scale Cross-Sectional Study

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Background: Dyslipidemia is a major modifiable risk factor for cardiovascular disease. This study aimed to determine the prevalence of lipid abnormalities and their association with sex and age among adults in Isfahan, Iran. Methods: This cross-sectional study was conducted at Nobel Laboratory, Isfahan, in 2024 in adults aged ≥18 years. Lipid parameters were classified using standard cutoffs: total cholesterol≥200 mg/dL, LDL≥100 mg/dL, HDL<50 mg/dL in women and<40 mg/dL in men, and triglycerides≥150 mg/dL. Chi-square tests and binary logistic regression were used to examine associations with sex. Women were the reference category. Results: A total of 105,586 individuals (mean age: 50.37±16.40 years, 53.8% female) participated. The overall prevalence of dyslipidemia was: high cholesterol 17.7%, high LDL 44.4%, low HDL 42.9%, and high triglycerides 34.7%. Low HDL affected 48.0% of women and 37.0% of men, while high triglycerides affected 29.9% of women and 40.3% of men. Women had significantly higher odds of high cholesterol (OR=1.256, 95% CI:1.222-1.291, p<0.001) and high LDL (OR=1.071, 95% CI:1.046-1.096, p<0.001), but lower odds of low HDL (OR=0.635, 95% CI:0.619-0.651, p<0.001) and high triglycerides (OR=0.633, 95% CI:0.618-0.649, p<0.001) compared to men. Age ≥50 years was significantly associated with all lipid abnormalities in chi-square analyses (all p<0.001). Conclusion: Dyslipidemia is highly prevalent in Isfahan, affecting nearly half the population for LDL and HDL abnormalities. Significant sex differences exist: men have worse HDL and triglyceride profiles, while women show higher cholesterol and LDL levels. These findings highlight the need for sex-specific prevention strategies and routine lipid screening.

Keywords: Dyslipidemia, Prevalence, Sex Differences, Iran

P150

The Association between Total Iron Binding Capacity (TIBC) and Renal Function Markers

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Introduction: Kidney disease disrupts key biochemical parameters. While Blood Urea Nitrogen (BUN) and serum creatinine are standard renal markers, Total Iron Binding Capacity (TIBC) reflects iron status and is affected by chronic inflammation. This study examined the link between TIBC and renal function. Methods: This cross-sectional analytical study was conducted in 2024 on individuals over 18 years old referred to the Noble Laboratory in Isfahan. Patients with severe liver disease, acute hematological disorders, and conditions affecting iron metabolism were excluded. Serum urea was measured using the enzymatic urease–glutamate dehydrogenase method, serum creatinine was determined by the Jaffe method, and TIBC was assessed using an indirect colorimetric assay. Analyses were performed twice: once for all individuals over 18, and once only for kidney patients (defined as creatinine ≥1.4 mg/dL). Data were analyzed using SPSS version 22, with a significance level of $P < 0.05$. Findings: In the group with normal creatinine (Cr<1.4 mg/dL), 20,577 individuals (mean age 44.4 ± 16.9 years; 65.9% female) were included. Significant inverse correlations were found between TIBC and BUN ($r = -0.132$, $p < 0.001$) and creatinine ($r = -0.103$, $p < 0.001$). In the group with elevated creatinine (Cr≥1.4 mg/dL), 857 individuals (mean age 65.07 ± 16.14 years; 30.8% female) were analyzed. Stronger inverse correlations were found between TIBC and BUN ($r = -0.326$, $p < 0.001$) and creatinine ($r = -0.453$, $p < 0.001$). Conclusion: TIBC shows a significant inverse correlation with BUN and creatinine, strengthening with declining kidney function. This suggests TIBC, potentially influenced by inflammation and altered iron metabolism in renal disease, may provide complementary information to standard renal markers.

Keywords: Blood Urea Nitrogen (BUN), Creatinine, Total Iron Binding Capacity (TIBC), Kidney Disease

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Seasonal Variations in Lipid Profile Components in Isfahan, Iran: A 2024 Cross-Sectional Study

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Background: Lipid profile components are influenced by various factors, including diet and physical activity, which may vary seasonally. This study aimed to investigate seasonal variations in cholesterol, LDL, HDL, and triglyceride (TG) levels among adults. Methods: This cross-sectional study was conducted at Nobel Laboratory, Isfahan, Iran, during 2024. Venous blood samples were collected from adults aged ≥18 years. Lipid parameters were measured using standard methods. Seasons were categorized as spring, summer, autumn, and winter. Data were analyzed using one-way ANOVA with Tukey's post-hoc test. Results: A total of 105,586 participants (53.8% female, mean age 50.37±16.40 years) were enrolled. Total cholesterol showed significant seasonal variation ($p<0.001$), with the highest levels in autumn (170.09±38.99 mg/dL) and lowest in spring (160.26±36.46 mg/dL). LDL levels were lowest in summer (94.98±26.52 mg/dL) and highest in winter (98.48±30.71 mg/dL) ($p<0.001$). HDL demonstrated marked seasonality ($p<0.001$), peaking in summer (51.58±12.96 mg/dL) and nadir in autumn (45.29±9.22 mg/dL). TG levels were highest in summer (145.60±81.22 mg/dL) and lowest in winter (135.73±70.45 mg/dL) ($p<0.001$). Post-hoc analysis confirmed significant differences between most season pairs for all parameters. Discussion and Conclusion: All lipid parameters exhibited significant seasonal variations. Cholesterol and LDL peaked in colder months (autumn/winter), while HDL peaked in summer. TG followed a different pattern with summer peaks. These findings have important implications for clinical practice: single lipid measurements should be interpreted with consideration of sampling season, and seasonal timing may influence cardiovascular risk assessment. Public health strategies for dyslipidemia management in Isfahan should account for these predictable seasonal fluctuations.

Keywords: Seasonal Variation, Cholesterol, LDL, HDL, Triglycerides

P152

Sex-Specific Associations between Kidney Function and Liver Enzymes: A Cross-Sectional Study from Isfahan, Iran

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Background: The interplay between kidney function and liver health is increasingly recognized, yet the relationship between estimated glomerular filtration rate (eGFR) and liver enzymes remains underexplored, particularly regarding sex differences. This study aimed to investigate the correlation between eGFR and liver enzymes and to identify independent predictors of eGFR using multiple linear regression. Methods: This cross-sectional study included 8,574 adults aged≥18 years from Nobel Laboratory, Isfahan, Iran. Pearson correlations were assessed overall and after stratification by sex. Multiple linear regression was performed to identify independent predictors of eGFR. Results: Participants (mean age 50.65±16.21 years, 54.7% female) had mean eGFR 80.20±16.78 mL/min, AST 53.63±31.11 U/L, and ALT 21.87±15.44 U/L. Overall, eGFR showed significant positive correlations with AST ($r=0.219$, $p<0.001$) and ALT ($r=0.103$, $p<0.001$). Striking sex differences emerged: in men, eGFR correlated positively with both AST ($r=0.080$, $p<0.001$) and ALT ($r=0.164$, $p<0.001$); in women, eGFR showed a perfect correlation with AST ($r=1.000$, $p<0.001$) but no correlation with ALT. Multiple linear regression revealed that age ($\beta=-0.415$, $p<0.001$), sex ($\beta=1.080$, $p<0.001$), AST ($\beta=1.058$, $p<0.001$), and ALT ($\beta=-0.096$, $p<0.001$) were independent predictors of eGFR, explaining 58.6% of its variance ($R^2=0.586$, $p<0.001$). Conclusion: The relationship between kidney function and liver enzymes is complex and sex-dependent. AST emerged as a strong positive predictor of eGFR, while ALT showed a weak negative association, consistent with previous studies suggesting differential roles of these enzymes in hepato-renal crosstalk. The striking sex differences-particularly the perfect AST-eGFR correlation in women-warrant further investigation and highlight the necessity of sex-stratified analyses.

Keywords: eGFR, AST, ALT, Kidney Function, Liver Enzymes, Sex Differences

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Inverse Association between Serum Magnesium and Glycated Hemoglobin in an Iranian Adult Population: A Cross-Sectional Study

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Background: Emerging evidence suggests that Magnesium (Mg) deficiency may contribute to impaired glycemic control, yet population-based data on the Mg-HbA1c relationship remain limited. This study aimed to investigate the association between serum magnesium levels and glycated hemoglobin (HbA1c) in a large sample of Iranian adults. Methods: This cross-sectional study was conducted at Nobel Laboratory, Isfahan, Iran, including 9,411 adults aged ≥18 years. Serum magnesium and HbA1c were measured using standard methods. Pearson-correlation was assessed overall and after stratification by sex. Linear regression was performed to identify independent predictors of HbA1c, adjusting for age, sex, and magnesium. Results: Participants (mean age 50.90±16.49 years, 57.1% female) had mean serum magnesium 2.14±0.13 mg/dL and mean HbA1c 5.82±1.12%. A significant inverse correlation was observed between magnesium and HbA1c ($r=-0.073$, $p<0.001$). This association was stronger in women ($r=-0.092$, $p<0.001$) than in men ($r=-0.051$, $p=0.001$). linear regression revealed that magnesium ($\beta=-0.091$, $p<0.001$) and age ($\beta=0.408$, $p<0.001$) were significant independent predictors of HbA1c, while sex showed no association ($\beta=0.012$, $p=0.212$). The model explained 17.2% of HbA1c variance ($R^2=0.172$, $F=646.96$, $p<0.001$). Conclusion: This study demonstrates a significant inverse association between serum magnesium and HbA1c in an Iranian adult population, consistent with previous research in diabetic patients. The stronger correlation in women warrants further investigation. Hypomagnesemia has been linked to insulin resistance through impaired tyrosine kinase activity at the insulin receptor level. Given that nearly half of diabetic patients may exhibit hypomagnesemia, routine magnesium assessment and potential supplementation could serve as a cost-effective adjunct to conventional glycemic control strategies.

Keywords: Magnesium, HbA1c, Glycemic Control, Iran, Cross-Sectional Study

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Association of Glycated Hemoglobin with Kidney Function Parameters in Diabetic Patients: A Cross-Sectional Study from Isfahan, Iran

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Background: Diabetic nephropathy is a major microvascular complication of diabetes mellitus and a leading cause of end-stage renal disease worldwide. This study aimed to investigate the association between Glycated-hemoglobin (HbA1c) levels and kidney function parameters (creatinine, blood urea nitrogen [BUN], and albumin) in a population of diabetic patients. Methods: This cross-sectional study was conducted at Nobel Laboratory in Isfahan, Iran, in 2023. A total of 486 diabetic adults (fasting blood sugar ≥125 mg/dL; mean age 61.29±13.13 years; 50.4% female) were enrolled. Pearson-correlation coefficients were calculated to assess bivariate associations, followed by multiple-linear-regression analyses adjusting for age and sex. Results: Mean HbA1c was 7.80±1.47%, creatinine 1.14±0.50 mg/dL, BUN 17.82±11.05 mg/dL, and albumin 4.00±0.27 g/dL. HbA1c showed a significant positive correlation with creatinine ($r=0.102$, $p=0.024$) and a significant negative correlation with albumin ($r=-0.158$, $p<0.001$). No significant correlation was observed between HbA1c and BUN ($r=0.073$, $p=0.106$). After adjusting for age and sex, the association between HbA1c and creatinine remained significant ($\beta=0.114$, $p=0.010$), as did the association with albumin (partial $r=-0.188$, $p<0.001$). Multiple-regression-analysis confirmed that HbA1c was an independent predictor of both creatinine ($\beta=0.114$, $p=0.010$) and BUN ($\beta=0.093$, $p=0.030$), while age was the strongest predictor of BUN ($\beta=0.333$, $p<0.001$). Conclusion: This study demonstrates that poor glycemic control, reflected by higher HbA1c levels, is independently associated with elevated creatinine and reduced albumin in diabetic patients. These findings align with previous research showing that hyperglycemia contributes to glomerular damage and albuminuria through mechanisms including oxidative stress, advanced glycation end-products, and activation of the renin-angiotensin system.

Keywords: HbA1c, Diabetic Nephropathy, Creatinine, Blood Urea Nitrogen, Albumin, Iran

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Consolidating Clinical Insights and Uncovering Novel Regulatory Mechanisms of Exosomal microRNAs in Obesity and Non-Alcoholic Fatty Liver Disease: A Systematic Review and Bioinformatics Analysis

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Obesity and non-alcoholic fatty liver disease (NAFLD) are interrelated metabolic disorders characterized by chronic inflammation, insulin resistance, and dyslipidemia. Although clinical identification of both conditions has become widespread, the molecular mechanisms underlying their concurrence are poorly understood. Recent evidence has shown that exosomal microRNAs (miRNAs) have essential regulatory roles in both diseases. This PROSPERO-registered systematic review (ID: CRD420251017335) explores clinical research regarding exosomal miRNAs in obesity and NAFLD, including patient demographics and biochemical factors. Literature was retrieved from MEDLINE, ISI Web of Science, and Embase. Bioinformatics analysis using miRWalk also revealed shared miRNAs, predicted target genes, and elucidated enriched pathways using Gene Ontology and KEGG. MiRNA-mRNA interaction was mapped to reveal critical regulatory hubs. The review found 93 and 24 miRNAs associated with obesity and NAFLD, respectively, that shared let-7b and miR-335-5p. Computational analysis using miRWalk demonstrated 40,410 overlapping miRNA interactions and 42 common target genes. Notably, miR-6085 and miR-6753-5p were most significantly associated with metabolic inflammation. Circulating exosomal miRNAs in the blood, including miR-122, miR-192, miR- 128, and miR-9-5p, were associated with histopathology, inflammation, and liver enzymes. MiR- 298, miR-342, and let-7d-5p were discovered to have optimal diagnostic potential (AUC $\geq$ 0.85) and performed better than the conventional ALT marker. ADIPOQ was discovered as a therapeutic target, which was modulated by miR-335-5p and let-7b. This study demonstrates the diagnostic and therapeutic potential of exosomal miRNAs in the differential diagnosis and therapy of NAFLD and obesity.

Keywords: Obesity, Nonalcoholic Fatty Liver Disease, microRNAs, Exosomes, Biomarkers

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Distribution of Immunoglobulin Subclasses in Patients Suspected of Monoclonal Gammopathy (MGUS and MGCS) in Iran

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Background: Monoclonal gammopathies encompass a spectrum of disorders with varying clinical significance. Accurate determination of immunoglobulin type and M component level is crucial for diagnosis, risk stratification, and monitoring. This study aimed to investigate the distribution of immunoglobulin subclasses and determine the frequency of MGUS and MGCS among suspected patients. Methods: In this cross-sectional study conducted at Nobel Laboratory in Isfahan, a total of 657 patients suspected of monoclonal gammopathy were selected from among individuals referred to this laboratory. Serum samples were evaluated using electrophoresis and immunotyping with the Sebia capillary electrophoresis system. Immunoglobulin type, light chain, M component level, and total gamma status were recorded and analyzed. Results: Of the total patients, 402 (61.2%) were male. Total gamma was normal in 65% of patients and abnormal in 35%. Based on M component level, 121 patients (18%) with total gamma >3 gr% were classified as MGCS, and 536 patients (82%) with total gamma <3 gr% as MGUS. The most common immunoglobulin patterns were IgG K (45.51%) followed by IgG L (26.33%). Other patterns included IgM K, IgM L, IgA L, IgA K, free light chains, oligoclonal, and biclonal patterns. Conclusion: Our findings indicate that both MGUS and MGCS are substantially represented among patients suspected of monoclonal gammopathy. In both conditions, IgG-associated monoclonal patterns—particularly IgG-κ and IgG-λ—were the predominant immunoglobulin subclasses. The observed distribution of immunoglobulin isotypes and light chains is consistent with previously reported patterns in monoclonal gammopathies. These results underscore the clinical importance of accurate immunoglobulin subclass identification in both MGUS and MGCS for diagnosis, risk assessment, and longitudinal patient monitoring, and provide valuable baseline data for future studies in this population.

Keywords: Monoclonal Gammopathy, MGUS, MGCS, Immunoglobulin Subclasses

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Detection of Infectious Agents and Drug Resistance in Sepsis by Multiplex PCR and Reverse Hybridization

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Background: Sepsis is a life-threatening condition and a significant cause of preventable morbidity and mortality globally. This study presents a opportunities for diagnosis, prognosis and therapeutics, antibiotic resistance through the perspective of bloodstream infection and sepsis. Methods: In this cross sectional study, 16 patients with bloodstream infection and sepsis were checked during 2023-2025. Multiplex-PCR and reverse dot blot hybridization were performed using kit and detected gram positive bacteria (Coagulase-Negative Staphylococci, Staphylococcus aureus, Streptococcus spp., Streptococcus pneumoniae, Streptococcus agalactiae, Streptococcus pyogenes, Listeria monocytogenes, Enterococcus spp.), gram negative bacteria (Pseudomonas aeruginosa, Acinetobacter baumannii, Neisseria meningitidis, Stenotrophomonas maltophilia, Escherichia coli, Klebsiella pneumoniae, Serratia marcescens, Enterobacteriaceae species, and Proteus/Morganella spp), fungi species)Candida albicans and Candida spp) and twenty antibiotic resistance markers. Results: Sepsis infection were identified in 25% (4/16) patients which all of them were men 62.5% (4/10). The GES, OXA24-like, OXA48-like, NDM and SIM genes were detected in three blood culture samples 18.75(3/16) from which carbapenemase-resistant Klebsiella pneumoniae was isolated. The detection rate of the mecA gene from methicillin-resistant Staphylococcus and Candida albicans isolates were 12.5% (2/16). The rates of the vanA and CTX-M genes from vancomycin- resistances, Enterococcus and β-lactam- resistances, Pseudomonas aeruginosa were identified 6.25% (1/16) and 6.25% (1/16), respectively. Conclusion: These organisms contribute to severe sepsis and septic shock due to their virulence and resistance profiles. Rapid diagnostic methods can significantly reduce the time to identification of organisms and resistance genes and have the greatest impact on improving time to optimal therapy.

