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CONGRESS ABSTRACTS

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The Message from the Congress Chairman

Dr. Sh. Hemmati
DCLS

In the Name of God

Dear colleagues, specialists, and professionals in the field of laboratory sciences The unparalleled role of medical laboratories in diagnosing, monitoring, and treating diseases is undeniable. Today, in a world where evidence-based medicine and precise diagnostics form the foundation of any advanced healthcare system, laboratories are considered the beating heart of the healthcare frameworks. Insufficient attention to diagnostic infrastructure and to the challenges faced by professionals in this field can have irreversible consequences for public health. Delays in disease diagnosis, increased treatment costs, reduced quality of services, and even the migration of key experts are all outcomes of neglecting this vital sector. However, amidst these challenges, there are opportunities for growth, transformation, and the advancement of laboratory sciences—opportunities we must seize with hope, knowledge, and collective effort. The future is bright because the importance of laboratories is increasingly recognized.

The recent pandemic demonstrated that laboratory diagnostics are the first and most critical step in controlling and managing diseases. Advances in diagnostic technologies have opened new horizons. Artificial intelligence, smart laboratories, novel molecular methods, and automation technologies not only enhance the accuracy and speed of diagnostics but also make our work more efficient and impactful. Our unity and advocacy can lead to positive change.

Active participation in health policymaking, engagement in scientific associations, and constructive interaction with decision-making bodies can strengthen the position of laboratory sciences in the country's healthcare system. We are not alone in this journey. With empathy, effort, and perseverance, we can turn challenges into opportunities and create a brighter future for the country's laboratories. This congress is a step toward that goal—an opportunity for collaboration, knowledge exchange, and paving the way for progress. Let us believe in a better future and strive for it.

The Message from the Congress Scientific Chair

Prof. A. H. Zarnani (DCLS, PhD)

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Dr. A. H. Naseri (DCLS)

Scientific Chairs

Dr. A. Shirin (DCLS)

Co-scientific chair in workshop affairs

Dr. F. Shaygan (DCLS)

Scientific manager and co-scientific chair in international affairs

In the Name of God

It is a distinct pleasure and honor to welcome distinguished guests and esteemed colleagues to the prestigious event of 16th international and 22nd national congress on Quality Improvement in Clinical Laboratories (QILC 2025), which will be held under the esteemed auspices of the International Federation of Clinical Chemistry (IFCC) and the European Federation of Laboratory Medicine (EFLM). This congress represents a vital opportunity for us, as members of the global laboratory medicine community, to share knowledge, and explore the latest advancements that are shaping the future of our field. Our focus this year is on the dynamic interplay between the past, present, and future of laboratory medicine with a particular emphasis on the transformative power of high-throughput technologies and artificial intelligence. We are living in an era of unprecedented technological progress, and the clinical laboratory is at the forefront of this transformation. The rapid evolution of high-throughput technologies has revolutionized the way we approach laboratory testing. These powerful tools enable us to process vast quantities of samples with remarkable speed and accuracy, opening new avenues for disease detection, personalized medicine, and large-scale research. From genomics and proteomics to metabolomics and beyond, high-throughput platforms are providing invaluable insights into the complexities of human health and disease. Equally transformative is the rise of artificial intelligence in healthcare. AI algorithms, with their ability to analyze complex datasets and identify patterns that would be impossible for the human eye to detect, are poised to revolutionize diagnostics. From automated image analysis in pathology and radiology to the development of sophisticated diagnostic algorithms, AI is empowering us to make more informed decisions, improve patient outcomes, and enhance the efficiency of our laboratories. This congress will delve into the exciting intersection of these two powerful forces: high-throughput technologies and artificial intelligence. We will explore how these advancements are being applied in various disciplines within laboratory medicine, including but not limited to precision medicine, infectious disease diagnostics and cancer diagnostics. In this congress, we will have the opportunity to hear from leading experts in their respective fields, engage in stimulating discussions, and network with colleagues from around the world. We are confident that this congress will be a resounding success, providing a platform for the exchange of ideas, the forging of new collaborations, and the inspiration for future innovations. Together, we can harness the power of high-throughput technologies and artificial intelligence to improve the quality of patient care and advance the field of laboratory medicine.

Thank you for joining us. We wish you all a productive and enriching congress.

The Message from the Congress Executive Chair

Dr. Gh. R. Hamzehloo
DCLS

In the Name of God

The integration of science and technology has undeniably transformed healthcare diagnostics, continuously driving us toward better patient outcomes. Today, as the healthcare landscape faces unprecedented challenges, emerging medical laboratory technologies serve as a beacon of hope, guiding us toward a future of more reliable, effective, and value-driven laboratory services for patients and the healthcare system.

The convergence of emerging technologies with healthcare diagnostics is fundamentally reshaping the field. From genetic insights to proteomic advancements and the power of artificial intelligence, these innovations collectively pave the way for a healthcare revolution.

In the near future, these technologies will enable the early detection of diseases, allowing for timely interventions and significantly improving patient outcomes. This shift from reactive, treatment-centered healthcare to proactive, preventive care is transformative. For example, advancements in genomics now facilitate the precise identification of genetic variations linked to disease susceptibility. This not only enables early diagnosis but also empowers healthcare providers to deliver personalized treatment plans tailored to an individual's genetic profile.

The 22nd QICL Congress will feature 23 scientific sessions and 40 workshops, focusing on key themes such as genomics, proteomics, and artificial intelligence, alongside other clinically and practically significant topics. Renowned experts and clinicians will lead these discussions, with keynote speeches delivered by internationally distinguished professors.

Simultaneously, the largest specialized exhibition of laboratory kits and equipment—now officially named the Iran Clinical Lab Expo (ICLE)—will be held alongside the congress. This exhibition will serve as a premier platform for the laboratory community and industry leaders to showcase the latest advancements in the field.

Despite economic challenges, including sanctions, currency restrictions, and the financial pressures caused by the elimination of government subsidies and currency allocation at the NIMA rate, we remain committed to addressing the needs of the laboratory community. Through the Quality Improvement Congress, we aim to provide valuable scientific, practical, and educational support to laboratory professionals.

Additionally, the Hakim Jorjani Festival will offer a warm and celebratory atmosphere where we will honor outstanding laboratory staff, technical managers, and student researchers. We will also pay tribute to distinguished figures in laboratory sciences and commemorate our colleagues and healthcare professionals who have dedicated their lives to this field and those we have sadly lost.

We look forward to the participation of laboratory professionals, researchers, and industry leaders in the Quality Improvement Congress, ensuring a successful and impactful event.

Congress Main Topics

Accreditation in Medical Laboratory Based on ISO 15189	**Dr. H. Bayat, DCLS**
Advanced Technologies in Blood Transfusion Practice from Donor Vein to Patient Vein	**Prof. A. Gharehbaghian, DCLS, PhD**
Advances in Viral Hepatitis Multi-Omics Research	**Prof. R. Jamali, MD**
Cancer Screening Tests: Evaluating the Evidence	**Dr. A. R. Lotfikian, DCLS**
Challenges and Advancements in Diagnosis and Management of Acquired Demyelinating Syndromes in Children	**Prof. M. R. Ashrafi, MD**
Challenges in Laboratory Diagnosis of Diabetes	**Dr. A. K. Niko Sokhan, MD**
Challenges in Laboratory Diagnosis of Thyroid Diseases	**Prof. A. Esteghamati, MD**
Clinical Implications of Antinuclear Antibodies and Anti-Phospholipid Antibodies: A Comprehensive Review	**Dr. M. Ghasem Zadeh Soroush, MD**
Cost-effectiveness in Laboratory Medicine	**Dr. A. R. Olyaei Manesh, PhD**
Emerging Fungal Infections and Diagnostic Updates in Invasive Mycoses	**Dr. M. Ghahri, DCLS, PhD**
Expert Talks	**Dr. Sh. Hemmati, DCLS**
Genomics and Transcriptomics: The Powerful Technologies in Precision Medicine	**Prof. A. R. Biglari, MD, PhD**
Harmonization of Clinical Laboratory Test Results	**Dr. R. Mohammadi, DCLS, PhD**
Immunological Testing in Organ and Tissue Transplantation	**Prof. A. A. Hamidieh, MD**
Innovative Diagnostic Methods in Clinical Microbiology (Bacteriology)	**Dr. B. Valizadeh, DCLS**
Latest Advances in Arbovirus Laboratory Diagnosis	**Dr. M. Norouzi, PhD**
POCT: Innovations and Challenges	**Dr. Gh. R. Hamzehlou, DCLS**
Professional Ethics in Medical Laboratories	**Dr. M. Sahebalzamani, DCLS**
Proteomics and Metabolomics in Laboratory Diagnosis	**Prof. F. Kobarfard, PhD**
Technological Advances in Today's Hematology Laboratories	**Dr. N. Vazifeh Shiran, PhD**
The Future Medical Laboratories: Sustainable and Eco-friendly	**Dr. M. Vanaki, DCLS**
Toward Application of Extracellular Vesicles in Laboratory Diagnosis	**Prof. A. H. Zarnani, DCLS, PhD**
Young Scientists	**Dr. F. Azizmohseni, DCLS**

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(in Alphabetic Order)

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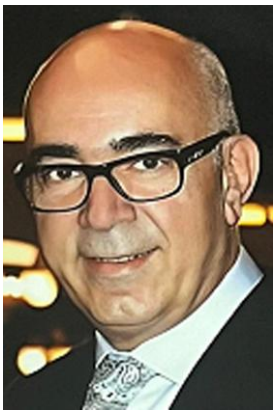

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ABSTRACTS

The 16th International & 22nd National Congress on Quality Improvement in Clinical Laboratory

Keynote Speech

O1-O5

O1

Lipoprotein(a): Why Measurement Matters and How to Achieve Lower Levels

Amirhossein Sahebkar 1 *

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Background: Lipoprotein(a) [Lp(a)] is a genetically determined lipoprotein that serves as an independent risk factor for various cardiovascular diseases, including atherosclerosis and calcific aortic valve disease. Method: A review of scientific literature using electronic databases. Results: Recent guidelines advocate for a one-time measurement of Lp(a) in all adults to identify individuals at high risk, as elevated levels can significantly impact cardiovascular outcomes. The concentration of Lp(a) is primarily influenced by genetic factors, with notable variations across different populations and genders. Despite the absence of approved medications specifically targeting Lp(a), innovative therapies are in advanced stages of clinical trials, showing promise in effectively lowering Lp(a) levels by up to 98%. These developments underscore the importance of measuring Lp(a) not only for risk assessment but also for guiding therapeutic interventions in both primary and secondary prevention settings. Emerging evidence indicates that Lp(a) measurement can facilitate personalized treatment approaches, including lifestyle modifications and pharmacotherapy options like PCSK9 inhibitors and antisense oligonucleotides. Furthermore, addressing knowledge gaps regarding Lp(a) biology and its clinical management is crucial for improving patient outcomes. Conclusion: Systematic screening and targeted interventions aimed at reducing Lp(a) levels are essential for mitigating cardiovascular risk, thereby enhancing overall cardiovascular health. The integration of Lp(a) measurement into routine clinical practice holds significant potential to reshape cardiovascular risk assessment and prevention strategies.

Keywords: Lipoprotein(a), Cardiovascular Disease, Risk Assessment, Measurement, Prevention Strategies

O2

Innovative Technological Advancements in Laboratory Medicine: Predicting the Lab of the Future

Khosrow Adeli 1 *

1- Head, Clinical Biochemistry Division and Senior Scientist, Research Institute, The Hospital for Sick Children; Toronto, ON, Canada- Professor and Vice-Chair, Department of Laboratory Medicine and Pathobiology, University of Toronto, ON, Canada- Past-President, International Federation of Clinical Chemistry and Laboratory Medicine (IFCC)

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Laboratory medicine is integral to public health and healthcare provision, and it relies on numerous analytical techniques to provide timely, objective data to healthcare professionals to guide disease prevention, diagnosis, treatment, and monitoring. Driven and defined by a culture of innovation, recent technological advances have revolutionized modern laboratory medicine and added significant value and visibility to its role in healthcare and clinical decision-making. Noteworthy innovations in laboratory automation, genomics, nuclear magnetic resonance spectroscopy, mass spectrometry, microfluidics, and electronic tools have changed the face of omics research. The growing application of these technologies, as well as their integration with microtechnology and point-of-care testing, has contributed to improved patient outcomes and narrowing of the clinical-laboratory interface to facilitate a patient-centered approach to healthcare. However, to adequately capitalize on these advancements, new tools such as artificial intelligence and data mining are needed to harness the exciting potential of medical big data derived from these novel techniques. In this presentation, I will provide an overview of the recent technological advancements in laboratory medicine, with a critical discussion on their clinical utility and future perspectives. The promise and potential for precision and personalized medicine will also be discussed and appraised, with specific attention paid to the contingency of its success on advanced information technology capabilities.