Keywords: Sepsis, Multiplex-PCR, K.Pneumoniae, P.Aeruginosa, C.Albicans

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Antifungal Susceptibility Patterns of Clinical Dermatophyte Isolates Using Broth Microdilution: Focus on Terbinafine and Itraconazole

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Bakground: Dermatophyte infections are globally prevalent, particularly in tropical and subtropical regions, and represent significant public health concern developing countries. Management typically requires topical and systemic antifungal therapy, but species show variable susceptibility, and rising resistance complicates treatment. Therefore, in vitro antifungal susceptibility testing is essential for guiding effective treatment. This study aimed to evaluate the antifungal susceptibility patterns of clinical dermatophyte isolates. Methods: Antifungal susceptibility testing was performed using the broth microdilution method according to the CLSI M38 (3rd edition) guideline on 43 dermatophyte isolates obtained from patients with dermatophytosis (38 Trichophyton tonsurans, 3 Microsporum ferrugineum, and 2 Microsporum canis). The isolates were tested against terbinafine, griseofulvin, ketoconazole, fluconazole, and itraconazole. Following plate preparation and inoculation with the fungal suspension, including appropriate positive and negative control wells, the microplates were incubated at 30 °C for 4 days, after which the minimum inhibitory concentrations (MICs) were determined. Results: The MIC ranges observed against the dermatophyte isolates were 0.031–0.5 µg/mL for terbinafine, 0.5–64 µg/mL for griseofulvin, 0.031–16 µg/mL for ketoconazole, 0.25–64 µg/mL for fluconazole, and 0.031–0.5 µg/mL for itraconazole. The MIC_{50}, MIC_{90}, and geometric mean values were determined for each antifungal agent, with terbinafine and itraconazole demonstrating the lowest values among the tested drugs. Conclusion: Based on the antifungal susceptibility results, within the tested concentration ranges, terbinafine and itraconazole demonstrated greater in vitro activity against clinical dermatophyte isolates compared with the other antifungal agents.

Keywords: Dermatophytes, Antifungal Susceptibility, Broth Microdilution

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Changes in mRNA Expression Profiles of Follistatin-Like (FSTL) Family Members in Muscle and Adipose Tissues of Obese Diabetic Patients: A Bioinformatics Analysis

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Background: Type 2 diabetes mellitus (T2DM) is a closely related metabolic disorder characterized by chronic inflammation, insulin resistance, and adipose tissue dysfunction. The follistatin-like (FSTL) protein family, identified as new myokines involved in the remodeling of adipose tissue, still needs to be well-characterized in the context of obesity-related T2DM. Methods: In this study, we bioinformatically evaluated FSTL gene expression profiles in skeletal muscle and adipose tissue using five transcriptomic datasets from the Gene Expression Omnibus. These datasets reflected samples of lean, normal-weight individuals (NW), obese non-diabetic individuals (OW), and obese individuals with T2DM (OW-T2DM). Differential expression was established using DESeq2 and limma, and functional enrichment was conducted using Gene Ontology, KEGG, and Reactome databases. Results: In muscles, no differences in the gene expression of these genes were noted in OW-T2DM versus NW individuals. Nonetheless, stratified by the stage of myogenic differentiation, FSTL1 and FSTL3 were significantly downregulated from myoblast to myotube regardless of glycemic status. Notably, FSTL3 was even more reduced in T2DM-derived myotubes. In adipose tissue, FSTL1 was highly upregulated in obese and diabetic individuals, while FSTL3 showed a trend, albeit non-significant, towards upregulation. Both genes responded to intensive lifestyle intervention. In contrast, FSTL5 and FSTL4 were lean-specific, with complete loss in both obese and diabetic adipose tissues. Functional enrichment analysis revealed the involvement of FSTL members in TGF-β and BMP signaling pathways. Conclusion:These findings highlight that this family behaves differently in various tissues and conditions, indicating they could be useful for research as diagnostic markers or treatment targets in obesity-related T2DM. Keywords: Gene Expression; Follistatin-Related Proteins, Muscles; Adipose Tissue; Diabetes

Keywords: Gene Expression, Follistatin-Related Proteins, Muscles, Adipose Tissue, Diabetes

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Purification of Human Liver Ferritin for Application as a Reference Standard Protein in Immunoassays

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Introduction Ferritin is a diagnostic biomarker in serum immunoassays for evaluating iron status in iron deficiency anemia and hemochromatosis [1]. Reliable quantification depends on high-purity ferritin standards, often prepared from human liver [2]. This study aimed to purify human liver ferritin via size exclusion chromatography and assess its application as an immunoassay reference standard [3]. Materials and Methods Human liver tissue was homogenized, followed by heat denaturation and ammonium sulfate precipitation. The ferritin-enriched fraction was further purified by size exclusion chromatography on Sephadex G-200. The purity was evaluated by SDS-PAGE under reducing conditions. Protein concentration was measured using BCA assay. The purified ferritin served as a calibrator or standard in a sandwich ELISA, compared to commercial standards. Results Sephadex G-200 chromatography produced a major peak at ~440–450 kDa, referred to ferritin's native 24-subunit structure. Reduced SDS-PAGE showed a strong protein band at 19 kDa (L subunits enriched in liver ferritin) with minimal contaminants, confirming high purity in comparison with control sample of native ferritin purified from human liver (BioRAD, USA). Chromatography collected fractions were concentrated and the amount of protein was determined using BCA assay. Absence of IgM contamination and non-specific interference was assessed by control ELISA. Finally, the application of purified ferritin was assessed using available commercial ELISA immunoassay kits, showing that the efficacy and sensitivity of purified ferritin as a standard protein in ELISA was as well as commercial human liver purified native ferritin (BioRAD). Conclusion The Sephadex G-200-based protocol effectively purified high-quality human liver ferritin. Its biochemical purity (SDS-PAGE) and strong ELISA performance support its use as a reliable, cost-effective reference standard for ferritin immunoassay, enhancing clinical measurement standardization and accuracy using the home-purified protein. Key words: Ferritin, Purification, Standard, Chromatography, Immunoassay References: [1] Milman N, Juul-Jørgensen B, Bentzon MW. Calibration of Abbott AxSYM Ferritin kit using the WHO Human Liver Ferritin International Standard 80/602. Eur J Clin Chem Clin Biochem. 1997;35:631-2. [2] Organization. WH. WHO

guideline: use of ferritin concentrations to assess iron status in individuals and populations. Geneva: World Health Organization. 2020. [3] Pagé M, Legueux J, Gauthier C. A three step purification procedure for human liver ferritin. Can J Biochem. 1980;58:494-8.

Keywords: Ferritin, Purification, Standard, Chromatography, Immunoassay

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Design and Development of a Guided Box for Precise Sampling in 96-Well Plates Using Reverse Numbering Strips

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Introduction: Accurate identification of the target well in 96-well plates is crucial, particularly in light-sensitive assays where ambient light must be minimized. Under such conditions, locating the correct well can be challenging for the operator. This study introduces a protective box for 96-well plates incorporating movable row strips and a guiding numbering system to improve well localization. Methods: For each plate row, a strip approximately twice the length of the plate was designed with a central aperture matching the size of a single well. On both sides of the aperture, numbers from 1 to 12 are printed in reverse order with spacing corresponding to the well intervals. As the strip moves from the left side of the plate toward the right, the numbers progressively align beneath the wells and ultimately display the correct well number. The operator can match this number with the reference row labeling to accurately locate the target well. Results: The proposed design significantly reduces human error in identifying target wells and prevents incorrect sample loading. Additionally, by covering all other wells, it protects the plate from ambient light exposure during light-sensitive experiments. Discussion: The combination of movable strips and reverse numbering enables accurate well positioning even under low-light conditions. This simple and low-cost design improves loading precision and enhances laboratory workflow in both research and diagnostic settings.

Keywords: 96-Well Plate, Precise Sample Loading, Light-Sensitive Assay, Protective Box, Human Error Reduction

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Six Year Study of Fungal Growth in Blood Culture of Patients in Ahvaz Imam Khomeini Hospital in Khuzestan Province

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Background: A positive fungal blood culture means the presence of fungus in the bloodstream. In most cases, fungal blood infections in hospitals are caused by *Candida* species, and this is a medical emergency. (1).Major risk factors of fungal bloodstream infection include immunosuppression and immunocompromised patients, organ transplant recipients, patients taking broad-spectrum antibiotics and ICU patients. (2).Examining the fungus in blood cultures and diagnosing it is vital, and it is better to start treatment for the patient as soon as possible and allow the healing process to take place, otherwise fungal bloodstream infections carry a high mortality rate and can lead to septic shock or organ failure(3).Methods:In this cross sectional descriptive study all patients with at least one positive blood culture were investigated from March 2020 to March 2026 in Ahvaz Imam Khomeini hospital in Khuzestan province.The total number of blood culture samples performed for patients was 75,959.The diagnostic technique was microscopic examination (20% KOH, methylene blue staining), Blood agar and Sabouraud Dextrose agar culture and CHROMagar Candida.Results:As a result of this 6-years epidemiological study on blood cultures and their examination for fungal diseases, out of 75,959 patients, 199 cases (0.26%), were positive for fungal diseases. 1,840 cases (2.42%), were also considered as contamination, indicating that if the pre analysis process had been carried out correctly, we might have had more positive fungal cases.According to the collected data, the highest number of positive yeast blood culture samples such as *Candida* species (especially *C. albicans*, *C. glabrata*, and *C. krusei*) which are the most common causative agents, were from patients admitted to the ICU (34%), and nephrology departments (18%), as well as NICU departments (11%).Conclusion:The presence of even the slightest sign of fungus in a blood culture is very important for detecting the presence of fungus in the patient's bloodstream and has clinical value. Although a positive blood culture result has high clinical value, it has low

sensitivity and further diagnostic tests and more precise methods are still needed to confirm it.Our research shows that fungi in the bloodstream remain a significant public health concern, especially in hospitalized patients. Early diagnosis of the disease and the correct selection of antifungal agents have a significant impact on accelerating the treatment process.

Keywords: Epidemiology, Fungi in blood culture, Fungi Infection, Bloodstream infection

The Clinical Importance and Application of Accurate Measurement of Low Hormone Levels

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Management of Laboratory Interferences in Immunoassays: A Systematic Review Focusing on Macroprolactin and Macro-TSH

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Background Immunoassay interferences are a significant cause of spurious hormone results in clinical laboratories, leading to misdiagnosis, unnecessary investigations, and inappropriate treatment. Macrohormones, particularly macroprolactin (complexed prolactin with immunoglobulin, causing pseudohyperprolactinemia) and macro-TSH (macro-thyrotropin, causing isolated pseudohyperthyrotropinemia), are key examples. Macroprolactin has reduced bioactivity but is detected in immunoassays, while macro-TSH delays clearance without affecting thyroid status. Methods This systematic review synthesized data from studies published up to 2025, identified through PubMed, Scopus, and other databases. Inclusion criteria: original studies and reviews reporting prevalence, detection methods (primarily polyethylene glycol [PEG] precipitation and gel filtration chromatography [GFC]), and clinical management of macroprolactin and macro-TSH in hyperprolactinemic or elevated TSH patients. Key searches included "macroprolactin systematic review prevalence PEG" and "macro-TSH prevalence interference." Meta-analyses (e.g., global prevalence of macroprolactinemia) and case series were prioritized. Exclusion: non-English studies or those without laboratory validation. Results Macroprolactin prevalence in hyperprolactinemic patients ranges from 10–25% globally (pooled 18.9% in one meta-analysis), with higher rates in asymptomatic cases. PEG precipitation (recovery <40–50%) is the primary screening method, with GFC as gold standard. Macro-TSH is rarer (0.6–1.6% in subclinical hypothyroidism cohorts), suspected in isolated TSH elevation (>10 mIU/L) with normal thyroid hormones. PEG recovery is typically <20–30%. Routine screening is not recommended due to low prevalence, but indicated for clinical discordance. Diagnostic algorithms emphasize clinical correlation, PEG screening for macroprolactin in all hyperprolactinemia, and selective for macro-TSH. Conclusion Recognition of macroprolactin and macro-TSH prevents misdiagnosis. Laboratories should adopt standardized PEG protocols, report monomeric fractions, and collaborate with clinicians. Routine macroprolactin screening is best practice; macro-TSH screening is targeted. This reduces unnecessary imaging/treatment and improves patient outcomes.

Keywords: Macroprolactin, Macro-TSH, Immunoassay Interference, Polyethylene Glycol Precipitation, Hyperprolactinemia, Hyperthyrotropinemia, Gel Filtration Chromatography

The impact of Laboratory Accreditation on the International Credibility and Acceptance of Laboratory Results

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Severe Microcytosis-Induced Pseudo-Thrombocytopenia: a Case Report and Laboratory Pitfall

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Automated counters, employing different methodologies with high speed and efficiency, have significantly contributed to clinical laboratories. These instruments yield precise and accurate results, crucial for diagnosing, treating, and monitoring patients. Nonetheless, these devices possess limitations and vulnerabilities that may influence test outcomes and, in certain instances, cause clinicians to be unsure of making informed decisions. We report a case of a 39-year-old pregnant woman whose initial platelet count, measured by an impedance-based analyzer equipped with automated discriminators, showed a significantly reduced platelet count. The delta check failed, prompting further analysis using a different hematology analyzer with fixed discriminator thresholds, which indicated a normal platelet count accompanied by uncertainty flags. Peripheral smear examination revealed severe microcytosis and erythrocyte fragments, which interfered with accurate platelet discrimi nation. This case emphasizes the rare pitfalls of impedance-based automated platelet count, particularly in cases of severe microcytosis. To determine platelet size distribution, automated counters use different techniques and discriminator strate gies (fixed or floating gates). In severe microcytosis, improper gate closure may lead to pseudo-thrombocytosis. However, in this case, the float-based device could not correctly differentiate between the two cell populations due to saturation of the two peaks related to red blood cells and platelets. This resulted in the incorrect identification of the border between plate lets and red blood cells, ultimately resulting in pseudo-thrombocytopenia. Modern hematology analyzers with laser-based technologies can help distinguish platelets from microcytic RBC fragments, but microscopic review remains essential for confirming results. This thought-provoking case highlights a rare but significant diagnostic pitfall. While microcytic red blood cell fragments typically result in pseudo-thrombocytosis, in exceptional scenarios, such as the one described, they may paradoxically cause a pseudo-thrombocytopenia. This phenomenon underscores the inherent limitations of impedance based hematology analyzers, which often struggle to differentiate between platelets and very small erythrocyte fragments in abnormal samples. To broaden diagnostic horizons and ensure accurate interpretation, laboratory professionals must be well-versed in the principles and limitations of their analyzers, remain attentive to potential sources of analytical error, and routinely perform microscopic reviews to confirm unexpected or questionable results.

Keywords: Automated Counters, Pseudo-Thrombocytopenia, Blood Morphology, Case Report

The Role of Medical Laboratories in Screening and Diagnosing Diseases in Newborns

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Epidemiology of Amino Acid Disorders Identified Through Newborn Screening Using Tandem Mass Spectrometry in Isfahan (2020-2025)

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Background: Inherited metabolic disorders (IMDs) represent a substantial cause of neonatal morbidity and mortality worldwide. Early identification through universal newborn screening (NBS) is essential to prevent irreversible neurological damage and long-term disability. Despite the recognized importance of NBS, epidemiological data on amino acid disorders in Iranian neonates remain limited. This study aimed to determine the prevalence and distribution of amino acid disorders detected by tandem mass spectrometry and to evaluate the impact of early diagnosis in an Iranian neonatal population. Methods: In this cross-sectional study, screening data from 600 Iranian neonates (300 males and 300 females) referred to Nobel Medical Laboratory between 2020 and 2025 were analyzed. Dried blood spot samples, collected between days 3 and 5 of life, were examined using tandem mass spectrometry (MS/MS). Quantitative amino acid profiles were obtained, and abnormal results were followed by confirmatory diagnostic testing according to standard clinical protocols. Results: Of the 600 screened neonates, 14 (2.3%) had abnormal amino acid profiles, and 8 (1.3%) were confirmed to have IMDs. Phenylketonuria (PKU) was the most frequently identified disorder (0.5%), followed by maple syrup urine disease (0.3%), tyrosinemia (0.3%), and homocystinuria (0.2%). Although the overall prevalence was higher in males than in females (1.7% vs. 1.0%), the difference was not statistically significant ($p > 0.05$). The mean age at diagnosis was 8 ± 12 days, facilitating prompt initiation of targeted therapeutic interventions. Conclusion: The observed prevalence of 1.3% highlights the critical role of universal NBS in the early detection of IMDs within the Iranian neonatal population. The predominance of PKU reinforces the continued need for robust screening infrastructure and timely confirmatory testing. Early diagnosis through MS/MS-based screening enables rapid intervention, mitigates irreversible complications, and supports cost-effective healthcare planning. These findings contribute valuable epidemiological evidence to inform national screening policies and optimize neonatal health outcomes.

Keywords: Metabolic Disorders, Newborn Screening, Tandem Mass Spectrometry, Amino Acid Disorders, Phenylketonuria, Neonatal Screening

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Evaluation of Plasma Phenylalanine and Tyrosine Levels by HPLC in Newborn Screening for Phenylketonuria: A Gender-Based Analysis.

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Background: Phenylketonuria (PKU) is an inherited metabolic disorder characterized by elevated phenylalanine (Phe) and reduced tyrosine (Tyr) concentrations, which may lead to irreversible intellectual disability if not detected and treated early. Newborn screening is essential for preventing these complications. This study aimed to evaluate plasma Phe and Tyr levels using High-Performance Liquid Chromatography (HPLC) and to assess gender-based differences in PKU prevalence. Methods: In this cross-sectional study, 300 neonates (150 females and 150 males) aged 8–12 months were screened. Plasma samples were collected in EDTA tubes and analyzed by HPLC with UV detection at 254 nm. Chromatographic separation was performed on a C18 column (250 × 4.6 mm, 5 µm) using sodium acetate buffer (pH 6.5) and acetonitrile as the mobile phase at a flow rate of 1 mL/min. PKU was defined as Phe >75 nmol/mL. Results: PKU was diagnosed in 60 neonates (20%). Female and male neonates each accounted for 30 cases (20% in each sex group). Consequently, the healthy control group comprised 120 females and 120 males, ensuring an equal sex distribution between the control groups. Mean Phe levels were significantly higher in affected neonates (987.6 ± 183.4 nmol/mL) compared to healthy controls (55.8 ± 5.3 nmol/mL) ($P < 0.001$). Tyr levels were significantly lower in the PKU group (30.2 ± 4.1 nmol/mL) than in healthy neonates (95.7 ± 13.8 nmol/mL) ($P < 0.001$). The Phe/Tyr ratio was markedly elevated in affected neonates (32.7) compared to controls (0.6). Conclusion: HPLC-based plasma analysis provides an accurate and reliable method for measuring Phe and Tyr in PKU screening. The significant biochemical differences between affected and healthy neonates support the diagnostic value of these markers. In this study, no substantial sex-based disparity was observed in the prevalence of PKU. Early detection through systematic screening programs remains crucial for preventing neurological complications and ensuring normal cognitive development.

Keywords: Phenylketonuria, Newborn Screening, HPLC, Phenylalanine, Tyrosine, Plasma, Gender Differences

The Role of Medical Laboratories in the Diagnosis and Monitoring of Common Diseases

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P167

Evaluation of Serum Calcium Status and Its Association with Chelating Agents in Patients with Beta-Thalassemia Major: A Cross-Sectional Study in Yasuj

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Background: Chelating agents are essential for reducing tissue iron accumulation in patients with beta-thalassemia major. Although modern therapies, including chelation, have improved life expectancy in these patients, treatment-related complications—particularly alterations in serum calcium levels—are increasingly reported. Given the importance of monitoring calcium status, careful evaluation of this parameter is necessary. Methods: In this cross-sectional descriptive-analytical study, 105 patients with beta-thalassemia major in Yasuj were evaluated during 2021–2022 using a census sampling method. Demographic, clinical, and laboratory data were collected through a standardized checklist. Prior to blood transfusion, 5 mL of blood was drawn into clot tubes from each patient, and serum calcium, ferritin, and thyroid function tests were performed using commercial kits. Data were analyzed with SPSS version 26, with statistical significance set at $P \leq 0.05$. Results: The mean age of patients was 24.48 ± 9.8 years; 55.8% were male. Forty percent of patients had undergone splenectomy. A significant negative correlation was observed between age and mean serum calcium levels ($r = -0.196$, $P = 0.045$). Additionally, a significant association was found between splenectomy and serum calcium levels ($P = 0.05$). No significant differences were observed between serum calcium levels and the type of chelating agent used ($P > 0.05$). Conclusion: Hypocalcemia may occur concurrently with beta-thalassemia major. Regular monitoring of serum calcium in these patients is recommended to facilitate early detection of this complication.

Keywords: Beta-Thalassemia Major, Iron Chelators, Hearing Disorders

P168

A Report for Multidrug-Resistant Isolates of Mycobacterium Tuberculosis in Golestan Province, North Iran

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Background: Iran had a moderate incidence of tuberculosis (TB), but Golestan province had a permanently higher TB incidence rate than the national average. Here, we aimed to characterize the drug resistance patterns Mycobacterium tuberculosis complex (MTBC) isolates circulating in the Golestan province. Methods: A set of 166 MTBC isolates were collected during July 2014 to July 2015 and subjected to drug susceptibility testing (DST) for first line anti-TB drugs; rifampin (RMP; 40 µg/mL), isoniazid (INH; 0.2 µg/mL), ethambutol (ETL; 2µg/mL) and streptomycin (STM; 4 µg/mL) on Lowenstein-Jensen (LJ) medium using proportional method. Results: The set of 148 (89.2%) isolates were pan-susceptible, and 18 (10.8%) were found to be any drug resistant, including; two (1.2%) MDR, three (1.8%) INH mono-resistant, 12 (7.2%) STM mono-resistant, and one isolate (0.6%) that resistant to INH and STM. In addition, the phenotypic DST for second-line anti-TB drugs was completed on two MDR isolates; both were resistant to ETL, but one of them showed resistance to CIP, OFX, LVX, AMK and KAN. Conclusions: In this study, we found an MDR isolate that was simultaneously resistant to RMP fluoroquinolones, determined as pre-extensively drug-resistant (pre-XDR) TB. Emergence of drug-resistant isolates is a significant barrier for TB control, then, it is important to conduct future studies to determine transmission pattern of drug-resistant isolates in this region.

Keywords: Mycobacterium Tuberculosis, Tuberculosis, Multidrug-Resistant

P169

Lip Metastasis in Colorectal Cancer: A Rare Case

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Background: Cutaneous metastasis from colorectal cancer (CRC) is uncommon and usually indicates advanced disease with poor prognosis. Metastatic involvement of the lip is particularly rare and may lead to delayed diagnosis due to its atypical presentation. Case Presentation: We report the case of an 82-year-old man who presented with an isolated, painless lesion on the lower lip accompanied by recent weight loss. Initial topical treatment was ineffective. Histopathological examination of the lip biopsy revealed features consistent with metastatic adenocarcinoma of gastrointestinal origin. Immunohistochemical analysis showed positivity for CK20, CEA, CDX2, SATB2, and a high Ki67 proliferation index (>75%), while CK7 and other non-gastrointestinal markers were negative. Abdominopelvic computed tomography demonstrated circumferential wall thickening of the left colon with regional lymphadenopathy, and additional imaging revealed hepatic and pulmonary metastases. Due to the patient's poor clinical condition, colonoscopy was not performed. The diagnosis of metastatic CRC to the lower lip was established based on imaging and immunohistochemical findings. The patient was treated with the FOLFOX chemotherapy regimen without clinical response; treatment was subsequently discontinued, and supportive care was initiated. The patient died five months after diagnosis. Conclusion: Lip metastasis is an extremely rare manifestation of CRC and signifies widespread disease with poor survival. This case highlights the importance of maintaining a high index of suspicion for metastatic disease when evaluating new cutaneous or mucosal lesions, particularly in elderly patients. Prompt biopsy and immunohistochemical evaluation are essential for accurate diagnosis.

Keywords: Lip Biopsy, Colorectal Cancer, Lip Metastasis

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Survival and Prognostic Factors in Patients with Pancreatic Cancer: A Population-Based Study from Northern Iran

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Background: Pancreatic cancer is associated with poor prognosis and high mortality. Identifying prognostic factors may improve risk stratification and management. This study aimed to evaluate survival rate and related factors among patients with pancreatic cancer in Guilan province, Iran. Methods: This study included fifty patients aged ≥18 years with pancreatic cancer. Demographic, clinical, and treatment-related data were collected. Survival was assessed using the Kaplan–Meier method, with comparisons performed by log-rank test. Univariate and multivariate Cox proportional hazards models were used to identify predictors of mortality. Results: Out of 50 included patients, 20 patients were female, and the mean age was over 60 years in 58% of patients. Most tumors were located in the pancreatic head (78%), and 56% of patients were diagnosed at advanced stages (III/IV). The mean and median survival times were 39.6 months and 9.0 months, respectively. One-, three-, and five-year survival rates were 45.2%, 31.3%, and 23.5%. Advanced disease stage (III/IV) was strongly associated with reduced survival (aHR = 3.32, p = 0.025). Underweight BMI was linked to increased mortality in univariate analysis (HR = 2.79, p = 0.016). In multivariate analysis, male sex (HR = 3.38, p = 0.016) and blood group O (HR = 2.86, p = 0.031) were independently associated with higher mortality. Conclusion: Advanced disease stage remains the strongest predictor of mortality in pancreatic cancer. Male sex, blood group O, and low BMI may also influence survival, highlighting the importance of early diagnosis and nutritional assessment.

Keywords: Survival Rate, Pancreatic Cancer, Mortality

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Analysis of Agglutination-Based Serological Tests in Hospitalized Patients with Gastrointestinal Symptoms

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Background and Aim: Gastrointestinal symptoms are frequent among hospitalized patients and often necessitate investigation of infectious causes, including brucellosis and enteric fever. Serological agglutination tests such as the Wright, 2ME Wright, Coombs Wright, and Widal tests are commonly employed as diagnostic screening tools. This study investigated the positivity rates of these tests in patients presenting with gastrointestinal symptoms during a 9-month period to enhance diagnostic accuracy and inform clinical decision-making. Methods: This study was conducted within the internal medicine department of a teaching hospital over a period of nine months. It focused on patients admitted with gastrointestinal symptoms, including fever, abdominal pain, and diarrhea. Blood samples were subjected to several diagnostic tests, including tube agglutination methods of the Wright test to identify total Brucella antibodies, the 2ME Wright teststandard for detecting IgG antibodies, the Coombs Wright test for incomplete antibodies, and the Widal test to assess antibodies against Salmonella typhi and paratyphi. In total, 103 Wright tests and 39 Widal tests were evaluated. Positivity was determined based on predefined serological titers aligned with relevant clinical guidelines. Results: During the study period, 103 tests were performed with standard tube agglutination methods. The results of this study were positive for the Wright test (9.7%), the 2ME Wright test (5%), Coombs Wright test (0%). Additionally, for the Widal test, 39 samples were analyzed, with no positive results reported (0%). Conclusion: This 9-month investigation revealed a small but notable yield from brucellosis serology, whereas Widal testing provided no diagnostic benefit. These results underline the necessity for the selective implementation of agglutination tests guided by clinical and epidemiological considerations. Future diagnostic approaches could benefit from integrating serological results with molecular and microbiological methods for a more comprehensive evaluation of gastrointestinal infections.

Keywords: Wright test, 2ME Wright Test, Coombs Wright, Widal Test, Gastrointestinal Symptoms

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The Increased C-Reactive Protein/Albumin Ratio and Platelet/MPV in Allergic Rhinitis and Asthma: Potential Biomarkers?

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Background: Allergic rhinitis and asthma are two common respiratory diseases with allergic etiology in the world's population. The pathogenesis of these two diseases is almost similar in terms of causing systemic allergic inflammation and type 2 immune response, so we focused on investigating the potential biomarkers like CRP/Albumin Ratio (CAR) and Platelet/MPV Ratio (PMR) in this regard. Methods: A total of 301 individuals were included in this study, which was done on pediatric patients diagnosed with allergic rhinitis (n=109) and controlled asthma (n=92) referred to Ahvaz Golestan Hospital's Clinic in Iran. Besides, (n=101) individuals with no history of infection or respiratory diseases were recruited as the control group. Venous blood samples were taken to perform biochemical tests and complete blood cell count after obtaining written consent from the patients. Results: The serum IgE levels, WBC and platelet counts, MPV, CRP, ENR, NLR, CAR, and PMR values were significantly higher in the allergic rhinitis and asthma groups compared to the control group ($P<0.001$). There were no statistically significant differences between ELR, MLR, MER, and PLR between the studied groups respectively ($P=0.083$, $P=0.989$, $P=0.067$, $P=0.154$). CAR and PMR tests can separate asthmatic patients from healthy individuals with a high sensitivity (68.48%, 65.22%) and specificity (74.26%, 77.23%) respectively. Conclusions: CRP/Albumin Ratio and Platelet/MPV Ratio are two independent supportive biomarkers with high sensitivity and specificity in distinguishing asthmatic patients from healthy individuals, but they are not considered very valid biomarkers in allergic rhinitis.

Keywords: Albumin, Allergic Rhinitis, Asthma, CRP, MPV, Platelet

P173

Association of C-Reactive Protein and Erythrocyte Sedimentation Rate with Type 2 Diabetes Mellitus and Non-Alcoholic Fatty Liver Disease

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Background: Type 2 diabetes mellitus (T2DM) and non-alcoholic fatty liver disease (NAFLD) are prevalent metabolic disorders that frequently coexist and share common pathophysiological mechanisms, particularly chronic low-grade systemic inflammation. Inflammatory biomarkers such as C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR) may reflect disease severity and metabolic burden; however, regional data on their comparative levels in patients with T2DM, NAFLD, and combined disease are limited. This study aimed to investigate the association between CRP and ESR with T2DM and NAFLD, to determine the prevalence of elevated inflammatory markers in these conditions, and to examine the correlation between CRP and ESR in different disease groups. Methods: In this cross-sectional study, 150 patients who attended Amir-Al-Momenin Hospital, Zabol, Iran, were enrolled and divided into three equal groups: T2DM, NAFLD, and T2DM with NAFLD. Demographic data, body mass index (BMI), CRP status, and ESR levels were recorded. Statistical analyses included ANOVA, chi-square tests, correlation analyses, and multivariable logistic regression, with statistical significance set at $p < 0.05$. Results: The mean age of participants was 46.01 ± 11.16 years. Significant differences were observed in age ($p < 0.001$) and ESR levels ($p < 0.001$) across groups, with the NAFLD+T2DM group being oldest (53.06 ± 9.05 years) and having the highest ESR (28.18 ± 13.32 mm/hr). Age >46 years was strongly associated with NAFLD+T2DM (OR = 7.20, 95% CI: 3.27–15.83, $p < 0.001$) and inversely associated with isolated T2DM (OR = 0.09, 95% CI: 0.04–0.22, $p < 0.001$). BMI was similar across groups and showed no significant association with disease status ($p = 0.781$). CRP positivity prevalence was 64.0% in T2DM, 62.0% in NAFLD, and 50.0% in NAFLD+T2DM, with no significant association ($\chi^2 = 2.364$, $p = 0.307$). ESR abnormality prevalence was 30.0% in T2DM, 20.0% in NAFLD, and 36.0% in NAFLD+T2DM, also without significant association ($\chi^2 = 3.195$, $p = 0.202$). Logistic regression revealed no significant associations between CRP or ESR and disease groups (all $p > 0.05$). The odds ratios for CRP and T2DM, NAFLD, and NAFLD+T2DM were 1.397 (95% CI: 0.694-2.812), 1.231 (95% CI: 0.614-2.466), and 0.587 (95% CI: 0.295-1.168), respectively. Overall correlation between CRP and ESR was weak and non-significant ($r = 0.107$, $p = 0.191$). However, disease-specific analysis revealed a

significant moderate positive correlation in the NAFLD-only group (r = 0.422, p = 0.002), while no correlation was observed in T2DM (r = 0.076, p = 0.602) or NAFLD+T2DM groups (r = 0.074, p = 0.608). Conclusion: While CRP and ESR are frequently elevated in patients with T2DM and NAFLD, they showed no significant independent associations with specific disease states in this study. The significant correlation between CRP and ESR observed exclusively in the NAFLD-only group suggests potential differences in inflammatory profiles across disease conditions. These findings indicate that CRP and ESR may not be sufficiently specific as standalone markers for distinguishing between T2DM, NAFLD, or their combination, highlighting the complex and multifactorial nature of inflammation in metabolic diseases

Keywords: Type 2 Diabetes Mellitus, Non-Alcoholic Fatty Liver Disease, C-Reactive Protein, Erythrocyte Sedimentation Rate

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Efflux Pumps and Glycopeptide Resistance in Clinical Enterococcus faecalis and Enterococcus faecium Isolates- 2024

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Background: Enterococci are important opportunistic pathogens in clinical settings, and the emergence of multidrug resistance is a growing concern. Efflux pumps such as emeA, efrA, efrB, and efmA may contribute to reduced susceptibility to multiple antimicrobials. This study investigated the prevalence of major efflux pump genes in clinical Enterococcus isolates and their association with vancomycin resistance. Methods: Enterococcus spp. were recovered from clinical specimens collected in Ganjavian Hospital, Dezful. Enterococcus strains were identified using the ddl gene amplification. Glycopeptide resistance was screened phenotypically, and the presence of vanA and vanB genes was confirmed by PCR. Subsequently, all isolates were tested by PCR for the presence of efflux pump genes. Results: In 73 isolates, 63% were identified as vancomycin-resistant Enterococcus, with vanA (100%). We detected the efflux pump genes emeA, efrA, efrB, and efmA in 39.7%, 39.7%, 42.5%, and 56.2% of the isolates, respectively. The results revealed a statistically significant association between Enterococcus species and the presence of specific efflux pumps. Notably, efflux pump efmA was predominantly identified in E. faecium, whereas the other pumps were more common in E. faecalis. A significant relationship was also observed between biofilm production and the presence of efflux pumps efrA and efrB. Interestingly, efflux pumps were predominantly detected in vancomycin-susceptible strains ($p< 0.05$). Conclusions: The presence of efflux pumps and vanA genes highlights the need to consider efflux-mediated resistance when interpreting antimicrobial susceptibility and when designing infection control and treatment strategies. Further studies on efflux activity assays are clarifying the functional role of these pumps in Enterococcus resistance.