O3

Utilizing Multiomics to Develop Novel Therapeutics for Immunological and Inflammatory Diseases

Mohammad Bohlooly 1 *

1- Translational Genomics, Centre for Genomics Research, Discovery Sciences, BioPharmaceuticals R&D, AstraZeneca, Gothenburg, Sweden

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Rapid technological advances in the field of large-scale omics is changing the way we make medicines. Within the last decade we have seen an increase in the sensitivity, scope and scale of Next Generation Sequencing and related technologies become available to scientists, and this is leading to a greater understanding in the fundamental molecular processes underpinning disease. Within pharma we have applied these approaches across the whole process of making novel medicines from target identification through drug discovery and to the clinic. We are now able to effectively combine multiomic and modal data(genomics, transcriptomics, proteomics, advanced imaging)to produce a more comprehensive view of normal, diseased and treated states both directly in humans and in pre-clinical models of disease. This data is being used not only within specific projects but combined across projects and external datasets with increasingly sophisticated AI approaches to build predictive knowledge graphs of disease across diverse patient endotypes. Furthermore, the recent trend in applying omics to the generation of normal and disease atlases directly from patient clinical material is improving the success of delivering medicines to the right patient, and also back-translating these learnings to improve the translatability of pre-clinical drug screening and disease models. These advances in omics technologies have also facilitated a paradigm shift from traditionally small molecule approaches to rational drug design in an expanding array of new modalities including therapeutic gene editing, cell therapy, RNA, oligonucleotide and advanced antibody/peptide and conjugate approaches, giving us different inroads to overcome the challenges of developing and delivering novel medicines. In this presentation we will describe how we are applying multiomics approaches to the biological understanding, drug development and treatment of a range of immunological and inflammatory disorders, and how these approaches will lead to more effective and safer personalizedmedicines across a broader spectrum of disease.

O4

Integrated Diagnostics: Evidence-Based Therapy Guidance in Oncology from Tumor Markers to Liquid Biopsy

Tomris Ozben 1 *

1- Specialist in Clinical Biochemistry Akdeniz University, Medical Faculty, Dept of Clinical Biochemistry Antalya Turkey

Diagnosing cancer at an early stage has utmost importance. Tumor markers ™are considered as one of the valuable tests for detection and follow up of malignant tumors. They are easily measured in body fluids, mainly in serum or plasma; the results are obtained rapidly, automated assays are available for many markers, and the costs for TM testing are relatively low. Despite their lack of specificity and sensitivity, they are useful in screening for early malignancy, aiding cancer diagnosis, determining prognosis, surveillance, predicting drug response or resistance, and monitoring therapy. Combination of multiple TMs as a panel for assessment, or as part of validated algorithms has improved their performances. Ongoing research helped to discover new TMs having increased sensitivity and specificity, but still TMs are not available for all tumors. The genomic profiles of cancer patients are highly variable which dramatically influence the development of the disease and the efficacy of potential treatments. Personalized healthcare–also called precision medicine–employs molecular diagnostics to test each patient's genomic variants as a guide to the best treatment. Personalized medicine provides the right drug to be given to the right patient, at the right dosage and at the right moment. Since ctDNA and CTC are representative of the entire tumor genome, analysis of tumor DNA from fluid samples is frequently referred to as "liquid biopsy – liquid profiling".ctDNA is a particularly promising circulating biomarker for risk assessment in cancer patients due to the simplicity of obtaining plasma DNA, the cost-efficiency of the process, the high specificity and sensitivity of the resulting data. Liquid biopsy can detect ctDNA in cancer patients and identify specific mutations that may have prognostic or therapeutic implications. ctDNA quantification and mutation analysis are novel oncologic biomarkers for diagnosis, follow-up and therapeutic management of cancer. Integration of TMs with other diagnostic modalities such as modern imaging techniques and the recent developments in molecular diagnosis and liquid profiling will advance diagnostic performance and improve management of cancer patients.

O5

The Importance of Molecular Allergy Diagnostics in Clinical Laboratory Medicine; Innovation for Better Management and Causal Treatment of Allergic Diseases

Alireza Ranjbar 1 *

1- Distinguished Professor, Molecular and Clinical Pediatrics, Immunology and Allergy, Bonn, Germany

Allergy diagnosis typically begins with a detailed medical history and careful assessment of symptoms. Traditional methods, such as the skin prick test and measurement of specific IgE antibodies in the blood, rely on native allergen extracts. These extracts contain a wide range of proteins and allergenic components, each with varying allergenic potency. As a result, IgE antibodies are detected against both major and minor allergens without distinction, making it difficult to differentiate true allergies from cross-reactivities. Apparent polysensitizations or double sensitizations to different allergens are often caused by cross-reactions. In such cases, molecular allergy diagnostics can significantly enhance analytical specificity and selectivity, allowing for a more accurate distinction between genuine allergies and cross-sensitizations. Moreover, some allergen components are present only in trace amounts within native extracts, potentially leading to false-negative results when extract-based diagnostics fail to detect sensitization to these minor components. Molecular allergy diagnostics can therefore greatly improve test sensitivity, an advantage particularly important in the diagnosis of insect venom allergies. Additionally, sensitization to certain allergen molecules-especially in food allergies-can be associated with a higher risk of severe clinical reactions, highlighting the importance of precise molecular identification. Allergen-specific immunotherapy (AIT), the only causal and disease-modifying treatment for allergies, also benefits from molecular diagnostics, enabling the accurate selection of patients who are most likely to respond to therapy.

Oral Presentation

Accreditation in Medical Laboratory Based on ISO

15189

O6-O10

O6

Meeting Accreditation Requirements in the Transport of Send-out Samples

Mojtaba Azadi *

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Transporting clinical specimens from a collection site to a laboratory located in a further place to perform tests is of the common processes in clinical laboratory practice. Protecting the specimen quality so that there is no impressive difference- regarding the decision making for the patients- between the results obtained from transported specimens compared with the pre-transportation is of the paramount importance. Achieving this important objective is a shared responsibility between the sending laboratory, the courier agent, and the receiving laboratory. Assuring the quality of specimen transport is part of Quality Management System criteria, and therefore of the assessment scopes by the accreditation bodies. In this presentation, the ISO 15189 (2022) document requirements regarding specimen transportation, and CLSI PRE06 (Draft 2025) guidance will be discussed; and at the end a report on an evaluation to study the preservation of TSH test quality, as the representative of protein hormones, will be presented.

O7

Evaluation of Problems with Implementing Quality Assurance in Analytical Phase in Medical Laboratories

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Background: Analytical phase is one of the three phases in the quality assurance of medical laboratories. Theimportance of the analytical phase is because of its requirements to sufficient knowledge of the laboratory managers in evaluation, and in addition, it requires the knowledge and abilities of the laboratory technicians because of their direct involvement in the laboratory processes. In this study, we have examined the level of knowledge of the laboratory technicians about the quality assurance requirements and the problems evolved with it. Methods: The present research is a descriptive-analytical study, and the population of the research consists of all the personnel of the technical departments of the selected laboratories in the city of Tehran, numbering 116 people. In this research, with the help of a 70-question questionnaire, we used the one sample t-test and one sample Wilcoxon test for the evaluation of the knowledge of the laboratory technicians, and we used the Likert scale for evaluation of the answers and the number 3 was established for the evaluation of the answers. The validity of this questionnaire was reported as favourable by 10 laboratory medicine experts. Data analysis was done using SPSS version 24. Results: Of the 116 participants in the study, 92(79.3%) were female, and 24 (20.7 %) were male. 48.3%of them were between 30 and 40 years of age,17.2 % under 30 years old, 21.6%between 40 and 50, and the others (12.9%) were over 50 years of age. 97.4%of them were graduates of laboratory medicine and 2.6% were graduates of microbiology, 54.3% of participants had less than 10 years of work experience and the rest (45.7%) had between 10 and 30 years of work experience. The average level of the knowledge of the laboratory technicians with the theoretical principles of quality assurance was about 3.15, which is acceptable considering the theoretical mean of 3 and the p-value of less than 0.05. However, the average level of knowledge with the practical methods of quality assurance was 2.7, which is unacceptable considering the theoretical mean of 3 and the p-value of less than 0.05. Conclusion: Although the average level of the knowledge of the laboratory technicians with the theoretical principles of quality assurance was acceptable but the average level of knowledge with the practical methods of quality assurance was unacceptable and needs to more training. It was also found that more than half (60%)of participants mentioned that they want to know more about the quality assurance processes and taking apart in the quality assurance training courses.

Keywords: Analytical Phase, Quality Assurance, Questionnaire, Laboratory Technicians, Knowledge

O8

Environmental and Personnel Challenges in the Implementation and Continuity of ISO 15789 Standard in Reception, Sampling, and Reporting Departments

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Introduction: It has been over a decade since the development of the ISO 15189 standard globally. However, the interest of clinical laboratories in Iran to obtain certification for this ISO is very low. Although a few laboratories have taken steps to acquire this ISO in recent years, there are unfortunately many challenges and concerns for the technical managers of laboratories. This article examines and identifies these challenges in the areas of reception, sampling, and reporting. Research Method: The study involved reviewing, evaluating, and analyzing retrospective data from patients, clients, and other types of laboratory customers, as well as personnel from the reception, sampling, and reporting departments, collected from a set of five laboratories. Findings: Unfortunately, the current environment of existing laboratories is not designed to meet laboratory standard needs(privacy preservation, related to the laboratory layout, section 2-2-5 of the ISO checklist).Regarding personnel challenges, the most significant issues include: Severe shortage of trained human resources Severe shortage of job applicants in the mentioned departments Extremly low motivation toaccept, implement, and maintain the accreditation process Inappropriate organizational culture and personal concerns of staff Discussion and Conclusion: Optimizing the space and physical layout of the laboratory environment in current conditions according to ISO standards. Providing solutions to reduce or eliminate personnel challenges.

Keywords: Medical Diagnostic Laboratory, ISO 15189, Accreditation

O9

Challenges in Accrediting Hematology Laboratories

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The hematology laboratory is a part of the general laboratory where not only the equipment, kits and reagents, SOPs and sample quality, but also the diagnostic skills of the individuals are very important, hence there are challenges in its quality control and accreditation that are less noticeable in others. In this department, despite the request for a CBC test, a large number of parameters are measured, the basis of measurement, normal range, Limit of Detection and Quantification and uncertainty of each differ based on age, gender and geography. In addition, the method of reporting morphology and differential count and diagnosing hematological abnormalities based on PBS also differ significantly. Although ICSH and CLIA recommendations for harmonization in reporting results have been published, their implementation in different laboratories is very diverse. The presence of visual graphs, their interpretation, descriptive and written reports, lack of standard criteria for PBS preparation, high sensitivity of whole blood samples to aging and pre-analytical errors, low TAT, presence of critical malignant diseases, existence of various types of internal and external quality control, as well as the presence of optional and additional parameters in addition to the standard parameters of the CBC test have also increased the complexity of the part in accreditation. Biochemistry test like FBS is one parameter, but CBC test can have up to 60 parameters in modern devices, so accreditation and quality control of one laboratory will have differences from one laboratory to another, which we will try to explain in this article.

Keywords: Accrediting Hematology, Laboratory Skills, Quality Control, Harmonization, Laboratory Errors

O10

Maintenance Challenges and Solutions to Maintain and Improve the 15189 Standard in Accredited Laboratorie

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“The laboratory shall establish, document, implement and maintain a management system to support and demonstrate the continued fulfillment of the requirements of the standard as stated in the objectives and policies.” National and international experience shows that once a management system is established, it will be difficult to maintain it. The main reason for this is the failure to comply with all or some of the quality management principles (QMP), and the reasons can be dependence on specific personnel, staff turnover, lack of awareness of staff at different levels and, most importantly, management commitment. “The laboratory shall continually improve the effectiveness of the management system, including pre-examination, examination and post- examination processes. This is achieved through the objectives stated in the policy and objectives.” It will be more difficult to improve the standard systems once the standard is established and maintained. The causes of stagnation of standards after establishment may be the formulation of unrealistic and non-operational policies and objectives resulting from a lack of awareness of the current situation and the ability to implement the operational plan. The solution to maintaining and improving the standard is to observe the seven principles of quality management.

Advanced Technologies in Blood Transfusion Practice

from Donor Vein to Patient Vein

O11-O15

O11

Using Advanced Technologies: Machine Learning and Artificial Intelligence Applications Related to Blood Donors

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Blood transfusion plays a pivotal role in patient care, treatment, and survival such as major surgery, cancer therapy, organ transplantation, hematological and bleeding disorders, or trauma and disaster preparedness. On the other hand, the main factors that affect blood transfusion activities include; the implementation of blood Transfusion establishment, existing blood donors' pool, efficient laboratory screening for TTIs, implementation of quality management system, and appropriate clinical use of blood products. In recent years, the advent of advanced technologies such as machine learning (ML) and artificial intelligence (AI) has brought significant transformations in various sectors, including blood transfusion establishments. Machine learning algorithms can analyze the historical data of donors and predict future trends and behaviors, helping to create personalized communication and engagement strategies, and encouraging donors to return and donate regularly. AI-equipped systems can provide predictive analyses, improving the efficiency and accuracy of blood donor eligibility assessments. AI systems can predict blood demand based on existing data, seasonal trends, and current events, ensuring blood transfusion centers maintain optimal inventory, be aware of shortages, and implement strategies to prevent wastage of blood and blood products. Additionally, advanced algorithms can increase the success rate of blood transfusions by better-matching donors to recipients, considering factors like blood type, medical history, and urgent needs. AI can also monitor equipment performance from collection to storage, predict potential failures, and ensure the reliability and safety of the blood donation process. Machine learning processes can identify fraudulent donors or suspicious patterns in donation records, increasing the protection of the blood transfusion cycle. AI can also help blood transfusion programs by automatically analyzing large datasets and providing timely monitoring and reporting.

Keywords: Blood Transfusion, Blood Donation, Machine Learning, Artificial Intelligence

O12

Advanced Technologies and Innovations in Blood Transfusion Practice

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Immunohematology, as one of the oldest branches of laboratory science, entered the academic arena with the discovery of ABO blood groups by Landsteiner and has witnessed a great transformation in this field over the past 120 years, and has had a positive and reciprocal impact on other branches of laboratory science. Immunohematology has evolved from a solely laboratory approach to blood banking and then blood transfusion medicine, moving from a test tube perspective to the clinic and focusing on collaboration and participation to patient-centered approach. In the field of laboratory diagnostics, it has remained faithful to the oldest method of antigen and antibody measurement (Agglutination - Hemagglutination), and transformed it into a test that is competitive with other methods of antigen and antibody measurement, and succeeded in dramatic change by combining agglutination with automation. The development of a gel-based antigen and antibody carrying card in a gel environment, which stops the reversibility of antigen and antibody reactions preventing false reactions, followed by its development in a microtube instead of a test tube greatly reducing the consumption of reagents, has enabled its development in small and large hospitals and its connection with blood transfusion services, managing vein to vein from donors to recipient and rendering error management using artificial intelligence and electronic cross match. The development of agglutination in other antigen and antibody detection methods and its competition with ELISA in terms of sensitivity and specificity has enabled its development in all laboratory areas for antigen and antibody detection, and it can be expected to bring a competitive cheap and efficient assay method to the field of medical diagnostic laboratories on a single platform.

Keywords: Immunohematology, Hemagglutination, Antigen-Antibody Reaction, Automation

O13

Using Machine Learning (ML) and Artificial Intelligence (AI) in the Management of Transfusion Related Adverse Reactions

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Background: Classification and management of transfusion related events is important for patients care and tracking of events. Artificial intelligence (AI) and machine learning (ML) increasingly take the step from just being interesting concepts to being relevant or even part of our lives. Managing of the transfusion related reactions can be easily done using AI based on symptoms and signs. Methods and Materials: An AI system should assess some cases scenarios to provide a diagnosis, severity, and traceability of the transfusion reactions. Data must be compared with traditional and common classification by experts. Results: Studies show that AI's classification accuracy varied widely. The AI classifies all TACO and TRALI cases, exceeding specialists' assessments. Conversely, it does not correctly identify cases such as DSTR. AI-generated responses included non-standard terminology, limited severity assessments, and no probability determinations. AI systems linked to cardiac monitors can detect changes in vital signs – temperature, heart rate, blood pressure, and oxygen saturation, and help prevent an impending adverse reaction. Conclusion: AI could have a role in helping healthcare providers to consider transfusion reaction categories that might be missed, but caution is advised in applying the AI's output to transfusion reaction classification.

Keywords: Transfusion Related Adverse Reactions, Artificial Intelligence, Machine Learning

O14

Best Practices in Blood and Blood Product Inventory Management: A Focous on Artificial Intelligencce Application

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Background: Blood and blood product inventory management is a critical challenge in healthcare. Traditional methods rely on manual data recording and empirical predictions, often leading to supply-demand imbalances, shortages, or wastage. These inefficiencies can cause severe crises, particularly in emergency situation Methods and Materials: Recent technological advancements, particularly in Artificial Intelligence (AI), have introduced machine learning algorithms capable of analyzing historical data to predict demand patterns. By integrating AI-driven models with existing inventory systems, blood storage and distribution can be optimized. Results: Studies indicate that AI-based inventory management significantly reduces blood wastage while ensuring adequate supply during emergencies. Predictive models enable better allocation of resources, leading to improved efficiency in healthcare facilities. However, the accuracy of AI models depends on high-quality data, and implementation costs remain a challenge Conclusion: Despite limitations, AI presents a promising future for blood inventory management. By reducing inefficiencies and enhancing supply chain resilience, AI-driven approaches can transform the field, ensuring optimal blood availability and reducing shortages. Future research should focus on improving data accuracy and cost-effective implementation strategies.

Keywords: Blood Inventory Management, Artificial Intelligence, Predictive Analytics

O15

Using Next Generation Sequencing (NGS) as an Advanced Technology for Blood Group Genotyping

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Background: Next-generation sequencing (NGS) is one of the new molecular methods for determining the genotype of blood groups. Molecular methods are very useful, especially in cases where serological methods are unable to determine the blood group. The technologies available in NGS include short-read sequencing or second-generation NGS, which includes Illumina and Ion Torrent Thermo Fisher technologies, which have an error rate of less than 1%, while third-generation NGS or long-read sequencing, which includes PacBio and Oxford Nanopore technologies, are fast but has an error rate of about 10%. Methods: In this study, more than 20 articles related to blood group genotyping using various NGS technologies were reviewed in the Pubmed database. Results: NGS is used in determining the blood group genotype of donors, resolving serological grouping discrepancies, examining poorly expressed blood group antigens, examining blood group chimerism, determining fetal blood group antigens in maternal plasma, and managing hemolytic disease of the newborn. Conclusion: Some challenges in the application of NGS in blood grouping include high cost, sequencing errors, especially in cases of complex polymorphisms, and technical errors that require standardization. Despite the existing challenges, NGS has great potential to revolutionize blood group genotyping.

Keywords: Next Generation Sequencing, Genotype, Blood Grouping

Advances in Viral Hepatitis Multi-omics Research

O16

O16

Advances in Multi-omics Approach in Viral Hepatitis

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Multiomics is a new strategy in personalized medicine that brings the data of numerous omic groups while approaching to the diagnosis and treatment of a disease. The genome, proteome, transcriptome, epigenome, and microbiome are among the most familiar omics in this regard. Viral hepatitis is a major cause of liver related morbidity and mortality worldwide. Hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), hepatitis D virus (HDV), and hepatitis E virus (HEV) are the most common viruses that infect hepatocytes and induce hepatitis. The Multi-omics is defined as the comprehensive study of the functions, relationships and roles of various types of molecules in biological cells. The multi-omics analysis has been proposed and considered key to advancing clinical precision medicine, mainly including genomics, transcriptomics and proteomics, metabolomics. The applications of multi-omics can show the origin of hepatitis viruses, explore the diagnostic and prognostics biomarkers and screen out the therapeutic targets for viral hepatitis and related diseases. To better understand the pathogenesis of viral hepatitis and related diseases, comprehensive multi-omics analysis has been widely carried out. This pannel mainly summarizes the applications of multi-omics in different types of viral hepatitis and extrahepatic manifestations, in order to provide new insight into their important role.

Keywords: Multiomics, Viral Hepatitis, Genomics, Proteomics, Transcriptomics, Metabolomics

Cancer Screening Tests: Evaluating the Evidence

O17-O19

O17

Application of Novel Biomarkers in the Screening of Hematological Neoplasms

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The landscape of hematologic malignancies is undergoing significant transformation due to the development of novel diagnostic tools and biomarkers. This presentation delves into the latest research findings that highlight their clinical relevance and potential applications in patient management. A key focus is the role of circulating tumor DNA (ctDNA)in various hematological malignancies, including lymphomas, multiple myeloma, myelodysplastic syndromes, and leukemia. A comprehensive meta-analysis demonstrates that ctDNA can be a powerful prognostic tool, enabling clinicians to track disease progression and treatment responses with greater accuracy We examine the impact of Wilms tumor mutations, identified as independent poor prognostic factors in pediatric acute myeloid leukemia(AML).Additionally, low expression levels of miR-214-5p are linked to more aggressive subtypes of pediatric anaplastic large cell lymphoma(ALCL)reinforcing the significance of microRNAs in influencing disease outcomes Further investigation reveals HNRNPH1 as a novel regulator of cellular proliferation and disease progression in chronic myeloid leukemia, providing insight into potential therapeutic targets. Moreover, we discuss the long non-coding RNA LINC00152and its crucial role in regulating the self-renewal of leukemia stem cells, which is associated with chemoresistance in acute myeloid leukemia The presentation also highlights the pivotal role of PSMB7 in the pathogenesis of multiple myeloma and its correlation with resistance to bortezomib, underscoring the need for personalized treatment approaches. We explore PHF6 mutations and their implications in hematologic malignancies, as well as the prognostic significance of a high count of CD68+andCD163+macrophages in mantle cell lymphoma Finally, we will compare various clinical testing modalities for the assessment of NPM1-mutant acute myeloid leukemia and present research highlights on mass cytometry's applications in hematologic malignancies. The advancements in this field promise to revolutionize early diagnosis and improve patient outcomes through more tailored therapeutic strategies. By integrating these various findings, this presentation aims to underscore the critical advancements in the field of hematologic malignancies and promote discussions on future research directions that can enhance diagnostic precision and personalized patient care.

O18

Counseling and Indication of Genetic Tests in Hereditary Breast and Ovarian Cancers

Marjan Yaghmaie *

Hereditary breast and ovarian cancers (HBOC) account for approximately 5–10% of breast cancers and 15–20% of ovarian cancers, predominantly driven by pathogenic variants in BRCA1 and BRCA2. Recent advances have expanded the scope of genetic testing to include moderate-risk genes (e.g., PALB2, CHEK2, ATM, RAD51C/D) as part of multigene panel testing. Current guidelines from NCCN (2024) and ESMO emphasize the importance of pre- and post-test genetic counseling to ensure informed decision-making, facilitate cascade testing in at-risk relatives, and optimize risk-reducing strategies. Genetic testing is indicated in individuals with early-onset breast cancer (<50 years), triple-negative breast cancer diagnosed before age 60, high-grade serous ovarian cancer at any age, bilateral or multifocal disease, male breast cancer, and those with relevant family history. Furthermore, universal genetic testing for ovarian cancer patients is now widely recommended, irrespective of age or family history, due to therapeutic implications. Counseling integrates risk assessment models (e.g., BOADICEA, Can Risk) and must address psychosocial aspects, variant interpretation, and implications for surveillance, risk-reduction (e.g., RRSO, mastectomy), and PARP inhibitor therapy eligibility. Testing approaches must also consider somatic vs. germline status in advanced cancers. Emerging data suggest disparities in access and uptake, highlighting the need for broader implementation of mainstreaming models and tele-genetics. This presentation will provide an updated overview of the clinical indications, gene panels, counseling frameworks, and the translational impact of genetic testing in HBOC management.

Keywords: Hereditary Breast Cancer, BRCA1/2, Genetic Counseling, Multigene Panel, Ovarian Cancer, PARP Inhibitors, Risk-Reduction, Cascade Testing

O19

Cancer Screening Evaluation: From Governance Policies to Evidence-Based Guidelines

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Cancer is the third leading cause of death in Iran. Given the increasing elderly population in Iranian society and the increasing risk of cancer, cancer screening programs should receive great attention. Of the 270 known cancers, nearly 50 percent are preventable and screening tests have been proven effective. Because most cancers are asymptomatic and slow-growing in the early stages, screening programs are very important and vital in the early detection of cancers. Success in cancer screening programs requires collaboration between clinicians, the private sector, and government support. Evidence-based interventions can increase adherence to recommended screening guidelines, but disparities in cancer screening uptake persist. Advances in medical research highlight the potential of artificial intelligence and minimally invasive screening tests as new horizons in early cancer detection.