Keywords: Vancomycin-Resistant Enterococcus (VRE), Efflux Pump, Biofilm, Antibiotic Resistance, PCR

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The Comparison of the Time of Normalization of CRP in COVID-19 Patients Who Received IV Dexamethasone in COPD and Non-COPD Patients in Qazvin in 2021

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Introduction: According to the results of the studies and the existence of a relationship between inflammatory factors in COPD patients who are infected with COVID-19 in epidemic conditions, this study aims to investigate the level of the inflammatory marker of CRP in COVID-19 patients with COPD, compared to people without COPD. Methods and materials:In this cross-sectional analytical study, the number of 76 COPD and non-COPD patients with Covid-19 who visited Buali Hospital in Qazvin in the first 6 months of 2021 were conducted. Two groups were divided by matching. After data collection, SPSS version 16 software was used for data analysis. The selection of patients' files was random. A significance level of less than 5% was considered.Results:The average age of the participants was 70.49 ± 14.71 years (with a range of 36 to 94 years). Most of the participants were men (71.1%) and the frequency of women was 28.9%. Our study showed that the average CRP normalization time in the COPD group was higher than the non-COPD group (7.84 vs. 6.42), but this relationship was not significant. Also, there was no significant relationship between inflammatory factors such as CRP and ESR, as well as blood factors such as lymphocytes, neutrophils, RBCs, and platelets between tow groups.In this study, between factors CRP 1 and CRP 2 CRP 2 and ESR, time and blood sugar, CRP 1 and neutrophil, time and neutrophils, time and platelets, the number of dexamethasone and platelets, and neutrophils and blood sugar in the COPD group were significantly correlated. also, in the group non-COPD, between lymphocytes and RBC, neutrophils and platelets, time and ESR, CRP 1 And the number of dexamethasone significant correlation was observed. as well as factors CRP 1 and ESR, time and dexamethasone, RBC and ESR, CRP 1 and time were significantly correlated in both groups.Conclusion And Discussion:The results of this study showed that the duration of

normalization of CRP between the two groups and other investigated parameters was not statistically significant. However, statistically significant correlations were observed between some inflammatory and blood factors. In our study, there was no difference in clinical response to intravenous dexamethasone and duration of hospitalization between people with and without COPD, which indicated that the severity of COVID-19 in patients with COPD is not more severe, contrary to popular belief. Based on this, perhaps more investigations are useful for the development and implementation of an effective treatment approach for the management of these patients.

Keywords: COVID-19, COPD, CRP, Dexamethasone, Inflammatory Factor

P176

The Future of Prostate Cancer Detection: Integrating Novel Biomarker Panels for Precision Diagnosis

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Background: Prostate-specific antigen (PSA) testing has improved prostate cancer detection but lacks specificity, leading to unnecessary biopsies and overdiagnosis of indolent tumors. More accurate, non-invasive tools are urgently needed to distinguish clinically significant disease. Methods: This review synthesizes evidence on emerging prostate cancer biomarkers with clinical applicability. Genetic, proteomic, and immunologic markers were evaluated, with emphasis on validated panels for clinical integration. Results: Promising biomarkers outperform PSA in specificity. These include urinary RNA markers (PCA3, TMPRSS2-ERG), circulating microRNAs (miR-375), and protein-based markers like prostate-specific membrane antigen (PSMA). Multiparametric panels—such as the 4Kscore and Prostate Health Index (PHI)—combine multiple biomarkers with clinical data to improve risk stratification and reduce unnecessary biopsies, particularly in men with PSA in the diagnostic grey zone. Conclusion: Integrated biomarker panels represent a pivotal advancement in personalized prostate cancer care, enhancing diagnostic precision and reducing invasive procedures. Widespread implementation requires standardization, cost-effectiveness analyses, and validation across diverse populations. Future efforts should develop clinical guidelines incorporating these panels into routine practice.

Keywords: Prostate Cancer, Biomarker, PSA, Diagnosis, Risk Stratification

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Seasonal Variations in Serum Vitamin D Levels in Central Iran: A Large Cross-Sectional Analysis

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Introduction: Vitamin D status fluctuates with seasonal sunlight exposure. Detailed population-level data characterizing this variation in central Iran are lacking. This study described the seasonal pattern of serum 25-hydroxyvitamin D levels in a large clinical sample from Isfahan. Methods: This cross-sectional analysis included 107,337 individuals with serum vitamin D measurements obtained from the Noble Laboratory in Isfahan. Vitamin D levels were measured using HPLC. Concentrations were categorized according to the season of blood draw (spring, summer, autumn, and winter). Seasonal differences were evaluated using one-way ANOVA followed by Tukey's post-hoc test in SPSS. Results: a total of 107,337 individuals (61.4% female) with a mean age of 48.67±16.5 years were participated. The overall mean vitamin D level was 35.9±14.7ng/mL. A highly significant seasonal variation was observed ($p<0.001$). Mean levels were lowest in winter (32.6±14.7ng/mL), intermediate in autumn (35.9±14.3 ng/mL), and highest in spring (37.3±14.9ng/mL) and summer (37.8±14.5 ng/mL). Post-hoc analysis confirmed that the winter mean was significantly lower than all other seasons ($p<0.001$), and the autumn mean was significantly lower than both spring and summer ($p<0.001$). No statistically significant difference was found between spring and summer levels. Discussion and Conclusion: The study reveals a clear seasonal rhythm in vitamin D status, with levels peaking in spring/summer and reaching a nadir in winter. These findings emphasize the necessity of considering the season of testing for accurate clinical interpretation of vitamin D status in this region and support the rationale for seasonal public health guidance regarding sunlight exposure or supplementation.

Keywords: 25-Hydroxyvitamin D, Seasonality, Iran, Cross-Sectional Study, Sunlight Exposure

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Prevalence of High-Risk HPV16 and HPV18 Among HPV-Positive Women in Isfahan, Iran: A Cross-Sectional Study

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Background: Human papillomavirus (HPV) is the most common viral sexually transmitted infection worldwide. Persistent infection with high-risk HPV types, particularly HPV16 and HPV18, is the primary cause of cervical cancer and other anogenital malignancies. This study aimed to determine the prevalence of HPV16 and HPV18 among HPV-positive women attending a diagnostic laboratory in Isfahan, Iran. Methods: This cross-sectional study was conducted at Nobel Diagnostic Laboratory in Isfahan, Iran, during the first quarter of 2025. Among 899 individuals referred for HPV testing, 300 patients (mean age 34.61±11.67 years; 96% female) tested positive for various HPV types. Viral DNA extraction and genotyping for HPV16 and HPV18 were performed using real-time PCR in the molecular laboratory. Results: Of the 300 HPV-positive patients, 79 (26.3%) were infected with HPV16 and 10 (3.3%) with HPV18. The remaining 211 cases (70.3%) consisted of other high-risk or low-risk HPV types. HPV16 was approximately eight times more prevalent than HPV18 in this population. Conclusion: Our findings demonstrate that HPV16 is the most common high-risk type among HPV-positive women in Isfahan, followed by HPV18. This distribution aligns with global patterns showing HPV16 as the predominant carcinogenic type in cervical cancer. The high prevalence of these oncogenic types underscores the critical importance of molecular screening for risk stratification and supports the implementation of prophylactic vaccination programs targeting HPV16/18 in Iran. Regular screening with high-sensitivity methods like real-time PCR remains essential for early detection and prevention of cervical cancer.

Keywords: HPV16, HPV18, High-Risk HPV, Cervical Cancer, Iran

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Circular RNAs in Diabetic Foot Ulcers: A Scoping Review of Clinical, Preclinical, and in Silico Evidence on Diagnostic and Therapeutic Potentials

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Background and Objective Diabetic foot ulcers (DFUs) involve chronic inflammation, impaired angiogenesis, oxidative stress, and disrupted fibroblast–keratinocyte interactions. Circular RNAs (circRNAs), a category of stable non-coding RNAs, have become essential regulators of these processes; nevertheless, their comprehensive functions in DFUs are still inadequately characterised. This scoping review integrated clinical, preclinical, and in silico evidence on circRNAs in DFUs to assess their diagnostic, mechanistic, and therapeutic potential. Methods Systematic searches of MEDLINE, EMBASE, Web of Science, and Google Scholar were conducted on July 16, 2025, according to the PRISMA-ScR guidelines. Eligible papers included clinical investigations of circRNAs in the tissues of patients with DFUs, preclinical animal models assessing circRNA-based therapies, and computational predictions of circRNA-miRNA-mRNA networks. Information was collected on circRNA expression, molecular targets, clinical associations, and therapeutic effects. Results Twenty-two studies (7 clinical, 13 preclinical, 2 in silico) were selected. Clinical studies found hsa_circ_PRKDC, hsa_circ_072697, hsa_circ_080968, and hsa_circ_0000907 to be associated with wound severity, tissue perfusion, and keratinocyte proliferation in patients with diabetic foot ulcers. Preclinical studies showed that delivery of mmu_circHIPK3, mmu_circMYO9B, and mmu_circ_Astn1 via exosomes or nanoparticles improved angiogenesis, epithelial regeneration, and wound closure. However, the silence of mmu_circ_0005654 reduced ferroptosis and inflammation. In silico analyses identified potential regulatory axes, such as hsa_circ_0089761/miR-146a-5p/SMAD4 (Mothers against decapentaplegic homologue 4) and hsa_circ_0049271/miR-24-3p/JUNB, that were associated with inflammatory-angiogenic pathways in this disease. Conclusions CircRNAs hold promise for the diagnosis and treatment of DFUs by modulating angiogenesis, inflammation, oxidative stress, and epithelial repair. Standard network-guided therapies are essential to translate circRNA-based strategies into clinical practice.

Keywords: Angiogenesis, Biomarker, Circular RNA, Diabetic Foot Ulcer, Exosomal Therapy, In Silico Network, Non-Coding RNA, Wound Healing

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Prevalence of Prediabetes and Diabetes Mellitus in Isfahan: A Comparative Analysis of FBS and HbA1c Criteria in a Large Adult Population

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Background: Diabetes mellitus (DM) and prediabetes are escalating public health challenges in Iran. Discordance between fasting blood sugar (FBS) and hemoglobin A1c (HbA1c) in disease classification reported globally. This study aimed to determine the prevalence of prediabetes and DM among adults in Isfahan using both FBS and HbA1c criteria and to examine their agreement across sex and age groups.Methods: This cross-sectional study included 74,621 adults from Nobel Laboratory, Isfahan, Iran (2024). Prediabetes and DM were defined using ADA criteria: FBS 100-125 and ≥126 mg/dL, HbA1c 5.7-6.4% and ≥6.5%, respectively. Prevalence was calculated overall and stratified by sex and age groups (18-44, 45-59, ≥60 years). Agreement between criteria was assessed using cross-tabulation.Results: Participants (mean age 52.8±16.1 years, 55.7% female) had mean FBS 106.0±31.9 mg/dL and HbA1c 6.01±1.27%. Based on FBS, prevalence was: normal 59.4%, prediabetes 25.3%, DM 15.3%. Based on HbA1c, prevalence was: normal 52.1%, prediabetes 25.6%, DM 22.3%. DM prevalence increased markedly with age, reaching 36.7% in those ≥60 years by HbA1c. Men had higher DM prevalence than women by both criteria (FBS: 17.4% vs. 13.6%; HbA1c: 24.1% vs. 20.9%). Concordant classification occurred in 69.5% of subjects, while 30.5% showed discordance between criteria. Due to the non-normal distribution of the data, Spearman's rank correlation coefficient was used to assess the linear relationship between FBS and HbA1c, revealing a strong positive correlation ($r = 0.603$, $p < 0.001$).Conclusion: The burden of prediabetes and DM in Isfahan is substantial, with nearly one in four adults affected by DM based on HbA1c. Significant discordance between FBS and HbA1c classification underscores the importance of using both tests for accurate risk stratification. The rising prevalence with age and male predominance align with national trends.

Keywords: Diabetes Mellitus, Prediabetes, Prevalence, HbA1c, Fasting Blood Sugar, Iran

P181

Association of Age and Sex with CD38 Expression in Chronic Lymphocytic Leukemia: A Cross-Sectional Study from Isfahan, Iran

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Background: CD38 expression is a well-established prognostic marker in chronic lymphocytic leukemia (CLL), associated with more aggressive disease and shorter treatment-free survival. While its prognostic value is widely accepted, the relationship between demographic factors and CD38 expression remains underexplored, particularly in Iranian populations. This study aimed to investigate the association between age, sex, and CD38 expression in CLL patients. Methods: This cross-sectional study included 48 CLL patients (mean age 65.10±12.57 years; 58.3% male, 41.7% female) referred to Nobel Laboratory in Isfahan, Iran. Peripheral blood samples were stained with FITC-conjugated anti-CD38 antibody and analyzed using Beckman Coulter flow cytometry. CD38 expression percentage was recorded. Pearson correlation and multiple-linear-regression were performed to assess associations with age and sex. Results: Mean CD38 expression was 9.70±20.76%. A significant inverse correlation was observed between age and CD38 expression ($r=-0.303$, $p=0.036$), indicating that older patients had lower CD38 expression levels. The difference in CD38 expression between males (13.33%) and females (4.62%) was not statistically significant ($p=0.099$). Multiple regression analysis confirmed that age ($\beta=-0.291$, $p=0.043$) was a significant independent predictor of CD38 expression, while sex showed no significant association ($\beta=0.190$, $p=0.179$). Conclusion: This study demonstrates a significant inverse association between age and CD38 expression in CLL patients, with older individuals showing lower CD38 levels. This finding aligns with previous studies showing age-related differences in CLL biology. The lack of significant sex differences is consistent with some previous reports. These results suggest that age should be considered when interpreting CD38 expression as a prognostic marker in CLL.

Keywords: Chronic Lymphocytic Leukemia, CD38, Age, Sex, Flow Cytometry, Iran

P182

The Role of Clinical Laboratories in the Detection and Monitoring of Carbapenem-Resistant Klebsiella pneumoniae: Implications for Patient Management in Central Iran

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Background: This study aimed to investigate the frequency and antibiotic resistance patterns of MDR, extensively drug-resistant (XDR), and CRKP, as well as the antibiotic resistance genes of Klebsiella pneumoniae (K. pneumoniae) isolates from patients' infectious samples from central Iran. Methods: This study examined 546 clinical samples of patients to identify K. pneumoniae. The isolates were investigated for their antibiotic resistance profile, extended-spectrum β-lactamase (ESBL), AMPC β-lactamase, carbapenemase resistance, sulfonamide, plasmid-mediated quinolone resistance (PMQR) along with their resistance genes by polymerase chain reaction (PCR). Antimicrobial susceptibility testing of the isolated K. pneumoniae strains was performed using the disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. The minimum inhibitory concentrations (MICs) of imipenem, meropenem, and colistin for carbapenem-resistant isolates were determined using E-test strips (Liofilchem, Italy) according to the 2021 CLSI guidelines. ESBL-producing isolates were identified using the combination disk diffusion and double-disk synergy tests, whereas AmpC β-lactamase-producing isolates were detected using the disk test and phenylboronic acid method. In addition, carbapenemase production was evaluated using the modified Hodge test (MHT), the modified carbapenem inactivation method (mCIM), and the EDTA-modified carbapenem inactivation method (eCIM) according to the 2021 CLSI guidelines.Results: Out of 546 clinical samples, 121 (22.1%) cases of K. pneumoniae were identified using culture and PCR methods. The K. pneumoniae isolates were most frequently recovered from urinary tract specimens (62, 51.2%), followed by respiratory specimens (48, 39.6%), wound specimens (11, 9.0%), and blood specimens (8, 6.6%). The highest antibiotic resistance rates were found for ampicillin (119/121; 98.3%), cotrimoxazole (78/121; 64.4%), and cefixime, cefotaxime, ceftriaxone, and ceftazidime as a group (77/121; 63.6%). Tigecycline, colistin, and fosfomycin were the most effective antimicrobial agents with 98.4%, 96.7%, and 95.9% susceptibility, respectively. Of the isolates, 51 (42.1%) were CRKP. All CRKP isolates were MDR. The most abundant genes were bla_{TEM} (77/77; 100%), $bla_{CTX\text{-}M1}$ (76/77; 98.7%), bla_{SHV}

(76/77; 98.7%) for ESBL; bla_{CIT} 28 (48.3%) and bla_{CMY-2} 26 (44.8%) for AMPC β-lactamase; and bla_{OXA-48} 46 (90.1%) and bla_{NDM} 36 (70.5%) for carbapenemase. Among the PMQR determinants, qnrB (25/52; 48%), qnrS (19/52; 36.5%), and qnrA (11/52; 21.1%) were positive from the isolates. Conclusions: Due to the high prevalence of MDR and CRKP in central Iran, tracking and immediate intervention are necessary for control and inhibition of K. pneumoniae resistant isolates. Tigecycline, colistin, and fosfomycin are the best treatment options in patients with CRKP in this geographical area.

Keywords: Multidrug-Resistant, Carbapenem-Resistant K. Pneumoniae, bla_{OXA-48}, bla_{NDM}, Iran

P183

Age-Related Variations and Waning Immunity in HBV Vaccine Protection: The Need for Ongoing Serological Surveillance

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Background: Hepatitis B virus (HBV) infection remains a major global public health concern despite the widespread implementation of vaccination programs. The persistence of protective immunity, particularly across different age groups and over time, is critical for evaluating long-term vaccine effectiveness and guiding booster dose policies. This study aimed to assess the seroprotection rate against HBV across age categories and to investigate temporal trends in immunity over a ten-year period. Methods: In this retrospective cross-sectional study, laboratory records of serum hepatitis B surface antibody (HBs-Ab) measurements collected between 2015 and 2026 were analyzed. After data cleaning and exclusion of invalid results, 4,617 individuals were included. Seroprotection was defined as an HBs-Ab titer ≥10 IU/L. Participants were stratified into predefined age groups, and annual seroprotection rates were calculated. Descriptive statistics were used to summarize antibody titers, and temporal trends were evaluated using year-by-year comparisons. Results: The overall seroprotection rate was 58.8%. Protective immunity varied across age groups, ranging from 51.5% in individuals aged 40–49 years to 66.3% among those aged ≥60 years. The median HBs-Ab titer was 23.81 IU/L, while the mean titer was 207.81 IU/L, indicating a right-skewed distribution. Analysis of annual trends revealed a noticeable decline in seroprotection over time, from a peak of 72.9% in 2019 to 44.1% in 2026, suggesting waning immunity at the population level. Conclusion: This study demonstrates substantial age-related variability and a significant downward trend in HBV seroprotection over the past decade. These findings highlight potential gaps in long-term immunity and underscore the need for periodic serological monitoring. From a public health perspective, the results support reconsideration of booster vaccination strategies, particularly for high-risk and middle-aged populations, to maintain effective protection against HBV infection.

Keywords: HBV, Seroprotection, Vaccination

P184

The Role of Clinical Laboratory Biomarkers in Early Detection and Monitoring of Non-Alcoholic Fatty Liver Disease (NAFLD)

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Background: Non-Alcoholic Fatty Liver Disease (NAFLD) is the most common chronic liver disorder worldwide, strongly associated with obesity, insulin resistance, and metabolic syndrome. Early detection and appropriate monitoring are essential to prevent progression to non-alcoholic steatohepatitis (NASH), fibrosis, cirrhosis, and hepatocellular carcinoma. Clinical laboratories play a central role in screening, diagnosis, and longitudinal assessment of disease progression. Objective: To review the role of laboratory biomarkers in the early detection and monitoring of NAFLD and to highlight non-invasive indices that improve risk stratification in public health settings. Methods: This narrative review is based on published literature indexed in PubMed focusing on laboratory biomarkers and non-invasive scoring systems for NAFLD assessment. Results: Routine biochemical markers such as alanine aminotransferase (ALT), aspartate aminotransferase (AST), and lipid profile remain first-line indicators in suspected NAFLD. However, their sensitivity is limited. Emerging biomarkers including high-sensitivity C-reactive protein (hs-CRP), cytokeratin-18 (CK-18), and markers of insulin resistance enhance early detection. Non-invasive scoring systems such as FIB-4 index and NAFLD fibrosis score have demonstrated significant utility in identifying patients at risk of advanced fibrosis, reducing the need for liver biopsy. Laboratory monitoring also supports evaluation of therapeutic response and disease progression. Conclusion: Clinical laboratory testing is fundamental in the early identification and monitoring of NAFLD. Integration of conventional biomarkers with validated non-invasive indices improves risk stratification and supports preventive strategies in population health management. Background: Non-Alcoholic Fatty Liver Disease (NAFLD) is the most common chronic liver disorder worldwide, strongly associated with obesity, insulin resistance, and metabolic syndrome. Early detection and appropriate monitoring are essential to prevent progression to non-alcoholic steatohepatitis (NASH), fibrosis, cirrhosis, and hepatocellular carcinoma. Clinical laboratories play a central role in screening, diagnosis, and longitudinal assessment of disease progression. Objective: To review the role of laboratory biomarkers in the early detection and monitoring of NAFLD and to highlight non-invasive indices that improve risk stratification in public health settings. Methods: This narrative review is based on published literature indexed in PubMed focusing on laboratory biomarkers and non-invasive scoring systems for NAFLD assessment. Results: Routine biochemical markers such as alanine aminotransferase (ALT), aspartate aminotransferase (AST), and lipid profile remain

first-line indicators in suspected NAFLD. However, their sensitivity is limited. Emerging biomarkers including high-sensitivity C-reactive protein (hs-CRP), cytokeratin-18 (CK-18), and markers of insulin resistance enhance early detection. Non-invasive scoring systems such as FIB-4 index and NAFLD fibrosis score have demonstrated significant utility in identifying patients at risk of advanced fibrosis, reducing the need for liver biopsy. Laboratory monitoring also supports evaluation of therapeutic response and disease progression. Conclusion: Clinical laboratory testing is fundamental in the early identification and monitoring of NAFLD. Integration of conventional biomarkers with validated non-invasive indices improves risk stratification and supports preventive strategies in population health management.

Keywords: Non-Alcoholic Fatty Liver Disease (NAFLD), Clinical Laboratory, Biomarkers, Non-Invasive Markers, Liver Enzymes, FIB-4 Index, Metabolic Syndrome, Disease Monitoring

P185

Determination of Antibiotic Resistance Pattern and Production of Extended-Spectrum Beta-Lactamases in Escherichia Coli Isolates Collected from Bagher-ul-Uloom Hospital in Ahar

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Background: Antibiotic resistance in pathogenic microorganisms in humans and animals is one of the most important challenges facing human societies. Extended-spectrum beta-lactamase enzymes (ESBLs) are the most important factor causing multiply resistance to antibiotics among Gram-negative bacteria, including Escherichia coli, as one of the most important bacteria causing opportunistic infections. This study aimed to determine the frequency of microbial resistance and the production of extended-spectrum beta-lactamases in Escherichia coli isolates isolated from Bagher-ul-Uloom Hospital in Ahar city. Methods: In this descriptive-cross-sectional study, 130 Escherichia coli isolates collected from patients hospitalized in Ahar Hospital (including 117 urinary tract infection samples, 3 blood culture samples, 6 wound samples, 3 tracheal samples, and 1 catheter sample) were identified during one year (April 2025 to April 2026) using standard biochemical methods and culture in specific media. The antimicrobial resistance pattern of the isolates was determined using the disk diffusion method and using common antibiotic disks in the region. Extended-spectrum beta-lactamase-producing isolates were identified using the combined disk method. Results: The highest antibiotic resistance among the isolates studied was observed to Ampicillin with 100% and Nalidixic acid with 85% resistance, and the lowest resistance was observed to Gentamicin with 20% and Ciprofloxacin with 33%. 46% of the isolates were found to produce Extended-Spectrum Beta-Lactamase, one of which was from the isolates obtained from blood samples and the rest were from the isolates obtained from urinary tract infections. Conclusion: According to the results of this study, the frequency of antibiotic resistance and the presence of extended-spectrum beta-lactamase-producing isolates, early identification of these resistant bacteria and the use of appropriate treatment strategies, correct and rational administration of antibiotics are essential in order to prevent and prevent the further spread of microbial resistance.

Keywords: Antibiotic Resistance, Extended-Spectrum Beta-Lactamases, Escherichia Coli

The Role of the Laboratory in Diagnosing Heart Attacks

P186-P188

P186

Dyslipidemia and liver enzyme abnormalities: findings from the PERSIAN Guilan cohort study

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Background: Dyslipidemia is a major metabolic disorder that contributes substantially to morbidity, mortality, and healthcare costs worldwide. Growing evidence indicates that lipid abnormalities play an important role in hepatic dysfunction. This study aimed to investigate the association between dyslipidemia and its individual components with elevated liver enzyme levels in participants of the Prospective Epidemiological Research Studies in Iran (PERSIAN) Guilan Cohort Study (PGCS). Methods: This cross-sectional analysis included 10,520 adults enrolled in the PGCS in Guilan province, Iran. Demographic characteristics, clinical information, and medication use were collected. Serum lipid parameters, total cholesterol, triglycerides, low-density lipoprotein cholesterol (LDL-C), and high-density lipoprotein cholesterol (HDL-C), as well as liver enzymes including alanine aminotransferase (ALT), aspartate aminotransferase (AST), γ-glutamyltransferase (GGT), and alkaline phosphatase (ALP) were measured. Multivariable logistic regression models were used to assess associations between lipid abnormalities and elevated liver enzymes reporting odds ratio (OR) and 95% confidence interval (CI), with statistical significance set at $p < 0.05$. ORs were also adjusted for some demographic and clinical characteristics using statistical models. Results: Among the participants, 53.6% were women, with a mean age of 49.74 ± 8.89 years; the largest age group was 45–54 years (36.6%). The mean body mass index was 28.14 ± 5.09 kg/m², and 39.9% were overweight. Alcohol use was reported by 13.3%, while 0.6% had fatty liver disease, 0.3% had hepatitis, 15.1% used lipid-lowering medications, and 16.5% reported hepatotoxic drug use. Abnormal levels of total cholesterol, triglycerides, LDL-C, HDL-C, ALT, AST, GGT, and ALP were observed in 40.3%, 43.1%, 29.0%, 41.5%, 19.4%, 4.6%, 11.6%, and 5.1% of participants, respectively. Elevated total cholesterol was significantly associated with higher odds of elevated ALT, AST, and GGT in fully adjusted models (ORs: 1.56, 1.46, and 1.85; all $p < 0.001$), but not ALP. Hypertriglyceridemia showed the strongest associations with elevated ALT and GGT (ORs: 1.76 and 2.10; $p < 0.001$). Elevated LDL-C was consistently associated with higher odds of elevated ALT, AST, and GGT, while low HDL-C was independently associated

only with elevated ALT (OR = 1.17; p = 0.004). Overall dyslipidemia was strongly associated with elevated ALT and GGT, with limited evidence for associations with AST and no association with ALP. Conclusion: Dyslipidemia is independently associated with abnormal liver enzyme levels, particularly ALT and GGT, highlighting the close interplay between lipid metabolism and hepatic function.

Keywords: Dyslipidemia, Metabolic Disorder, Liver Enzyme

P187

The Role of Laboratory Markers in the Diagnosis of Cardiac Diseases

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Background: Rapid and accurate diagnosis of acute myocardial injury is essential for patients presenting with chest pain. Cardiac biomarkers, including creatine phosphokinase (CPK), its myocardial band (CK-MB), and troponin, are pivotal in the diagnostic process. This study evaluates the patterns of these markers in symptomatic patients and emphasizes the laboratory's contribution to clinical decision-making. Methods: A cross-sectional analysis was conducted involving 146 patients with cardiac symptoms (chest pain, dyspnea) over a three-month period. Serum levels of CPK, CK-MB, and troponin I were measured. Patients were categorized into six groups based on the results (normal/high for enzymes, positive/negative for troponin). Descriptive statistics were utilized to summarize the findings. Results: Among the 146 patients, 103 (70.5%) had all markers within normal limits. Elevated CPK with normal CK-MB and negative troponin, indicative of skeletal muscle injury, was observed in 13 patients (8.9%). Fourteen patients (9.6%) exhibited elevated CPK and CK-MB with negative troponin, suggesting extensive muscle damage. The classic pattern of acute myocardial infarction, characterized by elevated CPK, CK-MB, and positive troponin, was identified in 11 patients (7.5%). One patient (0.7%) had elevated CPK, normal CK-MB, but positive troponin, indicating minor myocardial injury. Additionally, four patients (2.7%) presented with positive troponin despite normal enzyme levels, suggesting very early or micro-infarction. Overall, 16 patients (11%) tested positive for troponin, confirming myocardial damage. Conclusion: Laboratory markers, particularly troponin, are crucial for diagnosing cardiac injury. Isolated elevations in enzyme levels without corresponding troponin positivity often reflect non-cardiac conditions, highlighting the necessity for a combined diagnostic approach. Quality assurance in laboratory testing is vital for timely and accurate diagnoses, preventing unnecessary admissions or missed infarctions. This study reinforces the central role of clinical laboratories in managing patients with suspected acute coronary syndrome.A total of 100 human serum samples were tested simultaneously using both methods according to the manufacturers' guidelines. The analysis showed a high overall concordance rate of 97%, with both tests producing consistent results for 97 samples. However, three discrepancies were observed: one

sample was positive with the rapid test but negative with the ELISA, while two samples were positive with the ELISA but negative with the rapid test.

Keywords: Cardiac Diseases, CPK, CK-MB, Troponin, Diagnosis

P188

The Role of Clinical Laboratory in Early Diagnosis of Acute Myocardial Infarction Based on High-Sensitivity Cardiac Biomarkers

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Background: Acute myocardial infarction (AMI) remains one of the leading causes of global mortality. Rapid and accurate diagnosis significantly reduces morbidity and mortality. The introduction of high-sensitivity cardiac troponin (hs-cTn) assays has revolutionized diagnostic algorithms. However, accurate interpretation requires understanding biomarker kinetics and differentiation between myocardial infarction and non-ischemic myocardial injury. Methods: This analytical review was conducted based on ESC and AHA guidelines (2023–2024) and indexed PubMed publications. The 0/1-hour and 0/3-hour hs-cTn algorithms, 99th percentile cut-offs, and absolute delta changes were evaluated. Additional biomarkers including CK-MB, myoglobin, H-FABP, copeptin, and BNP were also reviewed. Results: High-sensitivity troponin demonstrated superior diagnostic accuracy and high negative predictive value in early presentation. Absolute delta changes showed greater precision in diagnosing type 1 MI compared to relative changes. Other biomarkers provided adjunctive value, particularly in reinfarction and prognostic assessment. Conclusion: The clinical laboratory plays a central role in modern AMI diagnosis. Dynamic troponin measurement, strict quality control, and integrated clinical interpretation are essential for distinguishing infarction from non-ischemic myocardial injury. Implementation of standardized algorithms reduces unnecessary admissions and improves therapeutic decision-making.

Keywords: Acute Myocardial Infarction, High-Sensitivity Troponin, Cardiac Biomarkers, Laboratory Diagnosis, Myocardial Injury

Workshops
W1-W44

W1

Design and Monitoring of Quality Indicators in Medical Diagnostic Laboratories: A Practical Approch Based on ISO 15189:2022 And CLSI QMS12:2022

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Given the critical role of medical diagnostic laboratories in healthcare systems and the importance of ensuring the quality of laboratory services, the effective design and monitoring of quality indicators has become a fundamental requirement of quality management systems. This workshop aims to enhance the practical knowledge and skills of laboratory managers, technical supervisors, and professionals in the design, implementation, and monitoring of quality indicators, with a specific focus on the updated requirements of ISO 15189:2022 and CLSI QMS12:2022. The workshop begins with an overview of core quality management concepts and the role of quality indicators in continuous improvement of laboratory performance. Key updates and requirements related to quality indicators in ISO 15189:2022 are reviewed and aligned with the guidance provided in CLSI QMS12:2022. Participants will learn how to identify critical laboratory processes across the pre-analytical, analytical, and post-analytical phases and understand the principles for selecting appropriate quality indicators based on a risk-based approach, quality objectives, and stakeholder needs .The practical component of the workshop focuses on the design and definition of quality indicators, including the development of calculation formulas, identification of data sources, establishment of acceptance limits, and methods for monitoring and analyzing indicator data. In addition, the relationship between quality indicators, risk management, nonconformities, and corrective and preventive actions is explained in an applied and practical manner. Through real laboratory examples and hands-on exercises, participants will gain the competence to establish an effective quality indicator monitoring system and to use performance data for informed decision-making, continuous quality improvement, and enhanced readiness for laboratory accreditation and assessment processes.

Keywords: Quality Indicators, Quality Management, ISO 15189:2022, CLSI QMS12:2022, Quality Improvement, Risk Management, Nonconformities and Corrective Actions, Laboratory Accreditation

W2

Microbiome-Based Interventions in Health Quality Improvement: Practical and Clinical Approaches

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This workshop aims to enhance healthcare professionals' capacity to apply microbiome-related evidence in clinical decision-making and health quality improvement. Growing evidence highlights the role of the microbiome in the pathogenesis and management of chronic diseases, functional disorders, and quality-of-life outcomes. However, translating this evidence into practical clinical interventions remains challenging. The workshop addresses clinical assessment of microbiome dysbiosis, relevant diagnostic indicators, and the evidence-based role of microbiome testing. Practical interventions including targeted use of probiotics, prebiotics, synbiotics, structured dietary modifications, and antibiotic stewardship strategies aimed at preserving microbial diversity will be discussed. The practical component focuses on case-based analysis of selected clinical scenarios, including functional gastrointestinal disorders, metabolic syndrome, high-risk patients, and quality-of-life improvement. Through interactive discussions, participants will become familiar with practical decision-making algorithms for microbiome-oriented interventions.