Challenges and Advancements in Diagnosis and Management of Acquired Demyelinating Syndromes in Children

O20-O24

O20

Myelin Oligodendrocyte Glycoprotein–Associated Disorders

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Acquired Demyelinating Syndromes (ADSs)of the central nervous system (CNS)are rare disorders, occurring with an approximate annual incidence of 9.8 per million children per year. They present with neurologic dysfunction caused by immune-mediated injury to the myelin sheath of the brain, optic nerves, and spinal cord. The pathogenesis often involves demyelination together with B cells and CNS antibodies. Two immunoglobulin G(IgG)antibodies recognized as playing an important part in demyelination are aquaporin4-antibody (AQP4-Ab) and myelin oligodendrocyte glycoprotein antibody (MOG-Ab). Myelin Oligodendrocyte Glycoprotein–Associated Disorders (MOGAD)have four main clinical phenotypes of (1) ADEM (2) ON (3) TM (4) Cortical encephalitis. Tumefactive lesions, cerebellar demyelination, cranial neuropathies, monofocal or polyfocal cerebral motor deficits, and occasionally a widespread progressive leukodystrophy-like pattern may also be seen. The diagnostic guideline of the International MOGAD Panel requires fulfillment of three criteria:1. Presence of one of six core clinical demyelinating events: optic neuritis, myelitis, ADEM, cerebral monofocal or polyfocal deficits, brainstem or cerebellar deficits, or cerebral cortical encephalitis. 2.Serum MOG-Ab positivity 3. Exclusion of MS and other demyelinating syndromes. Brain MRI may show widespread involvement of the supratentorial and infratentorial white matter that can over time develop into a leukodystrophy-like pattern. This may extend into the pons, middle cerebellar peduncle, medulla, or deep gray matter. Spinal imaging suspicious for MOG-Ab disease may show longitudinally extensive myelitis, a characteristic H-sign of the central cord, or a lesion of the conus medullaris. Suspected cases should have serum tested for MOG antibodies via live CBA for the IgG Fc or IgG1 secondary antibodies; importantly, laboratories should ideally report both quantitative(i.e., titers)and qualitative results(i.e., low-positive or high-positive).Despite variation in assay protocols across laboratories globally, high positivity is reliably predictive of true MOG-Ab positivity. Low-positive or borderline results less reliably differentiate MOG-Ab disease from other entities and should prompt reconsideration of other diagnoses, particularly MS. Intrathecal OCBs are not normally present. Elevated CSF white blood cells with pleocytosis is often present.

O21

Neuromyelitis Optica Spectrum Disorder (NMOSD) - Case Presentation and Discussion

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NMOSD is a CNS inflammatory disorder that preferentially affects the optic nerves and spinal cord but can also involve the area postrema, hypothalamus, and periaqueductal gray. NMOSD is much less common in children, with pediatric NMOSD accounting for 2% to 5% of all NMOSD cases. The median age of onset in pediatric NMOSD ranges from 10 to 14, and a female predominance is seen, particularly when onset occurs in the teenage years. The first clinical manifestations of pediatric NMOSD often include unilateral or bilateral optic neuritis, transverse myelitis, and brainstem/cerebellar syndromes. Simultaneous optic neuritis and transverse myelitis are seen in a minority of pediatric patients at the initial attack. When the area postrema is involved, hiccups and/or intractable vomiting may be part of the initial manifestations. Treatment of acute attacks includes high-dose IV methylprednisolone for 3 to 5 days, although plasma exchange should be employed early if little to no neurologic recovery is seen, given the propensity for disability accumulation in NMOSD. The majority of pediatric NMOSD cases (>90%) exhibit a relapsing course,72 and thus chronic preventive immunotherapy is often required to reduce the risk of future relapses and accumulating neurologic disability.

O22

Pathogenesis and Diagnostic Biomarkers in Acquired Demyelinating Syndromes

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Acquired demyelinating syndromes (ADS) represent a diverse spectrum of immune-mediated disorders affecting the central nervous system (CNS). Understanding the pathogenesis of ADS has advanced considerably, highlighting the roles of autoimmune processes, environmental triggers, and genetic predisposition. The identification of specific autoantibodies, such as those targeting myelin oligodendrocyte glycoprotein (MOG) and aquaporin-4 (AQP4), has transformed diagnostic approaches and improved disease classification. The pathogenesis of ADS involves complex interactions between innate and adaptive immunity, including the activation of T cells, B cells, and complement pathways. Recent studies emphasize the role of cytokine dysregulation and molecular mimicry in triggering autoimmune responses. Additionally, advances in neuroimaging, such as diffusion tensor imaging and advanced MRI techniques, provide insights into the microstructural damage associated with demyelination. This presentation focuses on the latest discoveries in the underlying mechanisms of ADS and the development of diagnostic biomarkers. Emphasis is placed on the clinical utility of biomarkers such as MOG and AQP4 antibodies, neurofilament light chain (NfL), and glial fibrillary acidic protein (GFAP) in differentiating between ADS subtypes and predicting disease course. These biomarkers, combined with cutting-edge imaging modalities, offer the potential for earlier diagnosis and personalized therapeutic strategies. References: Narayan, R., Simpson, A., & Fritsche, K. (2023). Advances in understanding the immunopathogenesis of acquired demyelinating syndromes. Nature Reviews Neurology, 19(4), 215-228. Levy,M., Wingerchuk, D. M., & Pittock, S. J. (2022). Diagnostic biomarkers in pediatric demyelinating diseases: Current status and future directions. The Lancet Neurology, 21(9), 789-799. 3. Kothur, K., Wienholt, L., &Brilot, F. (2023). Role of neurofilament light chain and other biomarkers in acquired demyelinating syndromes. Journal of Neuroimmunology, 377, 578095.d

O23

Overview of Acquired Demyelinating Syndromes in Children

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Acquired demyelinating syndromes (ADS) encompass a heterogeneous group of immune-mediated disorders of the central nervous system (CNS) that primarily affect the myelin sheath. These syndromes are particularly significant in pediatrics due to their potential overlap with other neurological conditions, including infections and metabolic disorders, and their long-term impact on development and quality of life. ADS in children can be broadly classified into monophasic and recurrent disorders. Monophasic presentations, such as acute disseminated encephalomyelitis (ADEM) and optic neuritis, are often triggered by infections or vaccinations and typically resolve without recurrence. Recurrent or chronic conditions include multiple sclerosis (MS), neuromyelitis optica spectrum disorder (NMOSD), and myelin oligodendrocyte glycoprotein antibody-associated disease (MOGAD). Advances in neuroimaging and the identification of specific biomarkers, such as MOG and aquaporin-4 antibodies, have significantly improved the diagnosis and differentiation of these disorders. This presentation provides an updated overview of ADS in children, focusing on clinical features, diagnostic criteria, and recent therapeutic advances. Early diagnosis and targeted treatment are critical to mitigating long-term neurological sequelae. Emerging therapies, including monoclonal antibodies and disease-modifying treatments, are reshaping the landscape of pediatric demyelinating disorders. Multidisciplinary care involving neurologists, immunologists, and rehabilitation specialists is essential to address the complex needs of these patients. References: Banwell, B., Bar-Or, A., & Arnold, D. L. (2021). Pediatric multiple sclerosis: Advances in understanding and management. The Lancet Neurology, 20(5), 400-414. Hacohen, Y., Absoud, M., & Wassmer, E. (2022). Spectrum of acquired demyelinating syndromes in children: From bench to bedside. Neurology Clinics, 40(3), 603-619. Yeh, E. A., Weinstock-Guttman, B., & Kennedy, J. (2023). Advances in diagnosis and treatment of pediatric demyelinating diseases. Journal of Child Neurology, 38(2), 123-134.

O24

Laboratory Evaluations to Aid Diagnosis in Acquired Demyelinating Syndromes

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Background: Demyelinating diseases, while often presenting with characteristic clinical and imaging findings, may occasionally manifest in atypical or "awkward" forms, leading to significant diagnostic challenges. These rare presentations, which may overlap with other neurological conditions, necessitate careful consideration of novel biomarkers, advanced imaging techniques, and specialized laboratory tests. Accurate diagnosis is crucial for appropriate management and timely treatment. Objective: To review the diagnostic strategies for identifying atypical demyelinating diseases (including Anti-MOG-associated disease, Neuromyelitis Optica Spectrum Disorder (NMOSD), Acute Disseminated Encephalomyelitis (ADEM), and variant forms of Multiple Sclerosis (MS)) with an emphasis on advanced laboratory testing and neuroimaging techniques that enhance diagnostic accuracy. Methods: A comprehensive analysis was conducted of the clinical and laboratory diagnostic features of atypical demyelinating diseases. Key diagnostic tools reviewed include magnetic resonance imaging (MRI), cerebrospinal fluid (CSF) analysis, autoantibody testing (e.g., anti-AQP4, anti-MOG), nerve conduction studies (NCS), and evoked potentials. Relevant case studies and recent clinical findings were also examined to better understand the role of these tests in distinguishing rare and unusual presentations. Results: MRI remains essential for identifying lesions, but atypical forms may display unusual lesion distributions or be misinterpreted as other neurological disorders. CSF analysis often shows minimal changes in conditions like MOGAD and NMOSD, with oligoclonal bands (OCBs) being absent in contrast to MS. Serum autoantibodies such as anti-MOG and anti-AQP4 are highly specific for MOGAD and NMOSD, providing essential diagnostic clarity. Electrophysiological testing demonstrates abnormal nerve conduction in GBS and CIDP, while visual evoked potentials (VEPs) are useful in differentiating MS and its variants. Conclusion: A comprehensive diagnostic approach that integrates advanced imaging, autoantibody testing, and electrophysiological studies is critical in the diagnosis of atypical or "awkward" demyelinating diseases. By combining these modalities, clinicians can more accurately identify rare and variant forms of demyelination, improving prognosis and treatment outcomes. Further research into emerging biomarkers and diagnostic technologies will refine early detection and differentiation of these complex disorders.

Keywords: Atypical Demyelination, Anti-MOG, NMOSD, ADEM, MS Variants, MRI, CSF Analysis, Biomarkers, Evoked Potentials

Challenges in Laboratory Diagnosis of Diabetes

O25-O30

O25

The Role of Microarray Genetic Test in Diabetes Management

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Microarray genetic testing facilitating the identification of diabetes-associated variants and the calculation of Polygenic Risk Scores (PRS). Early risk detection is improved through microarray analysis, identifying individuals with a high genetic predisposition to developing diabetes before clinical onset. Microarray-based subtyping of diabetes reveals five genetically distinct clusters—SAID, SIDD, SIRD, MOD, and MARD—enhancing the understanding of disease heterogeneity and guiding targeted care. Tailored treatment strategies can be developed based on genetic profiles, such as early insulin therapy for SIDD patients and weight-loss-focused interventions for those with SIRD. Preventive care is strengthened by genetic risk stratification, allowing for early lifestyle modification and clinical surveillance in high-risk individuals. PRS derived from microarray data also contributes to the prediction of late complications of T2D, such as diabetic nephropathy, retinopathy, and cardiovascular disease, enabling proactive monitoring and management.

O26

Screening and Diagnosis of Diabetes

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FPG, 2-h PG during 75-g OGTT, and A1C are appropriate for screening and diagnosis. It should be noted that detection rates of different screening tests vary in both populations and individuals. FPG, 2-h PG, and A1C reflect different aspects of glucose metabolism, and diagnostic cut points for the different tests will identify groups with incomplete concordance. Compared with FPG and A1C cut points, the 2-h PG value diagnoses more people with prediabetes and diabetes. Moreover, the efficacy of interventions for primary prevention of type 2 diabetes (i.e., preventing conversion of prediabetes to type 2 diabetes) has been demonstrated mainly among individuals with prediabetes who have impaired glucose tolerance (IGT) with or without elevated fasting glucose, not for individuals with isolated impaired fasting glucose (IFG) or for those with prediabetes defined by A1C criteria.

O27

Effects of Continuous Glucose Monitoring in Diabetes Managements

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Continuous Glucose Monitoring (CGM)systems have been extensively studied and recognized for their significant benefits in managing diabetes. Here are some key points highlighting their importance based on scientific articles:1. Improved Glycemic Control: CGM has been shown to improve glycemic control by reducing hemoglobin A1c(HbA1c) levels, average blood glucose levels, and glucose variability. This is particularly beneficial for patients with both type 1 and type 2 diabetes.2. Reduction in Hypoglycemia and Hyperglycemia: CGM helps in detecting asymptomatic hypoglycemia and hyperglycemia, allowing for timely interventions to prevent severe episodes. This is crucial for reducing the risk of complications associated with these conditions. 3. Enhanced Patient Quality of Life: By providing real-time glucose data, CGM enables patients to make informed decisions about their diet, exercise, and insulin dosing, thereby improving their overall quality of life. 4. Cost and Utilization Implications: While CGM improves outcomes, it also increases healthcare costs. However, it can lead to reduced inpatient utilization by preventing severe hypoglycemic events and hospitalizations. Clinical Applications - Type 1 Diabetes: CGM has been widely adopted and proven effective in managing type 1 diabetes, particularly in reducing severe hypoglycemia and improving HbA1c levels. -Type 2 Diabetes: Although less studied, CGM has shown promise in improving glycemic control for type 2 diabetes patients, especially those on intensive insulin regimens. - Real-World Evidence: Real-world studies have supported the clinical effectiveness of CGM across various diabetes populations, leading to expanded coverage and use. In summary, CGM systems are crucial for enhancing diabetes management by providing continuous glucose data, reducing glycemic variability, and improving patient outcomes. However, their adoption must be balanced with considerations of cost and accessibility.

O28

HbA1c Standardization

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Also called glyco hemoglobin is a form of hemoglobin that is chemically linked to a sugar (non_enzymatically). The formation of excess sugar hemoglobin linkage indicates the presence of excessive sugar in the blood stream and is an indicator of diabetes (HbA1c more than 6.4). There are several ways to measure glycated hemoglobin, of which HbA1C is a standard single test. HbA1C is measured primarily to determine the three month average blood sugar level and is usded as a standard diagnostic test for evaluating the risk of complications of diabetes and as an assessment of glycemic control (because of 3 months average life span of a red blood cell). Several techniques are used to measure hemoglobin A1C.Laboratories may use high performance chromatography, immunoassay, enzymatic assay, capillary electrophoresis, or boronate affinity chromatography (the last one is office based). The variation between these tests makes difficulties in practice. The best test for HbA1C determination is HPLC.

O29

Importance of Urine Microalbumin Measurement and eGFR Calculation in Diabetics

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1. Early Detection of Diabetic Kidney Disease (DKD): Urine microalbumin (albumin-to-creatinine ratio) detects low levels of albumin in urine, which is often the earliest sign of kidney damage in diabetes. Estimated Glomerular Filtration Rate(eGFR)reflects overall kidney function. A declining eGFR indicates progression of kidney disease. 2. Prevention of Progression: Timely identification of microalbuminuria allows for early intervention with ACE inhibitors or ARBs, glycemic control, and lifestyle changes, which can delay or prevent progression to chronic kidney disease (CKD)and end-stage renal disease (ESRD).3. Risk Stratification and Monitoring: Persistent microalbuminuria is associated not only with renal risk but also with increased cardiovascular risk. Regular eGFR monitoring helps track kidney function over time and guides dose adjustments of medications. 4. Treatment Optimization: Helps clinicians decide on intensity of glycemic, blood pressure, and lipid control. Supports decisions on use of nephroprotective agents (e.g., SGLT2 inhibitors, GLP-1 receptor agonists). 5. Guideline Recommendations: ADA, KDIGO, and other guidelines recommend annual screening of urine ACR and eGFR in all patients with type 2 diabetes and in type 2.

O30

Importance of NT- Pro BNP Test in Early Diagnosis of HF

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BNP is a 33-amino acid peptide that is produced by the stretching of the left ventricle of the heart. BNP is produced from a precursor peptide called ProBNP, which is produced after stress on the heart muscle and is broken down by the enzyme corin into BNP and NT-ProBNP. It is the active part of BNP, but measuring both is equally valuable. BNP is measured for early diagnosis of HF. In diabetic patients, cardio vascular disease are the most common cause of death, so timely diagnosis is very important, and with the help of laboratory measurement of BNP, HF can be diagnosed in the early stages.

Challenges in Laboratory Diagnosis of Thyroid Diseases

O31-O33

O31

The Effect of Biological Factors Such as Age and Pregnancy and Sick Euthyroid Syndrome on Thyroid Function Tests

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In certain clinical situations, the interpretation of thyroid function tests presents challenges. Infancy: After birth, TSH levels increase significantly. Neonatal screening programs have helped reduce the complications of congenital hypothyroidism. Pregnancy is associated with significant changes in thyroid function. Increases in hCG and TBG lead to changes in thyroid hormone levels. Early in pregnancy, TSH levels may decrease due to the effect of hCG. Old Age: TSH levels increase, but this increase is generally not accompanied by a decrease in T4 levels. This condition may lead to subclinical hypothyroidism, which has protective effects on the cardiovascular system. Treatment at this age should be done with caution to prevent over-treatment complications. Thyroid Screening in Pregnancy is debated as it may lead to over diagnosis. The American Thyroid Association recommends screening for women with risk factors for thyroid disease. Low T3 Syndrome occurs in stressful conditions such as surgery or infection. In these conditions, thyroid hormone measurement is not generally recommended unless there is suspicion of thyroid disease. Understanding these physiological changes is essential for accurate interpretation of tests and preventing incorrect diagnoses.

O32

Common Interferences in Thyroid Hormone Assays

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Thyroid function tests are prone to various interferences that can lead to misinterpretation, especially when results do not align with clinical presentation.1) Biotin, commonly taken as a supplement for hair, skin, and nails or in high doses for neurological conditions, interferes with immunoassays that rely on biotin-streptavidin binding. In sandwich assays like TSH, excess biotin can cause falsely low results, while in competitive assays (free T3 and T4),it can lead to falsely high levels. TRAb levels may also be elevated, mimicking Graves' disease. Stopping biotin 48–72 hours before testing is recommended. 2)Macro-TSH is a high molecular weight complex formed by TSH binding to IgG autoantibodies. It is detected by standard assays but lacks biological activity. It typically presents as isolated elevated TSH with normal T3 and T4 in asymptomatic patients. Confirmation requires techniques like PEG precipitation or gel filtration chromatography, though the latter is less accessible.3) Heterophilic antibodies, especially human anti-mouse antibodies (HAMA), can bind assay antibodies nonspecifically, leading to false results—most commonly falsely elevated TSH. Though modern assays include blocking agents, interference may still occur, especially in individuals exposed to animal proteins or certain immunotherapies. Awareness of these interferences is crucial for accurate diagnosis and avoiding unnecessary treatment.

O33

Evaluation of Autoimmunity and Thyroid Cancer Markers

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Autoimmune thyroid diseases are often evaluated by using antibodies, especially anti-thyroid peroxidase (TPOAb) and anti-thyroglobulin (TgAb). Thyroid autoimmunity, particularly Hashimoto's thyroiditis (HT), closely links to papillary thyroid carcinoma (PTC), with studies showing elevated thyroid-stimulating hormone (TSH) and thyroid autoantibodies (TPOAb, TgAb) as risk factors. Elevated TSH levels independently predict malignancy risk, often coexisting with autoimmune thyroid inflammation that may promote tumor growth. TPOAb demonstrates particularly strong predictive value, with levels >30 IU/mL increasing thyroid cancer risk in some studies. In follow-up monitoring of differentiated thyroid cancer, serum thyroglobulin (Tg)remains the primary tumor marker, but its reliability is compromised by TgAb interference. Approximately 20–25% of patients with differentiated thyroid carcinoma (DTC)exhibit TgAb at diagnosis, which can interfere with Tg measurement, leading to falsely low or undetectable Tg levels, especially when using immunometric assays. This interference complicates the interpretation of Tg as a tumor marker. Persistent or rising TgAb levels post-thyroidectomy are clinically significant. A decline in TgAb levels over time, particularly a reduction of more than 50% within the first year post-treatment, is associated with a low risk of recurrence. Conversely, stable or increasing TgAb levels may indicate residual disease or recurrence, necessitating further evaluation with imaging modalities such as neck ultrasound or cross-sectional imaging. Current guidelines recommend combining TSH monitoring with TgAb assessment and ultrasound surveillance, particularly for patients with autoimmune thyroid history. While TgAb persistence often correlates with lymphocytic thyroiditis, rising titers may indicate recurrence, necessitating advanced imaging.

Clinical Implications of Antinuclear Antibodies and Anti-Phospholipid Antibodies: A Comprehensive Review

O34-O37

O34

Summary of Diagnostic Strategies for ANA & APA

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This presentation outlines diagnostic approaches for detecting antinuclear antibodies (ANA)and antiphospholipid antibodies (APA), emphasizing their clinical relevance, testing methodologies, and interpretation. ANA Testing ANA is a hallmark of connective tissue diseases (CTDs), including systemic lupus erythematosus (SLE), Sjögren's syndrome, and systemic sclerosis. However, ANA positivity can occur in non-CTD conditions (e.g., autoimmune hepatitis, infections, malignancies) or healthy individuals (e.g., elderly, pregnant women). Testing is recommended only for patients with CTD symptoms, suspected autoimmune hepatitis, or juvenile idiopathic arthritis (JIA)follow-up. Indirect immunofluorescence (IIF)on HEp-2 cells is the gold standard due to its sensitivity, though labor-intensive and prone to variability. Solid-phase assays (ELISA, ALBIA) lack sensitivity for initial screening. ANA titers (≥1:160) and fluorescence patterns (11 essential nuclear/cytoplasmic patterns) aid differentiation between healthy individuals and CTD patients. Serial ANA monitoring is discouraged, as titers do not correlate with disease activity. Negative/low-positive ANA cases may require repeat testing if CTDsymptoms persist. Specific autoantibody testing (e.g., anti-SS-A, Jo-1) is recommended based on clinical suspicion, even with negative IIF. Antiphospholipid Antibodies (APA) & Syndrome (APS) APS is defined by clinical manifestations (thrombosis, pregnancy morbidity) with persistent APA. Laboratory criteria include lupus anticoagulant (LAC), anticardiolipin (aCL), and anti-beta2 glycoprotein I (anti-β2GPI) antibodies. Testing requires confirmation ≥12 weeks post-initial positive result to exclude transient causes (infections, medications). LAC testing involves a 3-step process but is affected by anticoagulants, unlike aCL/anti-β2GPI. Risk stratification depends on antibody profiles: high-risk (persistent LAC ± moderate/high aCL/anti-β2GPI), moderate-risk (negative LAC with high-titer aCL/anti-β2GPI), and low-risk (low-titer antibodies). Triple positivity (LAC, aCL, anti-β2GPI) correlates with severe complications. APA may also occur transiently or in infections, malignancies, or autoimmune diseases but lacks diagnostic significance without APS criteria. Conclusion Accurate ANA/APA testing requires context-driven strategies, emphasizing clinical correlation, appropriate methodologies, and repeat testing for APA confirmation. Proper interpretation reduces misdiagnosis and guides risk assessment in autoimmune and thrombotic disorders.

O35

From Detection to Disease: The Role of ANA Types in Predicting Autoimmune Diseases and Their Progression

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The antinuclear antibody (ANA) test is a fundamental serologic tool in the initial evaluation of systemic autoimmune rheumatic diseases (ARDs), particularly systemic lupus erythematosus (SLE). Although ANA positivity is a common feature of most systemic ARDs, it is not disease-specific and must be interpreted in the appropriate clinical context, supported by further immunologic assays. High ANA titers(e.g.,>1:320) are more likely to be clinically significant, especially in SLE; however, the absolute titer does not correlate with disease severity or prognosis. Importantly, ANA positivity can also be observed in healthy individuals and asymptomatic first-degree relatives of patients with autoimmune diseases, limiting its specificity. Additionally, rare cases of ANA-negative SLE have been documented. The pattern of ANA staining and the presence of specific autoantibodies—such as anti-dsDNA and extractable nuclear antigens (ENA)—provide greater diagnostic specificity. While not all autoantibodies are exclusive to a single disease, comprehensive autoantibody profiling enhances diagnostic accuracy and prognostic assessment without compromising sensitivity or specificity. In conclusion, ANA testing should be complemented by specific autoantibody assays, including anti-dsDNA and ENA panels, as part of a structured diagnostic workup in patients suspected of having systemic autoimmune disorders.