Keywords: Microbiome, Health Quality, Probiotics, Clinical Interventions

W3

Smart Management of Patient and Physician Relationships Using CRM Software in Medical Laboratories

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In today's healthcare environment, the quality of medical laboratory services is no longer defined solely by accurate test results or advanced technology. Effective and intelligent relationship management with patients and referring physicians has become a critical component in enhancing satisfaction, trust, and long-term engagement. This workshop, titled “Smart Management of Patient and Physician Relationships Using CRM Software in Medical Laboratories”, aims to introduce modern managerial approaches and the practical use of digital tools—particularly Customer Relationship Management (CRM) systems—in the laboratory setting. Participants will be introduced to the core concepts of CRM, including its role in optimizing the communication cycle with patients and physicians, identifying needs and expectations, managing feedback and complaints, and improving the overall client experience. The workshop will also cover how CRM systems contribute to the integration of information, reduction of communication errors, faster response times, and more informed managerial decision-making. The practical segment of the workshop will demonstrate real-life applications of CRM tools in medical laboratories. Strategies for successful implementation tailored to various laboratory sizes, organizational structures, and legal requirements will be shared. Special attention will be given to data security, confidentiality, and compliance with medical ethics and quality standards. This workshop is designed for laboratory directors, technical supervisors, and medical laboratory professionals seeking to improve service delivery and strengthen stakeholder relationships. By adopting CRM-based smart management, laboratories can build a more patient- and physician-centered system that enhances competitiveness, efficiency, and quality of care.

Keywords: Customer Relationship Management (CRM), Patient Relationship Management, Referring Physician Engagement, CRM Software in Medical Laboratories, Digital Transformation in Laboratory Medicine, Laboratory Service Quality, Patient Experience and Satisfaction, Complaint and Feedback Management, Laboratory Information System (LIS) Integration, Data Security and Confidentiality, Data-Driven Decision Making, Key Performance Indicators (KPIs), Artificial Intelligence in Healthcare Management

W4

Costing of Laboratory Tests: Basis for Tariff Decision-Making

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In the dynamic and competitive environment of healthcare services, accurately determining the cost of laboratory tests is vital not only for setting fair tariffs but also for efficient resource management and strategic planning. The traditional approach of allocating overhead costs based on volume (such as the number of tests) often distorts cost calculations, as it overlooks the complexity and actual resource consumption of different activities. Activity-Based Costing (ABC) emerges as a precise solution to this challenge. This method works by identifying the key activities in the testing process (from reception and sampling, preparation, performing the test, quality control, to recording and reporting the result). It then allocates overhead costs (such as specialized human resources, equipment, consumables, depreciation, and energy) not based on simplistic assumptions, but according to each activity's actual consumption of these resources. Applying this method in medical laboratories provides a scientific and equitable basis for tariff determination. This approach helps managers more accurately identify high-cost and low-cost services, optimize processes, and ultimately, base financial decision-making and pricing on reliable, real-world data. Consequently, adopting the ABC method is a fundamental step toward financial transparency and enhanced productivity in the laboratory system.

Keywords: Activity-Based Costing (ABC), Laboratory Costing, Clinical Diagnostic Laboratory, Laboratory Cost Management, Laboratory Service Tariff Setting / Pricing, Laboratory Test Cost Calculation, Laboratory Productivity / Efficiency, Financial Transparency, Activity Centers, Cost Driver

W5

Optimization and Troubleshooting in Real-Time PCR

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Real-Time PCR is one of the most advanced and precise laboratory techniques for detecting and analyzing genetic patterns, with wide applications in life sciences, medicine, and veterinary science. Its high accuracy and sensitivity have made it a cornerstone in molecular research, disease diagnosis, and monitoring of medical treatments. However, due to its technical complexity and the need for strict laboratory control, troubleshooting and optimization of Real-Time PCR processes are essential. Issues such as improper primer design, sample preparation errors, incorrect instrument settings, and human mistakes can lead to inaccurate results, negatively affecting diagnostic reliability. This workshop will focus on strategies for optimizing protocols and troubleshooting common challenges in Real-Time PCR. Participants will learn scientific approaches to overcome frequent problems, including precise instrument calibration, proper selection of reagents and consumables, and accurate data interpretation. The goal of this workshop is to enhance participants' practical skills in applying Real-Time PCR effectively, ensuring reliable and reproducible results in both research and clinical diagnostics.

Keywords: Real-Time PCR, Troubleshooting, Optimization

W6

Artificial Intelligence in Embryology and Andrology: Applications, Methods, and Challenges

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Artificial intelligence (AI) is revolutionizing the assessment of male fertility by providing more accurate, efficient, and objective sperm analysis. Traditional methods of sperm analysis are subject to variability and are subject to individual variation. AI algorithms, especially those that are machine-based, are addressing these challenges in sperm analysis by analyzing large datasets for patterns and predictive results. Significant applications of AI in sperm analysis, including decision-making, motility, and sperm morphology, are reducing human error. AI-based image analysis techniques are demonstrating accurate diagnostic accuracy, which in turn can identify subtle abnormalities that may be missed in non-automated assessments. In short, AI is increasing the accessibility of sperm analysis. These advances are intended to improve the diagnosis and treatment of male infertility and lead to better outcomes. Also, traditional pre-implantation embryo evaluation in assisted reproductive technologies is highly dependent on the embryologist's opinion, but the use of artificial intelligence can non-invasively measure the quality of the embryo and identify possible abnormalities, thereby increasing the chances of pregnancy and the birth of a healthy child.

Keywords: Artificial Intelligence, Embryology, Andrology, Reproductive Medicine

W7

Antibody and Peptide Bioconjugation: Techniques and Biomedical Applications

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Bioconjugation is a fundamental technology in modern biotechnology that enables the controlled coupling of biomolecules such as antibodies, peptides, proteins, enzymes, drugs, fluorophores, polymers, and nanoparticles to create functional bioconjugates with enhanced biomedical applications. This workshop provides a comprehensive overview of the principles, strategies, and practical applications of antibody and peptide bioconjugation in diagnostics, therapeutics, and biomedical research. Participants will be introduced to the chemistry of bioconjugation, including zero-length, homobifunctional, and heterobifunctional crosslinkers, as well as the criteria for selecting appropriate conjugation methods based on the desired application. The workshop will cover the preparation and characterization of antibody–enzyme, antibody–fluorophore, antibody–drug, antibody–polymer, antibody–nanoparticle, and peptide–carrier conjugates, highlighting their roles in immunoassays, lateral flow assays, targeted drug delivery, antibody–drug conjugates (ADCs), molecular imaging, and nanomedicine.Recent advances in the field, including site-specific conjugation technologies, engineered conjugation sites, smart linker design, and emerging payloads for next-generation therapeutics, will also be discussed. Emphasis will be placed on improving conjugate stability, functionality, and clinical performance. This workshop is intended for graduate students, researchers, and professionals working in biotechnology, immunology, pharmaceutical sciences, molecular diagnostics, and related biomedical fields who seek a practical and up-to-date understanding of bioconjugation technologies and their expanding applications.

Keywords: Bioconjugation, Antibody, Peptide, Crosslinker, Conjugation, Antibody–Drug Conjugate (ADC), Nanoparticles, Diagnostic Kits, Immunoassays, Targeted Drug Delivery

W8

Microbiology Quality Control in the Laboratory Quality Management System Based on ISO 15189 and CLSI Standards

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This workshop aimed to teach the principles and standards of various methods for controlling microbial contamination in items such as antiseptic wipes, colored liquids, ultrasound devices, tubes, and dry environments. It emphasized the importance of microbiological control in consumable items used in medical and cosmetic procedures. Microbiological control is crucial because the presence of microbial contamination can lead to serious consequences. For example, failure to control contamination in colored liquids and warm gels may result in infections and complications for patients, along with delays in treatment and increased healthcare costs.

Keywords: Quality Control

W9

The Importance of Micronutrients in Health

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Mineral elements and micronutrients in the structure of metalloproteins and in free form in body fluids ensure the survival and maintenance of cell function. Therefore, the body has strong mechanisms to maintain their vital concentration. Despite profound advances in measurement technologies in medical diagnostic laboratories, the importance of measuring and monitoring the concentration of minerals, heavy and toxic metals, trace elements and micronutrients in the prevention of diseases, especially in specific patients, has not been given sufficient attention. Micronutrients such as magnesium, manganese, zinc and selenium are elements responsible for cell growth and division, blood pH regulation and antioxidant defense system. Calcium, with its vital roles such as participating in the processes of muscle contraction and cell movement, blood coagulation, transduction and bone mineralization, is considered one of the most vital elements in human life, along with phosphorus. From its presence in the structure of DNA and RNA to its buffering role inside the cell, phosphorus ensures human survival and growth. Meanwhile, heavy metal elements such as lead can disrupt the vital roles of vital elements and lead to clinical effects. Therefore, elucidating the role of the above-mentioned elements, the laboratory challenges related to measurement, interpretation of results and monitoring their levels in various diseases, is an undeniable necessity that requires discussion and dialogue among experts in the field of medical diagnostic laboratories.

Keywords: Micronutrient Deficiencies, Toxicity and Clinical Signs, Metallic Elements, Vitamins

W10

Management Requirements, Risk Strategy and Reports of Result

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This workshop provides a comprehensive exploration of the ISO 15189:2022 standard, the international benchmark for quality and competence in medical laboratories. The program begins with an in-depth analysis of Management Requirements, highlighting the evolution of leadership roles, organizational structure, and the framework for continuous quality improvement. A central pillar of the workshop is Risk Management, a critical focus of the 2022 revision. Participants will learn how to integrate risk-based thinking into laboratory workflows, focusing on identifying and mitigating potential hazards to ensure patient safety and clinical effectiveness. Furthermore, the session will examine the Impact of ISO 15189 on Laboratory Performance, demonstrating how compliance leads to enhanced diagnostic accuracy, operational efficiency, and strengthened stakeholder trust. To conclude, an Overview of Accreditation Requirements will be presented, offering a practical roadmap for laboratories seeking to navigate the formal accreditation process and achieve international recognition for their technical excellence. Overview on test report requirements Clause 7.4.1.2 of the ISO 15189 standard states: Results shall be reviewed and authorized for reporting before they are issued. The laboratory shall ensure that authorized personnel review the test results and evaluate them based on internal quality control and, where appropriate, with available clinical information and previous test results. Considering this issue, the final review and control of laboratory results is one of the most critical and important steps in the post-test process. This article aims to introduce a preventive and multi-stage quality control model that minimizes reporting errors by creating different layers of review and checks. Methodology and Methods: In this model, a multi-layered structure is designed in which each result undergoes successive and defined stages of control and checks by different levels of expertise and supervision before final approval. The central core of this model is the response check group. Findings: Implementation of this model over a 10-month period resulted in a significant reduction in potential clinically significant errors. The system also enhanced process transparency, decision traceability, and a culture of collective accountability in the laboratory. Conclusion: The proposed model goes beyond the minimum requirements of the standard, providing maximum protection against reporting errors through intelligent controls at various levels. This model is recommended as a suitable solution for laboratories committed to continuous quality improvement.

Keywords: ISO 15189:2022 Implementation, Risk-Based QMS, Patient-Centered Quality, Technical Competence, Reporting of results

W11

Quality Assurance and Technical Qualification

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This workshop explores the operational implementation of ISO 15189 requirements in microbiology. Key focus areas include the validation of conventional and molecular methods, stringent quality control of culture media, and equipment calibration. Participants will learn how to ensure technical competence and align complex diagnostic workflows with international standards to minimize laboratory errors.

Keywords: Validation & Verification, Traceability, ATCC, Reference Strains / ATCC Control, Culture Media Validation

W12

Operational Quality Control and Comparability of Results

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1-Internal Quality Control (IQC): Statistical quality control for quantitative measurement methods based on CLSI Statistical Quality Control (SQC) plays a fundamental role in ensuring the accuracy and reliability of laboratory test results. Its primary objective is the early detection of significant changes in the stable performance of measurement procedures—changes that, if not identified promptly, may lead to the reporting of erroneous patient results and inappropriate medical decision-making. Failure of a quality control system to detect out-of-control conditions with clinical consequences is directly associated with an increased risk to patient safety. The selection of measurement procedures in medical laboratories must be based on the alignment of their analytical performance with clinical requirements. In this context, Total Allowable Error (TEa) is widely used as a key indicator to define medical quality requirements, specifying the maximum permissible error that does not adversely affect clinical decision-making. To evaluate the stable performance of measurement procedures in terms of imprecision and bias relative to TEa, the Sigma Metric is commonly applied. Derived from the concept of process capability and the Six Sigma approach, this metric is expressed as a numerical value and demonstrates an inverse relationship with the probability of method failure. The application of the sigma metric facilitates the design of effective statistical quality control strategies and contributes to the reduction of laboratory errors with potential clinical consequences.
2-External Quality Assessment (EQA) & Comparability: Ensuring Accuracy This workshop is designed to inform accreditation assessors with a practical and harmonized understanding of ISO 15189:2022, Clause 7.3.7.3, focusing on the effective use of External Quality Assessment (EQA) and alternative approaches for monitoring the validity of examination results in medical laboratories. The workshop addresses the intent, requirements, and assessor expectations related to EQA participation, and the circumstances under which interlaboratory comparisons (small ILCs) other than EQA may be appropriately applied. Key topics include interpretation of Clause 7.3.7.3 within the risk-based framework of ISO 15189:2022, alignment with ILAC-P9:01/2024, and evaluation of laboratory EQA participation plans in relation to scope, examination methods, and clinical risk. Emphasis is placed on assessing the availability, appropriateness, frequency, and representativeness of EQA schemes, as well as the laboratory's justification and evidence when EQA is unavailable or unsuitable. The workshop also covers assessor approaches to reviewing performance outcomes, investigation of unsatisfactory results, implementation of corrective actions, and Verification that alternative methodologies adequately ensure result validity. Through case-based discussions and assessor-focused guidance, the workshop promotes

consistent, objective, and technically sound assessments, supporting harmonized accreditation decisions and reinforcing confidence in the competence of medical laboratories operating under ISO 15189:2022.

Keywords: Statistical Quality Control, Westgard Rules, Proficiency Testing, Metrological Traceability, Comparability of Result

W13

Necessary Steps in the Laboratory to Obtain ISO 15189

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Steps that must be taken in the laboratory to apply for ISO certification

Keywords: Certification

W14

From KPIs to Decisions: Measuring and Tracking Laboratory Growth

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This workshop is designed to teach the design and application of Key Performance Indicators (KPIs) in laboratory settings. Participants will learn the concept of KPIs and their difference from operational metrics, and how to align and design indicators based on organizational strategic objectives. The course covers methods for defining and analyzing performance indicators across areas such as organizational growth, sales and market development, human resource productivity, cost control, process performance, and patient/customer satisfaction. It also introduces principles of goal setting, benchmarking, trend monitoring, and performance deviation analysis. A key part of the workshop focuses on designing management dashboards and using performance data for better decision-making. Participants will learn how to apply a data-driven approach to analyze current performance and improve organizational processes. In conclusion, the workshop helps managers and specialists use KPIs to effectively monitor the laboratory's growth path and make more informed decisions to enhance performance and achieve organizational goals.

Keywords: Process Control, Growth Path, Laboratory Business Growth, Managerial Decision-Making, Key Performance Indicators (KPIs), Performance Monitoring, Data-Driven Approach

W15

From Challenges to Growth: Developing a Laboratory Development Plan

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A laboratory owner-manager, while being responsible for compliance with quality and regulatory requirements, must also think like a business leader and plan strategically for the future of their laboratory. In today's rapidly changing environment, economic pressures, technological advances, and evolving market expectations compel managers to consciously design paths for growth, resilience, and sustainability—going beyond day-to-day operations. This process requires the right mindset and practical decision-making tools. In this workshop, participants will become familiar with managerial thinking approaches and a set of practical tools tailored to the real conditions of medical laboratories in Iran. Topics such as strategic thinking, growth mindset, environmental analysis, data-driven decision-making, and viewing quality as a value-creating factor will be explored. The workshop will also address how to link quality requirements with development objectives, manage risks, and enhance resilience under conditions of uncertainty. Within this framework, the concept of strategic transformation is introduced as a gradual and manageable process, helping managers implement necessary changes without causing organizational shocks, while aligning with the laboratory's capacity and resources. Finally, the laboratory business model will be examined so that participants can understand the relationship between revenue, costs, and development, enabling them to design a realistic, actionable, and contextually appropriate plan for sustainable growth in their laboratories.

Keywords: Strategic Thinking, Growth Mindset, Laboratory Management, Quality & Compliance, Strategic Transformation, Resilience, Business Model

W16

Interference of Abnormal Hemoglobins in HbA1c Measurement

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HbA1c measurement is considered a gold standard for monitoring long-term glycemic control in diabetic patients and plays a critical role in clinical decision-making. However, the presence of abnormal hemoglobins and hemoglobin variants may interfere with HbA1c measurement, leading to inaccurate results and potential misinterpretation. This workshop provides an overview of hemoglobin structure and common abnormal hemoglobin variants such as HbS, HbC, HbE, HbD, and thalassemias. The mechanisms of interference caused by these variants in commonly used HbA1c measurement methods, including HPLC, immunoassays, enzymatic methods, and capillary electrophoresis, will be discussed. The session highlights differences in susceptibility of various analytical methods to hemoglobin variants and emphasizes the importance of selecting appropriate methodologies based on patient population characteristics. Strategies for identifying suspicious HbA1c results, interpretation challenges, and the use of alternative glycemic markers such as fructosamine and glycated albumin will also be reviewed. The aim of this workshop is to enhance the knowledge of laboratory professionals and clinicians to minimize analytical errors and improve the accuracy of glycemic assessment in patients with abnormal hemoglobins.

Keywords: HbA1c, Abnormal Hemoglobin, Analytical Interference, HPLC, Diabetes

W17

Clinical Importance of Accurate Low Level Measurement of Hormones and Critical Biomarkers

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Accurate measurement of low analyte concentrations represents one of the most critical challenges in modern clinical laboratory medicine, particularly when clinical decision making occurs near the analytical limits of detection and quantification. Several hormones, including thyroid stimulating hormone (TSH), estradiol, testosterone (AMH) Anti Mullerian Hormone, adrenocorticotropic hormone (ACTH), cortisol, parathyroid hormone (PTH), and beta human chorionic gonadotropin (β hCG), have clinical decision thresholds located at very low concentration ranges. Inadequate analytical sensitivity in these assays may result in misclassification of disease status, inappropriate treatment decisions, or delayed diagnosis. Beyond classical hormones, a group of non hormonal but clinically critical biomarkers—such as high sensitivity cardiac troponins (hs cTn), N terminal pro B type natriuretic peptide (NT proBNP), D dimer, procalcitonin (PCT), and high sensitivity C reactive protein (hs CRP)—play a pivotal role in rule out and early diagnostic strategies. Although these analytes are not hormones by biological definition, their clinical interpretation is strongly dependent on reliable measurement at very low concentrations, often near the limit of quantification. From an analytical perspective, both hormonal and non hormonal biomarkers share a common framework: dependence on clearly defined limits of blank (LoB), limits of detection (LoD), limits of quantification (LoQ), and acceptable precision at low concentration ranges, as outlined in CLSI EP17 and related guidelines. This workshop focuses on the analytical and clinical implications of low level measurements, integrates regulatory expectations for in vitro diagnostic (IVD) assays, and provides practical guidance for laboratories to ensure reliable interpretation of low concentration results in real world clinical practice.

Keywords: Analytical Sensitivity, LOD, LOQ, Hormones, Cardiac Biomarkers, EP17

W18

Design and Implementation of a Performance-Based Incentive Payment System in Medical Laboratories: A Framework for Quality Improvement, Productivity, and Organizational Equity

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This workshop aims to present the principles, structures, and practical methods for designing and implementing incentive-based payment systems in medical laboratories. As laboratories face challenges such as limited financial resources, the need to maintain staff motivation, variations in workload across sections, quality requirements, and the demand for transparent compensation, establishing a fair and measurable incentive model has become increasingly important. Participants will learn the core principles of performance-based incentive design, including the definition of quantitative and qualitative indicators, weighting of specialized laboratory activities, differentiation among job roles, and incorporation of variables such as educational level, work experience, shift type, on-call duties, quality performance, productivity, interdepartmental collaboration, and professional compliance. Practical examples of executable formulas and calculation frameworks adaptable to real laboratory settings will also be presented. A key part of the workshop will focus on implementation challenges, common design errors, conflict-reduction strategies, and methods for aligning incentive systems with laboratory quality improvement, patient safety, and service development goals. This workshop provides a practical managerial framework for laboratory directors, technical supervisors, section heads, and professionals interested in laboratory performance management and healthcare economics.

Keywords: Incentive Payment, Performance-Based Compensation, Medical Laboratory, Productivity, Quality of Services, Performance Evaluation, Human Resource Management, Laboratory Economics

W19

Sample Collection and Management in Fungal Diseases: From Bedside to Lab

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Proper sample collection and management play a crucial role in the rapid and accurate diagnosis of fungal diseases. This three-facilitator interactive workshop introduces participants to types of clinical samples, proper collection, transport, and laboratory preparation methods. The role of the laboratory in processing samples and effective collaboration with clinical teams for improved diagnostic quality is emphasized. Real clinical scenarios and laboratory samples are interactively reviewed, allowing participants to become familiar with practical sample handling procedures.

Keywords: Common Fungal Diseases, Timely Diagnosis, Clinical-Laboratory Collaboration, Interactive Workshop

W20

PGTA and ERT in Practice: A Comprehensive Workshop on Personalized IVF

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Preimplantation genetic testing for aneuploidy (PGT-A) and endometrial receptivity testing (ERT) are integral components of personalized medicine in assisted reproductive technology, designed to optimize embryo selection and embryo–endometrium synchronization. PGT-A is performed through comprehensive chromosomal analysis of trophectoderm biopsies obtained from blastocyst-stage embryos, most commonly using next-generation sequencing. By identifying euploid embryos for transfer, PGT-A supports efficient embryo prioritization, enhances implantation potential, and contributes to improved reproductive outcomes across a range of clinical indications. ERT focuses on the molecular assessment of endometrial receptivity through the evaluation of gene expression profiles associated with the window of implantation. This approach enables individualized determination of endometrial readiness in natural or hormone replacement cycles, allowing personalized timing of embryo transfer. Accurate alignment of embryo development with endometrial receptivity is a key factor in achieving successful implantation. This workshop will present the biological foundations, laboratory methodologies, and clinical application of PGT-A and ERT within contemporary IVF practice. Participants will gain practical insight into test workflows, result interpretation, and integration into clinical decision-making. Emphasis will be placed on the complementary use of embryonic genetic assessment and endometrial evaluation to address both major determinants of implantation success. By combining PGT-A and ERT, clinicians can implement a structured, individualized approach to fertility treatment. This workshop aims to provide reproductive specialists, embryologists, and laboratory professionals with actionable knowledge to support precision-based reproductive care.

Keywords: PGTA, ERT, Personalized IVF

W21

WHONET Software

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WHONET is a free software developed by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance for laboratory-based surveillance of infectious diseases and antimicrobial resistance. The principal goals of the software are: to enhance local use of laboratory data; and to promote national and international collaboration through the exchange of data. WHONET can be used by individual laboratories or as part of a national and international surveillance network.

Keywords: WHONET Software, Antimicrobial Susceptibility Testing, Bacteria

W22

Calibration in Automated Laboratory Systems (Immunochemistry): Interpretation, Correction and Enhancing Quality Control Performance

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Precise calibration of automated laboratory instruments remains one of the most critical challenges and determining factors in achieving reliable and clinically valuable results. In this program, laboratory technician will understand the scientific and practical principles of calibration, the standardized execution of steps, optimal use of calibrator materials, and adherence to manufacturer guidelines and international standards. Special emphasis is placed on interpreting results, identifying errors, and tracing sources of instrument malfunction to maximize the accuracy, stability, and repeatability of tests. This workshop will address correcting results, preventing common errors, and improving calibration quality. Participants will learn how to integrate calibration processes within a comprehensive quality assurance framework. Using real-world examples, problem-solving, and sample data analysis, the ability to make evidence-based decisions and enhance instrument performance will be strengthened. Upon completion of the workshop, participants will be able to confidently perform calibration of automated instruments, identify and correct deviations, and, by applying scientific and practical strategies, elevate the quality and accuracy of laboratory results to a higher level. This workshop is designed for laboratory technicians, supervisors, quality control officers, and lab technical directors.

Keywords: Calibration, Calibrator, Automated Instruments, Troubleshooting, Quality Assurance

W23

Foundations and Practical Principles of the Immunofluorescence Assay (IFA) Method in the Identification and Detection of Autoantibodies in Modern Medical Diagnostic Tests

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Indirect immunofluorescence assay (IFA) remains one of the most sensitive and, at the same time, one of the most challenging diagnostic methodologies in medical laboratories. The quality of its diagnostic output depends more than that of many other assays on technical proficiency, analytical judgment, and standardized interpretation. This workshop has been designed with a critical, experience-based approach to move beyond conventional instructional formats and to focus on the factors that directly determine diagnostic quality. Within this educational program, participants will be introduced to underlying but decisive elements affecting IFA performance—elements that are frequently overlooked in routine laboratory practice and that contribute to result variability, non-reproducible reporting, and reduced diagnostic reliability. The workshop content includes in-depth analysis of pre-analytical and analytical phases, management of technical errors, informed selection of kit based on type of substrate, and interpretation of immunofluorescence patterns in specialized clinical applications, including autoimmune, gastrointestinal, rheumatologic, and neurological testing. Special emphasis is placed on the standardization of pattern interpretation in accordance with internationally recognized frameworks, particularly the International Consensus on ANA Patterns (ICAP). In addition, concepts related to quality assurance, assay validation, inter-laboratory harmonization, and systematic documentation are addressed in a practical and application-oriented manner. At the conclusion of the workshop, participants will have developed a structured and evidence-based perspective on the appropriate execution and clinically reliable interpretation of IFA, as well as an enhanced understanding of the role of this methodology in improving diagnostic quality and laboratory performance. The workshop is specifically intended for professionals seeking substantive quality improvement rather than repetition of routine laboratory practices.

Keywords: Immunofluorescence Assay, Troubleshooting

W24
Cell Counter QC Materials; Chalenges and Solutions

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1- An overview of Sigma Metrics–based quality control, 2- Challenges in the selection of allowable total error in the hematology department, 3- The effect of environmental factors on Cell counter QC material , 4- Correct procedures for handling Cell counter QC material to achieve an optimal CV, 5- Technical challenges of hematology analyzers and their effect on Cell counter QC material, 6- The Effect of hematology analyzer reagents on Cell counter QC material, 7- Identification of factors affecting each hematology index based on cell counter results and graphs

Keywords: Cell Counter QC Material, Hematology Auto Analyzer, Quantitative Quality Control, Challenges and Solutions

W25

Evidence-Based Hematology: The Laboratory Role in Clinical Decision-Making

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Hematology, as one of the dynamic fields of medicine, is continuously confronted with a growing body of new evidence. The appropriate application of this evidence in clinical decision-making requires a systematic and evidence-based approach. This workshop is designed to familiarize participants with the principles and practical applications of Evidence-Based Medicine in hematology. Practical examples of common challenges in the diagnosis and management of hematologic disorders, including coagulation disorders, anemias, and hematologic malignancies, will also be discussed. The workshop will be conducted in an interactive, case-based format and aims to enhance participants' practical skills in applying scientific evidence in the clinical setting. It is expected that, by the end of the workshop, participants will have improved abilities in critically appraising evidence, making informed clinical decisions, and continuously updating their clinical knowledge in the field of evidence-based hematology.

Keywords: Clinical Laboratory, Common Hematological Diseases, Patient Management, Interpretation of Laboratory Results

W26

Standardization and Quality Assurance Challenges in the Coagulation Laboratory: 2025 Updates and Best Practices

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This practical workshop emphasizes the latest advancements in coagulation testing standardization. Participants will explore key 2024–2025 updates, The program covers core principles of quality control (QC) and quality assurance (QA) in coagulation laboratories, their practical implementation in Iranian settings, and addresses local challenges (e.g., preanalytical errors, reagent lot variability, DOAC/new therapy interferences, and resource limitations). Interactive case discussions, real-world problem-solving, and expert insights ensure actionable takeaways for daily lab practice.

Keywords: Coagulation Standardization, QC/QA, CLSI 2025, Local Challenges

W27

Coagulopathies: From Diagnosis to Interpretation and Commenting

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This practical-educational workshop focuses on achieving hands-on mastery in the coagulation laboratory and specifically addresses the technical challenges in the diagnosis and follow-up of von Willebrand disease (vWD). Participants will become familiar with the key fundamentals of coagulation tests, common technical pitfalls and traps in vWD-related assays, and optimal troubleshooting strategies. The program includes interactive real case discussions, analysis of laboratory results, and expert opinion exchange to facilitate more accurate diagnosis of bleeding disorders — especially vWD — in the Iranian laboratory setting. Additionally, interpretive commenting (Interpretative Commenting) in coagulopathies will also be discussed in the later part of the workshop.

Keywords: Von Willebrand Disease, Technical Challenges, Coagulation Testing, Interpretative Commenting

W28
Preliminary and Advanced Quality Control

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Today, the accuracy and precision of laboratory results and its quality control have become one of the important and strategic dimensions in laboratory management, and obtaining ISO-15189 is considered one of the practical goals in the globalization of a laboratory. Unfortunately, academic courses and university syllabi have not been able to meet the needs of laboratories, and given the lack of a precise and relevant field of study, the expansion of quality control and sigmametric sciences, the introduction of advanced software, national and international requirements and laws and guidelines, and different personal interpretations of some quality control laws, it became necessary to provide a comprehensive workshop to educate and communicate new changes and present the main concepts of quality control and its surrounding sciences in order to create a suitable opportunity for the organizational growth of the quality control department in laboratories. In this regard, the above workshop will be designed and presented at two levels: introductory and advanced.

Keywords: Quality control, Sigmametric, ISO-15189, Accuracy, Precision

W29

Statistical Quality Control Using the Sigma Metric Approach

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The purpose of the statistical quality control program is to determine scientific indicators and monitor them to improve the quality of laboratory results, which ensures the use of new sigma metric methods instead of traditional methods and provides laboratories and physicians with improved quality of output results using modern methods. Quality assurance is intended to create trust among laboratory staff, patients, and physicians in laboratory results and, as a result, increase confidence in laboratory achievements. Scientific criteria include the closeness of the results and the closeness of the results to the actual value: Accuracy / imprecision, Accuracy / inaccuracy, Accuracy or realism of the results. Practical criteria include issues that must be observed in setting up and performing each test: Speed, Price, Required specialist personnel, Required devices, Safety. No matter how appropriate the practical criteria are, if the scientific criteria are not acceptable, the answers obtained from the method used will not be reliable.

Keywords: Sigma Metric, Precision, Accuracy

W30

How to Manage Patients Suspected to Human Papilloma Virus (HPV) Infection in the Molecular Laboratories? Sampling Principles

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Proper genitourinary sampling for HPV diagnosis is of paramount importance. Besides of females, HPV identification in male has been considered in recent medical services worldwide. One of great challenges is suboptimal sampling especially from men which results in falsenegative reporting due to inadequate cell yielding. The aim of this workshop is to deliver to the audiences the key determiants of proper sampling, how to do the sampling, how difficult it is, and how can mitigate those problems.

Keywords: HPV, Stigma, Cervical Cancer, Genital Wart

W31

Oncogenic Viruses in Iran: A Practical Approach to Screening Program Management and Specimen Collection

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Oncogenic viruses contribute significantly to the global cancer burden. Accurate knowledge of their transmission, pathogenesis, prevention, screening, and diagnosis is essential for improving the quality of laboratory services and health care. This workshop focuses on the clinically and epidemiologically significant oncoviruses in Iran, centering primarily on Human Papillomavirus (HPV) and its role in cervical and other related malignancies. The session will review the molecular basis of viral carcinogenesis and the epidemiological status of oncoviruses. We will discuss primary and secondary prevention strategies, the role of vaccination, risk-based screening program design and management, selection of appropriate assays, and algorithms for managing abnormal results. The practical segment of the workshop is dedicated to pre-analytical standards, including the selection of proper specimen types, correct collection techniques, labelling, transport, storage, sample acceptance/rejection criteria, contamination prevention, and quality control. Furthermore, a targeted overview will cover the Hepatitis B and C viruses, Epstein-Barr Virus, HTLV-1, and HHV-8/KSHV, as well as their associations with malignancies. Participants will gain insight into the implementation challenges of screening and diagnosis in Iran, responsible interpretation of laboratory results, and the critical role of effective communication between the laboratory, clinicians, and the health surveillance system.

Keywords: Oncogenic Viruses, HPV, Viral Carcinogenesis, Cervical Cancer, Cancer Screening, Vaccination, Molecular Diagnostics, Laboratory Quality Control, Pre-Analytical Standards, HBV/HCV, EBV, HTLV-1, HHV-8/KSHV, Health Surveillance

W32

Reawakening Ancient Viruses: The Role of HERVs in Carcinogenesis

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Human endogenous retroviruses (HERVs), which constitute approximately 8% of the human genome, are relics of ancient retroviral infections in germline cells and play a dichotomous role in oncogenesis. On one hand, they contribute to tumor progression through mechanisms such as insertional mutagenesis, chromosomal rearrangements, and functioning as promoters or enhancers for oncogenes. For instance, HERV-K envelope proteins have been demonstrated to induce Ras/ERK signaling pathways, thereby stimulating and strengthening the epithelial–mesenchymal transition (EMT) process, which consequently enhances metastatic potential, particularly in breast carcinogenesis. On the other hand, the transcriptional reactivation of HERVs can stimulate a potent antitumor immune response. This occurs primarily via viral mimicry mechanisms, wherein HERV-derived double-stranded RNA (dsRNA) intermediates are sensed by pattern recognition receptors such as RIG-I and MDA-5, triggering a robust type I interferon response. Furthermore, the translation of HERV open reading frames (ORFs) generates tumor-specific antigens (TSAs) that can be presented on MHC class I molecules, effectively priming cytotoxic T lymphocytes (CTLs) to recognize and eliminate malignant cells. Given the preferential expression of various HERV types in a range of solid tumors—including hepatocellular carcinoma (liver), gastric, lung, breast, ovarian, and renal carcinomas—HERVs have emerged as promising diagnostic biomarkers and therapeutic targets. However, a fundamental paradox remains: it is still unclear whether HERV reactivation is the primary driver of malignant transformation or merely an epigenetic bystander effect resulting from global DNA hypomethylation and histone acetylation changes that accompany tumorigenesis.