O36

Antiphospholipid Antibodies: Diagnostic Value, Prevence, and Clinical Impact in Autoimmune Disease

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Antiphospholipid antibodies (aPLs), including lupus anticoagulant (LA), anticardiolipin antibodies (aCL), and anti-β2-glycoprotein I (anti-β2GPI), are key biomarkers in antiphospholipid syndrome (APS), a prothrombotic autoimmune disorder. Their clinical significance in predicting thrombotic events varies based on antibody type, titer, and persistence. LA demonstrates the strongest association with thrombosis, particularly venous thromboembolism (VTE)and arterial events (e.g., stroke) and is considered the most predictive single marker. High-titer IgG aCL and anti-β2GPI antibodies (≥40 GPL/MPL) also correlate with increased thrombotic risk, especially arterial events, though with lower specificity than LA. IgM isotypes are less clinically significant. Triple positivity (LA, aCL, and anti-β2GPI) confers the highest thrombotic risk, with a 30–50% recurrence rate despite anticoagulation. Persistent antibody positivity (>12 weeks apart) is critical for diagnosis and risk stratification, as transient aPLs (e.g., from infections) rarely predict thrombosis. Additionally, non-criteria antibodies (e.g., anti-phosphatidylserine/prothrombin) may enhance risk assessment in seronegative APS. Clinically, LA and triple positivity guide long-term anticoagulation decisions. Patients with these profiles often require lifelong warfarin over direct oral anticoagulants (DOACs), which are less effective in APS. However, isolated low-titer aCL/IgM antibodies may not warrant aggressive therapy, emphasizing the need for personalized management. Beyond thrombosis, aPLs predict obstetric complications (e.g., recurrent miscarriage), though anti-β2GPI antibodies are more specific for placental insufficiency. Emerging evidence links aPLs to microvascular thrombosis and non-thrombotic manifestations (e.g., cognitive dysfunction), broadening their clinical relevance. In conclusion, LA and high-titer IgG aPLs, particularly in combination, are robust predictors of thrombosis, guiding therapeutic intensity. Standardized testing, risk stratification, and monitoring are essential to mitigate morbidity in APS patients.

O37

Autoantibodies in Pathophysiology of Autoimmune Diseases: ANAs & APLAs

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Many physicians and laboratorians recognize the autoantibodies merely as diagnostic, prognostic or monitoring tools in their routine practice, but in fact, these self-made anti-self molecules, besides the contributing as a diagnostic/classification criterion, have different impacts on the body systems of the human patients affected by autoimmunity or even autoimmune disease. Pathophysiologically, the autoantibodies may have or may not have any etiologic role in the development of autoimmune disorders and hence, may cause a variety of immunopathologic lesions such as cell (or cell matrix)damage and inflammation through complement activation, antibody mediated cell cytotoxicity(either in the form of cell lysis, cell stimulation, or cell paralysis),immune complex deposition in critical tissues and organs, etc., generally based on the very 4 (nowadays at least 8!) common hypersensitivity mechanisms, except types I and IV hypersensitivity reactions. Interaction of autoantibodies with soluble, non-cell-bound molecules (e.g. plasma proteins) may also exert some noxious outcomes. Autoantibodies usually develop after a breakdown in immunologic tolerance(either central or peripheral) against self antigens (e.g., in inflammatory conditions, post-viral non-specific polyclonal activation, via molecular mimicry, etc.),but there are other conditions(especially factors related to age, sex, genetics and environmental) which compromise the regulatory mechanisms of self tolerance and may result in the production of autoantibodies, even in asymptomatic healthy appearing individuals ,even in non-relatives of patients with autoimmunity. However, the real underlying mechanisms remain unclear. A variety of autoantibodies, including different types of anti-nuclear antibodies(or ANAs, which comprise about tens of characterized antibodies against around hundred identified antigens in the eukaryotic nucleus, especially anti-double stranded DNA and anti-smith antibody)and different types of anti-phospholipid antibodies(or APLAs which include three main types of anti-cardiolipin, anti-beta 2 glycoprotein I, and lupus anticoagulant)cause different pathologic events in autoimmune diseases, and will be explained in detail during the lecture. They will be reviewed in comparison and contrast regarding the aspects of titer, isotype, target autoantigen, function and clinical correlation. Laboratory investigations are also to be discussed!

Keywords: Autoantibodies, Diagnosis, Prognosis, Monitoring, Hypersensitivity, Autoimmunity, Laboratory Tests

Emerging Fungal Infections and Diagnostic Updates in Invasive Mycoses

O38-O43

O38

Pancoast Syndrome Secondary to Invasive Aspergillosis: A Clinical Case Report

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Pancoast syndrome, typically associated with apical lung tumors, is a rare clinical entity when caused by invasive fungal infections. We present a case of a 52-year-old male with a 10-year history of poorly controlled diabetes mellitus, who presented with severe left shoulder pain, weakness, and radiculopathy consistent with Pancoast syndrome. Imaging revealed a left apical lung mass with adjacent rib destruction and brachial plexus involvement. Further evaluation identified a history of recurrent infections, including parotid and prostatic abscesses, both culture-positive for Aspergillus fumigatus. Histopathological examination of the lung lesion confirmed invasive aspergillosis. The patient was managed with systemic antifungal therapy (Amphotericin B and voriconazole) and adjunctive pain control, resulting in gradual clinical improvement. This case highlights the importance of considering invasive fungal infections, particularly in immunocompromised hosts, as a rare but treatable cause of Pancoast syndrome. Early diagnosis and targeted antifungal therapy are crucial for favorable outcomes in such complex presentations.

Keywords: Pancoast Syndrome, Invasive Aspergillosis, Diabetes Mellitus

O39

New Approaches in Laboratory Diagnosis of Invasive Fungal Infections

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Invasive fungal infections (IFIs) pose significant diagnostic challenges due to their high morbidity and mortality, requiring advances in laboratory diagnosis. Conventional diagnosis approaches including histopathology and culture on the specimens obtained from the normally sterile areas are enough for the definitive diagnosis of IFIs however, in many cases they are not feasible. So, the reliance on traditional methods hampers early diagnosis of infection. Recent developments have focused on enhancing traditional methods and introducing innovative technologies. Key approaches include the use of non-culture-based methods are promising. Matrix-assisted laser desorption/ionization time-of-flight is promising in the accurate identification of fungal species such as Aspergillus and Fusarium from clinical samples. Additionally, sero-diagnosis such as the galactomannan (GM) assay and beta-D-glucan (BD) testing are other useful approaches. These assays facilitate early diagnosis by detecting specific fungal components in serum or bronchoalveolar lavage fluid, although variability in sensitivity and specificity remains a concern. Molecular techniques, including PCR and next-generation sequencing (NGS), allow for rapid detection of fungal pathogens directly from clinical specimens, potentially improving diagnosis timelines significantly. In addition, point-of-care testing technologies are being developed to simplify the diagnostic process. Lateral flow devices for cryptococcal antigen detection represent this trend, providing rapid results that can offer timely treatment decisions. Overall, these advances represent a shift toward more accurate and efficient diagnostic strategies for IFI, ultimately aiming to improve patient outcomes and reduce the economic burden associated with these infections.

Keywords: Diagnosis, Non-Culture-Based Methods, Point-of-Care Testing Technologies, Invasive Fungal Infections

O40

Importance of Prompt and Accurate Diagnosis of Invasive Candidiasis

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The incidence and prevalence of invasive candidiasis (IC) are influenced by various factors, including geographical region, healthcare systems, patient demographics, and environmental conditions. The burden of the disease is significantly higher among hospitalized patients worldwide, (~100 per 100,000 admissions). Patients in the ICU are particularly affected, with incidence rates reaching 5.5 to 7 episodes per 1,000 ICU admissions. Neonates, especially preterm infants, are also at a greater risk for candidemia, with rates of up to 12 cases per 100,000 births. While most available data focus on candidemia, the incidence of invasive abdominal candidiasis (which may occur with no or only transient candidemia) is likely much higher. Candida species are responsible for approximately 3% of bloodstream infections (BSIs) and are the fourth most common cause. Although IC can be diagnosed clinically, it is often discovered during autopsy. Early diagnosis is crucial, as specific antifungal treatments can be effective. The overall sensitivity of blood cultures in diagnosing invasive candidiasis is around 50%, with a limit of detection (LOD) of ≤1 CFU/mL. Non-culture diagnostic tests for IC, including Manan antigen detection, anti-manan antibody testing, β-D-glucan detection, and PCR assays, can identify a greater number of patients with IC when used and interpreted correctly. These methods can help better direct antifungal therapy for patients most likely to have IC, reducing the reliance on empirical treatments and the emergence of antifungal resistance. In this review, we will discuss the importance of early and timely diagnosis of invasive candidiasis, highlighting the advantages and limitations of each diagnostic method.

Keywords: Invasive Candidiasis, Diagnosis

O41

Emerging and Reemerging Fungal Diseases

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Background: Emerging fungal infections may be used to denote infections that have newly appeared in the population or those that are rapidly increasing in incidence or geographic range. Also Re-emerging fungal disease have been known for some time, had fallen to such low levels that they were no longer considered public health problems and are now showing upward trends in incidence or prevalence worldwide or have appeared in areas where they were not previously found. The epidemiology of these infections has changed during the past 20 years. The incidence has increased, and the population of patients at risk has expanded to include those with a broad list of medical conditions, such as: solid-organ transplantation, hematopoietic stem cell transplantation (HSCT), cancer, receipt of immunosuppressive therapy, AccquiredImmuno Deficiency Syndrome (AIDS), premature birth, advanced age and major surgery. The aim of this study was to provide a brief presentation about emerging and re-emerging fungal disease in Iran. Methods: In this study, we checked out available literatures concerning emerging and re-emerging fungal disease in Iran. Databases searched were MEDLINE (PubMed), Web of Science, Scopus, Science Direct and the Scientific Information Database (SID). Results: Zygomycosis and aspergillosis are emerging fungal disease and Candidiasis due to non-albicans Candida species, trichosporonosis, cryotococcosis, malasseziasis (due to non-furfur species) and infection due to saprophytic moulds such as Fusarium spp, Alternaria spp and Curvulariaspp are emerging disease in Iran, over the past 20 years. Conclusion: The discovery of “new” species and the widening of geographic distributions of previously recognized organisms emphasizes that our understanding of fungal epidemiology is critically dependent on global collaborative efforts. Changes in hosts susceptible to infection, practice patterns, and diagnostic methods, and possibly changes in climatic influences, will likely continue to alter the epidemiology for years to come.

Keywords: Emerging Fungal Disease, Reemerging Fungal Disease, Iran

O42

Challenges in Diagnosis of Misdiagnosed Laboratory Cases

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Clinical manifestations of fungal and non-fungal diseases are not always helpful to make definite diagnosis. Many Fungi are able to develop similar clinical Manifestations e.g. fungal infection of nail which could not be differentiated by type of the fungus (dermatophyte or non- dermatophyte). On the other hand, one species of a dermatophyte can produce different clinical pictures. In addition, the clinical presentation of mycotic infections may mimic other diseases caused by bacteria, viruses or parasites. Also, many patients self-medicate or use inappropriate drugs to change the primary clinical picture of their disease. In this presentation several fungal infections mimicking other diseases and vice versa are discussed. In addition some misdiagnosed cases are presented. To investigate different mycotic diseases mimicking non fungal skin diseases, more than 10 cases are included in this study. Some of the patients had history of 3-4 years' misdiagnosis. Among those, several patients were followed up until definite diagnosis obtained and proper treatment performed. The data and information about several misdiagnosed cases with skin lesions were obtained. With their consent, pictures from their skin lesions also were obtained for follow up and fungal disease education. Definite diagnosis is not possible if clinical history of the patient is unknown. Obtaining a perfect and accurate clinical history from such patients in addition to exact sampling and perfect Lab. diagnosis is strongly recommended.

Keywords: Clinical Picture, Mycotic Disease, Mimicking Diagnosis, Iran

O43

Candida Auris in Healthcare Settings: Where Does It Come From? Why Should We Worry?