Keywords: HERVome, HERV, Transcriptional Reactivation, Tumorigenesis, HERVome

W33

Body Microbiome and Their Impact on Health and Disease

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Body micro biome composes of billion-billions of germs - bacteria, viruses, fungi, parasite, which distributed in skin, mucosal surface & gut, urinary system, respiratory system etc. The primary function of these microbiome is to combact with virulent microbes which provide a wide range of infections. For example: when gut microbiome is distrupted dysbiosis occur, and many vitamins, essential amino acids can't absorbed and impairment of immune system, neural system. And even psychiatric illness are implemented. Skin microbiom, potentially inhibit the colonization of virulent microbes.
But when the skin is injured some of these microflora introdust subcutanous and implement many local and systemic disease. Staphylococcus aureus, which is resistant to methicillin (oxacillin) vancomycin are a real threat for world health. Vaginal microbiome such as Lactobacillus and some streptococci help the GU tract from invasion of harmful organism. So integrity of immune system is profoundly related to these microbiome's. Staphylococcus aureus although may be regarded as microbial flora of skin but its antibacterial resistance to oxacillin, methicillin, vancomycin, can produce a wide array of patuogenic (virulent factors) that make a great challenge to world health. The world health organization claims that during 2030-2050 about 10 millions.

Keywords: Microbiome

W34

NGS-Based Diagnostic Genomics in Liquid Biopsy

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In this specialized workshop, the importance and application of Next-Generation Sequencing (NGS) in the analysis of liquid biopsy samples, as well as its role in the intelligent molecular diagnosis of diseases, particularly various types of cancer, will be explored. Liquid biopsy, as a novel and minimally invasive approach for disease diagnosis and monitoring, provides access to valuable molecular information through biological samples and, in recent years, has gained a prominent position in precision medicine, diagnostic genomics, and the development of intelligent molecular diagnostic strategies. In this workshop, participants will become familiar with the fundamental principles of liquid biopsy, the different types of applicable samples, its clinical applications in disease diagnosis, and the capabilities of NGS in identifying genetic and molecular alterations. In addition, the overall workflow of this process, from sample collection and preparation to sequencing, data processing, bioinformatic analysis, and interpretation of results, will be discussed in order to provide a comprehensive understanding of the role of this technology in achieving intelligent molecular diagnosis. The aim of this workshop is to provide participants with a comprehensive understanding of the pathway through which a liquid biopsy sample is transformed into interpretable genomic data that can be applied in clinical diagnosis. This program can offer a valuable opportunity for students, researchers, and professionals in the fields of genetics, genomics, biotechnology, bioinformatics, and laboratory sciences to become acquainted with one of the most important modern approaches in intelligent molecular diagnosis and personalized medicine.

Keywords: Liquid Biopsy, Next-Generation Sequencing, NGS, Diagnostic Genomics, Intelligent Molecular, Diagnosis, Cancer, Bioinformatics, Precision, Medicine, Genomic Analysis, Molecular Diagnosis

W35

The Myers-Briggs Type Indicator (MBTI) and Its Application in Managing Communication with Medical Laboratory Stakeholders Based on Clauses 5, 6, and 8 of ISO 15189:2022

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Establishing effective communication with internal and external stakeholders of medical laboratories and continuously improving such communication are among the fundamental factors for successful, sustainable, and patient-centered laboratory management. Recognizing individualistic differences, communication preferences, and interaction styles can serve as a supportive approach to enhancing the quality of organizational and professional relationships. The Myers-Briggs Type Indicator (MBTI) provides a framework for understanding differences in communication styles by focusing on individualistic preferences across four main dichotomy dimensions, including Extraversion–Introversion, Sensing–Intuition, Thinking–Feeling, and Judging–Perceiving. According to the framework individuals can be described through sixteen personality types and four broader patterns proposed by David Keirsey as Guardian, Artisan, Idealist, and Rational temperaments. The conscious application of MBTI can support laboratory managers and staff in strengthening leadership, developing a quality culture, enhancing personnel competence, improving teamwork, supporting continual improvement, managing risks, and enhancing stakeholder experience. These concepts are aligned with the requirements of Clauses 5, 6, and 8 of ISO 15189:2022. As for internal stakeholders (laboratory personnel), understanding individual differences may contribute to improved organizational communication, appropriate assignment of responsibilities, facilitation of change management and innovation, reduction of workplace conflicts. Additionally, it can contribute to designed training programs based on learning preferences, enhancement of teamwork effectiveness, and development of leadership skills. External stakeholders includes referring physicians and patients. As for the first, understanding communication preferences may contribute to more effective presentation of laboratory results, laboratory consultation, efficient responses to scientific inquiries, introducing new laboratory services, management of scientific disagreements, and improvement of physicians' satisfaction and trust. As for the second, considering differences in communication preferences may improve patient education, reduce anxiety, enhance responses to questions and concerns, support complaint management, increase trust, and improve patients' overall experience with laboratory services. In conclusion, MBTI should not be used as an instrument for judging, selecting, or categorizing individuals. Rather, it can be considered as a supportive instrument for developing communication skills, leadership capabilities, and human relationship management within medical laboratories.

Keywords: ISO 15189:2022; Medical Laboratory Accreditation; Myers-Briggs Type Indicator (MBTI); Medical Laboratory Management; Stakeholder Communication Management; Effective Communication; Quality Culture

W36

Laboratory Approaches to the Diagnosis of Bleeding Disorders, Inhibitor Testing, Molecular Quality Assurance, and Prenatal Diagnosis of Hemophilia

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Von Willebrand disease (VWD), first described over 100 years ago, remains the most common inherited bleeding disorder and continues to present significant diagnostic challenges. Although major advances have been made in understanding von Willebrand factor (VWF) biology, accurate diagnosis is still complicated by phenotypic variability, assay limitations, and overlap with other mild bleeding disorders. Over the past century, VWD diagnosis has evolved from clinical recognition based on bleeding symptoms to a combined clinical–laboratory approach incorporating VWF antigen, functional assays, factor VIII levels, and multimer analysis. More recently, genetic testing and next-generation sequencing have improved subtype classification and provided new insights into disease heterogeneity, particularly in type 2 variants. However, interpretation of borderline laboratory results and the clinical significance of many VWF variants remain ongoing challenges. This centenary presentation highlights the progress in VWD diagnostics and emphasizes the importance of integrating bleeding assessment tools with advanced laboratory and genetic methods. Future approaches combining quantitative phenotyping, molecular diagnostics, and population genomic data are expected to refine diagnostic accuracy and support more personalized management of patients with VWD.

Keywords: Von Willebrand Factor, Molecular Diagnosis, Genetics, Inherited Bleeding Disorders

W37

Comprehensive Reference for Laboratory Monitoring of Athletes in Various Conditions (Physiological and Clinical Health, During Intense Training, etc.)

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The systematic assessment, monitoring, and interpretation of laboratory test results alongside athletes' biometric data, both prior to the initiation of training and throughout the training process, provide valuable insights into the body's physiological responses to exercise and nutrition. Such evaluations enable athletes, coaches, and sports medicine professionals to better understand individual adaptations to training, thereby minimizing interruptions caused by illness, sports-related injuries, and overtraining. Through the analysis of key biological markers associated with energy metabolism, recovery, immune function, and hormonal balance, sports medicine laboratories offer comprehensive biomarker panels specifically designed for athletes. These assessments provide evidence-based support in several critical areas, including:
Genetic Testing and Athletic Talent Identification. Genetic testing can assist novice athletes in selecting the most appropriate sport, determining their optimal playing position or athletic role, and tailoring individualized training programs according to their genetic predisposition, metabolic profile, and physiological characteristics. Maximizing Recovery. Laboratory evaluation of recovery-related biomarkers can determine whether the body is adequately recovering following physical exertion. Insufficient recovery may indicate excessive training loads, which can lead to chronic inflammation, physiological stress, reduced athletic performance, fatigue, and overtraining syndrome. Enhancing Athletic Performance Performance-related biomarkers are analyzed to identify physiological limitations and opportunities for improvement, enabling athletes to achieve their maximum performance potential. Monitoring hormones, stress biomarkers, vitamins, and other biochemical indicators provides valuable information regarding the body's current physiological status and helps athletes overcome performance plateaus. Optimizing Nutritional Status Nutrition is often a decisive factor distinguishing championship-level performance from competitive failure. Specialized laboratory testing can identify individual deficiencies in vitamins, minerals, and other essential nutrients. Interpretation of these findings facilitates the development of personalized nutritional strategies aimed at optimizing metabolism, improving physiological function, and maximizing athletic performance.
Maintaining Hormonal Balance Hormones play a fundamental role in regulating physiological function and athletic performance. Laboratory testing can identify clinically significant hormonal imbalances that adversely affect energy production, muscular strength, recovery, and overall performance, including conditions such as testosterone deficiency. Biomarker analysis enables athletes to maintain optimal hormonal homeostasis during periods of intensive training. Monitoring Athletic Progress Serial

laboratory assessments allow athletes and coaches to objectively monitor key health and performance indicators over time. Longitudinal evaluation of these biomarkers provides scientific evidence regarding the effectiveness of modifications in training programs, nutritional interventions, and recovery strategies.
Injury Prevention Laboratory investigations can detect early signs of inflammation, physiological stress, or nutritional deficiencies before clinical symptoms or injuries become apparent. Early identification of these risk factors enables timely intervention, reducing injury risk and helping athletes maintain consistent progress toward their performance goals.

Keywords: Athlete Monitoring, Biomarkers, Genetic Testing, Athletic Performance, Recovery, Nutrition, Hormonal Balance, Overtraining, Injury Prevention

W38

Implementing Intelligent Quality Monitoring System: The Experience of "Peer Group" Program in Iranian Clinical Laboratories

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This workshop explores the transition from traditional QC to intelligent continuous monitoring systems (Peer Group). Topics include bias and CV analysis within peer groups, systematic error identification, and strategies to reduce measurement uncertainty in biochemistry and hematology. The goal is to achieve a common numerical language among laboratories and enhance patient safety

Keywords: Quality Monitoring, Peer Group, Uncertainty, Biochemistry, Hematology

W39

Uncertainty of Quantitative Results Based on ISO 20914

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All the measurements, including the quantitative results in medical laboratories, are subject to uncertainty. Therefore, it's important to be familiar with the concept of uncertainty; the resources of uncertainty; and the mathematical calculations to estimate measurement uncertainty in medical laboratory .The ISO 20914 document provides practical guidance for the estimation and expression of the measurement uncertainty of quantitative measurand values produced by medical laboratories. In this workshop, the participants will learn how to apply ISO 20914 document in their practice. Over the presentation, the theoretical concepts will be discussed; and several real world examples will be exercised.

Keywords: Measurement Uncertainty, ISO 20914, Medical Laboratory, Quantitative Analysis, Uncertainty Estimation

W40

Interpretation of Flow Cytometry Graphs Along with the Analysis of Some Cases of Hematological Disorders

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The flow cytometer works by focusing the suspension into stream of individual cells which pass through a series of lasers to excite the fluorescent dyes. Healthcare providers commonly use it to evaluate bone marrow, peripheral blood and other fluids in your body. Flow cytometry is a modality with ever increasing application in modern hematological practice. This is due to the rapidity of obtaining results, ease of use and increasing power to detect abnormal populations of cells. Flowcytometric immunophenotyping remains an indispensable tool for the diagnosis, classification, staging, and monitoring of hematologic neoplasms. The last 10 years have seen advances in flow cytometry instrumentation and availability of an expanded range of antibodies and fluorochromes that have improved our ability to identify different normal cell populations and recognize phenotypic aberrancies, even when present in a small proportion of the cells analyzed. Phenotypically abnormal populations have been documented in many hematologic neoplasms, including lymphoma, chronic lymphoid leukemias, plasma cell neoplasms, acute leukemia, paroxysmal nocturnal hemoglobinuria, mast cell disease, myelodysplastic syndromes, and myeloproliferative disorders. Developments in instrumentation and reagents have increased the sensitivity of detection and flow cytometry is now used to monitor patients after treatment where very low levels of residual disease may be present. This allows more precise delivery of therapy and prediction of the outcome of treatment. The most important factor that can limit the use of flow cytometry is the quality of the sample, so placing samples in the correct bottles and timely transportation to the laboratory is crucial.

Keywords: Flowcytometry, Hematology, Leukemia, Lymphoma, Malignancy

W41

Air Pollution and Human Health: Intra- and Extracellular Changes and Their Effects on Laboratory Tests

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Air pollution has a complete impact on the health of residents of all ages and may cause respiratory and inflammatory diseases. In addition, air pollution can also cause the genetic alterations through the cellular and molecular changes in the human cells and effects on extracellular vesiclues, contribute to the development of various types of cancer and dead .Understanding of this silent changes and their laboratory findings is a major step toward preventing dangerous diseases.

Keywords: Air Pollution, Clinical Trials, Inflammation, Heavy Metal Elements, Immune System

W42

Dealing with Diabetic Ketoacidosis

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Diabetic ketoacidosis is a serious and life-threatening complication of diabetes. Diabetic ketoacidosis is a complex metabolic condition characterized by hyperglycemia, ketoacidosis, and ketosis. Metabolic acidosis is the most common finding in DKA, and patients' glucose levels are usually between 250 and 500 mg/dL. Diabetic ketoacidosis occurs primarily in patients with type 1 diabetes, but it can also be seen in patients with type 2 diabetes. Despite advances in self-care for diabetic patients, DKA accounts for approximately 50% of hospitalizations in young diabetic patients. The exact incidence of DKA is unknown, but it is estimated to be about 1 in 2000 diabetic patients. Conclusion: DKA is a medical emergency that can be life-saving and reduce the risk of mortality with timely diagnosis and comprehensive treatment goals. Paying attention to the patient's history, clinical signs, laboratory signs, and changes in the patient's neurological status and consciousness can help in
making a correct, timely, and accurate diagnosis of this medical emergency.

Keywords: Ketoacidosis, Ketonuria, Ketonemia, Diabetes

W43

The Impact of Organizational Culture on Laboratory Accreditation

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This workshop addresses key requirements and approaches related to medical laboratories, including risk management based on ISO 22367, quality and competence requirements based on ISO 15189, safety requirements based on ISO 15190, social responsibility based on ISO 26000, ESG, HSE management systems, artificial intelligence management based on ISO/IEC 42001:2023, service excellence based on ISO 23592, customer complaints and satisfaction based on ISO 10002 and ISO 10004, and brand evaluation based on ISO 20671.

Keywords: Risk Management, Quality Management, Laboratory Safety, Social Responsibility, ESG, Artificial Intelligence, Service Excellence, Brand Evaluation

W44

A Semi-Workshop on: Skin Immunodiagnostic Tests
(Emphasizing Mantoux Tuberculin Test in Practice)

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Although in vivo tests do not account for a large proportion—either in number or variety—of routine medical laboratory tests, which are predominantly in vitro, they play a decisive role in the diagnostic decision-making process for certain allergic and infectious diseases. Although there are ongoing debates regarding the appropriate setting and qualified personnel for performing some skin tests—particularly the allergy prick test—not only between clinical physicians and laboratory/basic-science physicians, but also among physicians from different specialties (including pulmonology, pediatrics, otolaryngology, gastroenterology, dermatology, and others), and although even Medical Council regulations lack sufficient clarity to resolve these issues, such disagreement is not observed with respect to the Mantoux tuberculin skin test. At present, there also appears to be little inclination among specialists in infectious diseases, internal medicine, pulmonology, gynecology, and other fields to use this test as an office-based diagnostic procedure. Unfortunately, tuberculosis remains one of the most important public-health challenges worldwide. Fortunately, one of the diagnostic tools that can assist in detecting this disease—particularly its latent form—is the tuberculin skin test, which can be readily performed in Iran and is frequently requested by physicians. Therefore, having accurate scientific knowledge about this test is essential. This workshop will address the most appropriate methods for performing the test, including injection technique, reading, reporting, and interpretation. It will also discuss common errors at different stages of the procedure, with the aim of improving awareness among medical and laboratory professionals. During the workshop, several skin tests will be performed practically, and the technical aspects of conducting the test will be presented through live demonstrations. For this reason, the program goes beyond the usual format of nominal “workshops,” which are often merely lecture-based. It is therefore described as a semi-workshop.

Keywords: Immunodiagnosis, Skin Test, Allergy, Infectious Diseases, Tuberculosis, Tuberculin Test

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Laboratory & Diagnosis

Official Journal of the Iranian Association of Clinical Laboratory Doctors

Vol. 18, No. 72, Supplement Issue, September 2026