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Understanding the leading causes of mortality worldwide is imperative for improving human lifespan and quality. Humanity has been afflicted historically by the emergence and spread of infectious diseases, which remain a leading cause of death globally. According to data published by the World Health Organization in "The Top 10 Causes of Death, 2020," as of 2019, lower respiratory infections resulted in 2.6 million deaths worldwide. To put these numbers in perspective, the Centers for Disease Control and Prevention (CDC) ranked COVID-19 as 3rd new leading cause of death in the U.S., where it claimed 416,893 lives as of 2021. The COVID-19 outbreak global fatality rate was reported to be at least 3 million while tuberculosis claims approximately 1.5 million livesyearly. Malaria was responsible for 619,000 global deaths in 2021 alone. Fungal infections (FIs)are major public health threats acknowledged as medically relevant as recently as the 1980s, potentially due to their mild health impact on humanity. The most common fungal infections affect the skin and mucosa, with skin fungal infections afflicting close to 1 billion people. Invasive mycoses continue to be increasingly correlated to high morbidity and mortality rates globally. The emerging multidrug-resistant pathogenic yeast Candida auris is associated with high morbidity and mortality among immunocompromised patients, and COVID-19 hospitalized patients who have been admitted to intensive care units(ICUs).Transmission of C.auris is facilitated by its ability to colonize the skin and other body sites and persist on surfaces and medical devices for prolonged periods. This species has rapidly spread to six continents and has emerged as a fungal pathogen of major concern, being recognized as an important cause of nosocomial outbreaks of invasive candidiasis in Asia, Europe, Latin America, South Africa, and the U.S. Candida auris is now classified as an urgent threat to public health by the U.S Centers for Disease Control and Prevention. The Global Antimicrobial Resistance Surveillance System (GLASS)of WHO has highlighted the need for global surveillance schemes to identify and monitor antifungal resistance in Candida. Currently, no specific preventive and therapeutic approach against C. auris infection exists. Hence, there is significant interest in enhancing our understanding of this emerging pathogen to understand its environmental source and transmission routes to prevent disease and improve patient outcomes. Six distinct clades of C. auris were identified initially, including the South Asian Clade (I), the East Asian Clade (II), the South African Clade (III), and the South American Clade (IV), the fifth clade (V) and recently sixth clade have been described. Remarkably, colonization by C.auris of the skin or mucosa occurs before the invasion and systemic infection, and colonization may be a significant reservoir for cross-contamination. Researchers must thoroughly understand the public health implications of this multidrug-resistant pathogen. This review highlights the concerns associated with fungal infections as neglected diseases and deep dives into the fascinating yet enigmatic profile of Candida auris. Ultimately, our discovery is a reminder that much about C.auris remains to be learned and underscores the need for vigilance in areas where C.auris has not yet emerged.

Keywords: Candida auris, Multidrug-Resistant, CDC, WHO

Expert Talks

O44-O47

O44

Expert Talks

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This panel features three expert speakers who explore various aspects of modern technologies and quality assurance in medical diagnostic laboratories. Dr. Mehrad Vanki, in his presentation titled "Modern Technologies in Medical Laboratories: Threat or Opportunity?" introduces the most significant emerging technologies, including artificial intelligence, full automation, nanosensors, and advanced information systems. While highlighting the benefits of these technologies—such as increased speed, accuracy, and efficiency—he also addresses challenges like high costs, technical complexity, and potential job displacement. Dr. Reza Mohammadi, speaking on "Quality Assurance of Lab Results: Challenges and Solutions," emphasizes the importance of strict quality control processes. He outlines obstacles such as limited access to reliable testing kits and economic constraints, proposing solutions like enhanced training, revised pricing structures, and other measures to improve quality. Next, Dr. Hassan Bayat, in his lecture "Hemoglobin A1C: Harmonization, Standardization, and Quality Requirements," discusses the role of this test in diabetes management. He underscores the need to align results with international standards such as IFCC and NGSP to ensure accuracy and reliability. This panel provides a comprehensive overview of the role of technology and quality assurance in advancing laboratory services.

O45

Quality Assurance of Examination Results: Challenges and Solutions

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Ultimate aim of a medical laboratory is reporting examination results having acceptable accuracy for clinical applications. For quality assurance of these results, prerequisite requirements are: (1) Selection of appropriate approved measurement kit, (2) Verification of characterstics of this measurement kit, and monitoring its performance. For doing these actions, medical laboratory faces many challenges, which can be placed in three groups: (1) accessibility to appropriate approved measurement kit, (2) Cost-benefit ratio of procurement and using this kit, and (3) Doing right verification and monitoring processes and procedures right. In Iran, because of existing political and economic problems, medical laboratory could not have important active role in solving the first two challenges. In contrast, medical laboratory role in doing right thing right, is paramount. For this purpose, qualified, trained and with positive attitude personnel, and also appropriate software, are required. The most important challenges are in context of (1) selecting allowable errors, (2) selecting processes and procedures, and (3) data analysis and interpretation of the derived results. Unfortunately, in many cases, professionals (1) have not good understanding of allowable error and correct selection or calculation of them, especially in modified condition against basic condition; (2) do not use appropriate procedures for verification and monitoring; and (3) do not use correct analysis and interpretation. Solutions are: (1) Improving the political and economic situation in order to accessibility to appropriate measurement kits, along with improving cost-benefit ratio through correcting tariffs and improving employee attitude by improving their wages; (2) Making fundamental changes in university education to improve educational content of disciplines related to medical laboratory, especially quality assurance and quality management; and (3) Creating laboratory networks having central laboratories for performing examinations and satellite laboratories for mainly collecting specimens, along with supplying resources (personnels, equipment, materials, and software) for doing the right thing right.

Keywords: Quality Assurance, Right thing, Challenges, Software

O46

New Technologies in Medical Laboratory Threat or Opportunity

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Medical laboratories have been widely influenced by new technologies and advanced equipment. These developments have increased the accuracy, speed, and quality of services, but at the same time they have also brought challenges. The most important new technologies and equipment are listed along with their advantages and disadvantages: 1-Artificial Intelligence (AI) and Machine Learning Advantages: Increased accuracy in diagnosis / Rapid analysis of large volumes of data / Reduced human error / Improved clinical decision-making Disadvantages: Need for accurate and abundant data for training / Possibility of errors in the event of incomplete or incorrect data / Complexity in implementation and need for specialized knowledge / Concerns about the transparency of algorithms and liability for errors2. Total Laboratory Automation (TLA) Application: Transport, load, prepare, and analyze samples automatically Advantages: Increased speed of testing / Reduced need for human resources / Improved quality control / Reduced contamination and sampling errors Disadvantages: Very high cost of purchase and maintenance / Need for large physical space / Reduced job opportunities at lower levels / Need for specialized repairs and support 3. Digital Pathology Systems 4. High Technology for Molecular Diagnosis & genetics 5. Nano-sensors 6. Advanced Information Systems (LIS and modern HIS)7. Next-generation Point-of-Care Testing (POCT) Equipmentsummary: New technologies in medical laboratories have not only improved the quality of services, but also paved the way for more accurate, faster, and personalized medicine. However, the success of using these technologies requires investment in human resource training, technological infrastructure, and change management.

O47

Hemoglobin A1C: Harmonization/ Standardization, Analytical Performance Specifications

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Nowadays, diabetes is one of the most common non-contagious diseases that if diagnosed late and/or not controlled appropriately, would lead to various clinical, economic, and psychotic outcomes. Hemoglobin A1C (HbA1C) test is of the important tests for screening, diagnosis, and controlling diabetes. To provide clinicians and patients with the HbA1C results that is helpful, assaying this measurand in clinical laboratories must (a) be harmonized/standardized against approved international reference procedures/materials, and (b) meet analytical performance specifications. Over this presentation, the process of harmonization/standardization of HbA1C test as well as its analytical performance specifications, especially according to the IFCC, will be discussed.

Genomics and Transcriptomics: The Powerful Technologies in Precision Medicine

O48-O51

O48

The Challenges and Potential in Developing miRNA as Biomarkers and Therapeutic Tools (Small RNAs And the Big Picture in Liver Disease)

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MicroRNA as one of the most important components of transcriptome are small non-coding RNA which have key roles in post-transcriptional regulation of gene expression. Our group have previously demonstrated a microRNA signature associated with successful liver regeneration in auxiliary liver transplantation (ALT). We have demonstrated in an in vitro model that this miRNA signature induces cell proliferation, a key component of regeneration. We aim to develop this signature into a clinical biomarker to predict outcome in liver disease and investigate its potential role as an anti-cancer agent. In this presentation, I demonstrate that there is a circulating microRNA-based regeneration linked signature which is associated with improved clinical outcomes for patients with acute liver failure (ALF) from acetaminophen (APAP) toxicity and hepatitis C. We incorporated this signature into a prognostic model with clinical variables and demonstrated that it outperformed conventional clinical models in predicting mortality in APAP ALF. Using a murine model of liver cancer supported by in vitro studies; we were able to demonstratethat regeneration-linked microRNA influenced tumourbehaviour with complete growth inhibition induced across multi-lineage cancer. In conclusion, we have demonstrated the potential prognostic utility of circulating microRNA across liver disease which require further exploration to improve conventional prognostic models. The potential role of regeneration-linked microRNA as an anti-cancer represents a novel target for the development of a therapeutic agent in an area of need.

O49

Metabolomics in Medical Diagnosis: Newborn Screening for Inherited Metabolic Disorders by FIA-MS/MS as a Case Study-Current State and Challenges in Doing Good and Avoiding Harm

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Monitoring of patients with inherited metabolic disorders (IMDs)using dried blood spot (DBS)specimens has been routinely used since the inception of newborn screening (NBS)for phenylketonuria in the 1960s.The introduction of flow injection analysis tandem mass spectrometry (FIA–MS/MS) in the 1990s facilitated the expansion of NBS for IMDs. This has led to increased identification of patients who require biochemical monitoring. Monitoring of IMD patients using DBS specimens is widely favoured due to the convenience of collecting blood from a finger prick onto filter paper devices in the patient's home, which can then be mailed directly to the laboratory. Ideally, analytical methodologies with a short analysis time and high sample throughput are required to enable results to be communicated to patients in a timely manner, allowing prompt therapy adjustment. The advancement in analytical technology has led to the development of numerous assays to detect analytes at low concentrations(pmol/L)in DBS specimens that can be used to monitor IMD patients. In this review, we discuss the pre-analytical, analytical and post-analytical variables that may affect the final test result obtained using DBS specimens used for monitoring of patients with an IMD. Additionally, we discuss the current state & Issues of FIA-MS/MS that have been introduced into NBS for IMDs. We will consider the balance required to harness the potential of this method whilst maintaining the benefits and reducing the risks for harm associated with all screening.

O50

Innovative Approaches in Genomics and Transcriptomics for Precision Medicine

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Advancements in genomics and transcriptomics are fundamentally reshaping the landscape of precision medicine. With the emergence of next-generation sequencing technologies and large-scale molecular profiling, clinicians and researchers now have powerful tools to understand disease mechanisms at the genetic and transcriptional levels. This presentation will explore how integrative analyses of genomic variants and gene expression data are being used to develop personalized diagnostic and therapeutic strategies. Special attention will be given to the role of transcriptomics, particularly RNA sequencing, in revealing gene activity patterns that are critical for distinguishing disease subtypes and predicting treatment response. The clinical application of transcriptomic biomarkers is opening new pathways for tailored interventions in oncology, rare diseases, and immune-related disorders. While these technologies offer great promise, the translation of omics data into clinical settings presents several challenges, including issues related to data interpretation, standardization, and regulatory oversight. This talk will provide an overview of the scientific, clinical, and ethical dimensions of applying genomics and transcriptomics in precision medicine, with reflections on the future of personalized healthcare in Iran and beyond.

O51

The Evolution of Genomics and Personalized Medicine and Its Path in Iran

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The Human Genome Project (HGP), completed in 2003, was a landmark in human genetics that provided the first complete human genome sequence. It identified approximately 20,000–25,000 genes, uncovered the complexity of gene expression, and demonstrated that 99.9% of human DNA is shared among individuals, with just 0.1% accounting for individual variations. These discoveries laid the groundwork for modern genomics and personalized medicine. The advent of next-generation sequencing (NGS) technologies led to the development of large-scale genome variation databases such as 1000 Genomes, UK Biobank, and Genome Aggregation Database. These databases have played a pivotal role in linking genetic variants to disease; however, Middle Eastern populations, particularly Iranian, remain significantly underrepresented. To address this gap, the Iranome Project (www.Iranome.com or www.Iranome.ir) was launched in 2016 to provide a comprehensive Iranian genomic variations catalog. Samples were collected across the country from above 30-year-old healthy, unrelated volunteers of Iranian ancestry, based on a routine blood and urine test, clinical examination, and ancestry verification up to three generations. The project was conducted in two phases. Phase I included 800 individuals from eight Iranian ethnic groups: Arabs, Azeris, Balochs, Kurds, Lurs, Persians, Persian Gulf Islanders, and Turkmen. Phase II added 400 individuals from four additional Iranian ethnicities: Gilaki, Mazani, Sistani, and Zoroastrian. In total, over 1.5 million variants were identified, 308,311 (19.6%) of which were novel. Remarkably, only 0.6% of these novel variants displayed counterparts with the Greater Middle East Variome Project, highlighting Iran's unique genetic landscape. The Iranome database substantially enhances molecular genetic diagnostics, particularly for rare disorders in Iran. Moving from concept to the realization of Personalized Medicine in Iran needs major investments in expanding genomic infrastructure, such as more comprehensive local genomic databases, and also requires a more integrated pathway, facilitating dialogue and cooperation for capacity-building and integration of genomic medicine in Iranian healthcare system infrastructure.

Harmonization of Clinical Laboratory Test Results

O52-O56

O52

Harmonization of Medical Laboratory Test Results

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Despite the serious problems in standardization of different measurement procedures which in most cases may make it impossible to do it, harmonization of different measurement procedures of a given measurand in order to produce equivalent results, is possible. Lack of harmonization among different measurement procedures (MPs) of an analyte is due to presence of systematic error which is express as bias. Depending on how to estimate bias, it could be addressed at two levels, each one with different responsible for its identification and mitigation: levels I and II, with responsibility of kit manufacturer and laboratory, respectively. According to ISO 15189:2022, When in a medical laboratory either different methods or equipment, or both, are used for an examination, and/or the examination is performed at different sites, a procedure for establishing the comparability of results for patient samples throughout the clinically significant intervals shall be specified. Reporting unequivalent results which may be due the presence of bias in different MPs of a given measurand, can result in wrong medical decision making and ultimately harm to patient. So, inter-laboratory and intra-laboratory harmonization of different MPs of a given measurand have critical importance for patient safety. In this regard, AI-driven harmonization could be a transformative approach.

Keywords: Harmonization, ISO 15189, Patient Safety, AI

O53

Harmonization Between Different Measurment Procedures of a Measurand: Who Is Responsible? Laboratories or Manufacturers

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Lack of harmonization among different measurement procedures (MPs) of an analyte is due to presence of systematic error which is express as bias. In optimal condition, bias is determined against a reference measurement procedure (RMP) or certified reference material (CRM) which is necessary for MP standardization. In most conditions, RMP or CRM is not available and bias of a given MP is determined against results of other MPs for the same measurand, which is called relative bias and its estimation and mitigation is necessary for harmonization of different MPs of the same analyte. In any case, using commutable samples, such as human fresh serums, is necessary for estimating relative bias. Participation in external quality assessment (EQA) or Inter-laboratory comparison (ILC) programs, is a common way for estimating bias. In these programs, sample are usually noncommutable. So, it isn't possible to estimate relative bias among different MPs of a measurand, and only estimation of a laboratory MP relative to peergroup target value is possible. Depending on how to estimate bias, it could be addressed at two levels, each has a different responsible. At level I, bias may be determined against RMP (or CRM) or other MPs of the same measurand, which can be called sublevels Ia and Ib, respectively. Manufacturers are responsible for both sublevels. Level II has three sublevels. Sublevels IIa is against peer group target value, IIb is for different MPs of a measurand in a laboratory, and IIc is seen within a MP. In any case, Laboratory is responsible.

Keywords: Harmonization, Standardization, Measurement Procedure, Bias

O54

One Patient, One Result: AI-Driven Harmonization for Patient Safety in Multi-Lab Testing

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In contemporary healthcare, patients often undergo diagnostic tests at multiple laboratories, which can lead to discrepancies in test results due to variations in methodologies, reference ranges, and reporting formats. These inconsistencies compromise clinical decisions and patient safety. AI-driven harmonization presents a transformative approach to addressing this challenge by standardizing lab results across diverse facilities. Laboratory discrepancies—stemming from differing instruments and calibration systems—pose risks such as misdiagnoses, delayed treatments, and compromised patient outcomes. To mitigate these risks, AI-powered algorithms can analyze large datasets to correct biases, enable predictive quality control, and facilitate interoperability in lab information systems (LIS). These strategies ensure consistent, accurate, and reliable lab results, directly enhancing patient safety by minimizing diagnostic errors, reducing repeat testing, and improving treatment accuracy. Achieving comprehensive AI-driven harmonization requires adopting global standards, integrating AI into LIS, expanding external quality assessment programs, securing regulatory support, and fostering collaboration among lab professionals. Ultimately, harmonization is about more than aligning numbers—it's about delivering a future where "one patient, one result" becomes a standard, empowering clinicians and safeguarding lives.

O55

Comparability of Examination Results of Different Methods: A Requirement of ISO 15189

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Depending on their necessity or convenience, patients may interface with different laboratories or a large laboratory for testing, which measure same analyte using different methods/instruments. According to the requirements of the ISO 15189 standard, it is necessary that the results obtained from different methods/instruments for the same analyte be comparable to avoid their misinterpretation by the physician by using a common reference range. Although there is no consensus method for the comparability test, various methods such as CLSI EP31, linear regression, and Student's t-test can be used. The laboratory must have a documented procedure for performing comparability testing that properly specifies how to select the most stable method, the type of sample and number of samples required, the test acceptance criteria, and the statistical test used. If there is disagreement between the results, the laboratory should achieve such agreement by performing calibration, modifying the calibration, or changing the line equation (slope and intercept). If such agreement is not achieved through appropriate measures, such differences are further addressed by defining and reporting different reference intervals.

Keywords: Comparability of Results, Different Methods, Same Analyte, Statistical Test

O56

Leveraging Big Data Analytics to Determine Laboratory Reference Intervals, Enhance Test Result Interpretation, and Optimize Clinical Decision Making

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In the ever-evolving landscape of healthcare, the integration of big data analytics has emerged as a transformative force, particularly within the domain of laboratory medicine. This presentation explores the paradigm shift brought about by harnessing the power of big data analytics to revolutionize diagnostic processes, enhance patient outcomes, and streamline laboratory operations. The vast and intricate datasets generated in laboratory medicine present a unique opportunity to extract valuable insights that can significantly impact clinical decision-making. By applying advanced analytics techniques to large-scale datasets, healthcare professionals can uncover patterns, trends, and correlations that were previously hidden, paving the way for more accurate and personalized diagnostics. This presentation will delve into the key aspects of utilizing big data analytics in laboratory medicine, particularly the integration of laboratory datasets to establish comprehensive reference intervals for biomarkers of health and disease. Furthermore, recent advances in application of big data analytics in harmonization of population reference intervals across Canada will be presented and discussed. The impact of big data analytics extends beyond clinical applications to optimize laboratory operations and resource utilization. Big data analytics-driven insights can enhance workflow efficiency, reduce costs, and improve overall laboratory performance. Additionally, it highlights the role of real-time analytics in responding swiftly to emerging public health challenges, such as infectious disease outbreaks. In conclusion, this presentation will emphasize the transformative potential of harnessing big data analytics in laboratory medicine, shaping a future where data-driven insights drive advancements in diagnostics, patient care, and healthcare system efficiency. As the healthcare landscape continues to evolve, the integration of big data analytics stands as a pivotal catalyst in unlocking the full potential of laboratory medicine for improved patient outcomes and enhanced healthcare delivery.

Immunological Testing in Organ and Tissue Transplantation

O57-O62

O57

HLA Typing Methods: The Balance Between Cost and Quality

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Human leukocyte antigen (HLA) typing is a genetic test used to match patients and donors for bone marrow, cord blood, or organ transplants. The HLA system consists of a group of genes that are crucial for the immune system. HLA proteins, also referred to as markers, aid the immune system in distinguishing between cells that are part of the body and those that are foreign. The HLA region contains the most polymorphic genes in the human genome with more than 40,000 common and well-documented alleles is linked to a growing number of disease conditions. Initially, HLA typing relied on phenotypic determination but has now shifted towards molecular methods like real-time PCR, sequence-specific oligonucleotides, and sequencing-based techniques. Numerous studies have highlighted the importance of HLA matching in enhancing patient outcomes post-transplantation. In solid-organ transplants, HLA-DRB1 is crucial for renal organ allocation, while hematopoietic cell transplants prioritize HLA A, -B, -C, -DRB1, DQB1 & DPB1 matching. Like most polymorphic genes in humans, HLA typing is challenging due to allele ambiguity and the pairing of alleles with each other. HLA typing is influenced by knowledge of HLA haplotypes, and rapid typing techniques. NGS as a high-throughput method has reduced testing costs and increased response speed with great accuracy. However, Sanger sequencing remains the gold standard for high-resolution HLA typing. In a new typing method, amplifying the long reads of the HLA region before sequencing can solve phasing problems in analyzing the alleles, although quality control in all typing method is critical.

Keywords: HLA typing, HSCT, Transplantation

O58

Monitoring of Latent and Active Infections Before and After Transplantation

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Patients with compromised immune systems post-transplantation are more susceptible to latent or active pathogens. Viral infections are a significant cause of morbidity and mortality following hematopoietic stem cell transplantation (HSCT) and Solid Organ Transplantation (SOT). The risk of viral infections or reactivation post-HSCT is influenced by the level of immunosuppression and the duration of immunodeficiency. While many viral infections may initially be asymptomatic in affected patients, they can lead to severe complications during periods of immunosuppression. Viruses can also disrupt immune reconstitution after HSCT, affecting graft-versus-tumor effects and graft-versus-host disease. Commonly observed viral infections include CMV, EBV, HSV, VZV, Parvovirus B19, Adenovirus, BK polyomavirus, and respiratory viruses such as influenza and COVID-19. Fungal pathogens can lead to severe morbidity and mortality in HSCT and organ recipients. The incidence of invasive fungal infections in solid organ transplant (SOT) recipients ranges from 3.1% to 42%. The distribution of potential agents varies depending on the transplanted organ and transplant procedure. Invasive fungal infections (IFIs) often occur within 3-6 months post-transplantation and are predominantly caused by yeasts, with Candida species being the most common culprits. Cryptococcus species and other rare yeast fungi can also be responsible for IFIs, while Aspergillosis and zygomycosis are the most frequently reported mold infections. The other cause of fungal infection is Pneumocystis jirovecii (PCP). Patients presenting with PCP may show signs of fever, cough, dyspnea, and in severe cases, respiratory failure. So, in the context of transplantation, monitoring latent and active pathogens before and after the procedure is Inevitable.

Keywords: Infections, HSCT, SOT, Transplantation

O59

The Significance of Killer Immunoglobulin Like Receptor Typing in Hematopoietic Stem Cell Transplantation

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Lifesaving therapy for hematological malignancies can be provided throughallogeneic hematopoietic stem cell transplantation (aHSCT). When no fully matched HLA donor is available, aHSCT can therefore be performed with mismatched unrelated donors (MMUD), umbilical blood cord (UBC) stem cell products, or haploidentical (haplo-) related donors. The role of natural killer cells in early immunity against tumors has been indicated. Cytolytic function are carried out by germline-encoded receptors and their ligands, such as major histocompatibility complex (MHC) molecules. MHC class I molecules are interacted with by two main groups of receptors n NK cells: CD94/NKG2 and immunoglobulin superfamily KIR. KIR have a high degree of polymorphism and are segregated independently of MHC molecules. Studies have indicated the alloreactivity, which happens when NK cells express inhibitory KIR that are not engaged by the MHC class I molecules present on the recipient' cells, triggers GVL without promoting GVHD because of the ability to sense missing self-ligands. The strong connections in clinical studies are encouraging for KIR-related NK alloreactivity use in HSCT especially in donor selection in haplo-HSCT, donor selection in case of the 9/10 MMUD and adjustments of immunosuppressive therapies in all aHSCT. Prospective studies are being conducted on both adults and pediatric populations at the moment. It is worth mentioning that KIR/MHC interactions have also extensively been described in the genetic prediction of cancers and the consequences of solid tumors, pregnancy disorders or viral disease clearance, exploring the potential outcomes and power of this exceptional system that is slowly uncovering its secrets.

Keywords: Natural Killer Cells, KIR, HSCT, MHC

O60

Anti-HLA Antibody Assays in the Modern Era

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Maintaining reliance on a physical cross-match in organ transplant is, in many ways, redundant, and eliminating the physical cross-match in selected transplant scenarios will decrease ischemia time and facilitate organ sharing over greater distances. We recognize that this position will not be universally embraced. Reasons for such reticence may include: local resources, comfort level with interpretation of solid-phase testing, or a general unwillingness for change. Nonetheless, since many transplant programs worldwide are adopting this practice, it is apparent that the widespread utilization of the virtual cross-match is inevitable. Thus, we should advocate for continued education of HLA laboratories and support global standardization of HLA practices. Increased utility of the virtual cross match combined with judicious use of a physical cross match is the new standard. In such modern era, we should consider different discrepancies between the results of both cross-matches. Approximately 20% of cases may have a positive Flowcytometric cross-match and a negative virtual cross-match, with 90% of these cases being positive solely for B cells. Another discrepancy that can be found in approximately 5% of cases is having a negative Flowcytometric cross-match and a positive virtual cross-match. It is important to discriminate between those two scenarios so that educated transplant decisions can be made and appropriate post-transplant therapies can be utilized.

Keywords: Anti-HLA Antibody, Physical Cross-match, Virtual Cross-match

O61

Chimerism: A Key Point in Monitoring of Hematopoietic Stem Cell Transplantation

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Chimerism analysis is a crucial method for monitoring hematopoietic stem cell transplantation (HSCT) in various hematologic diseases. This abstract provides an overview of molecular biology techniques used to study chimerism post-transplantation, focusing on their advantages and disadvantages. Short tandem repeats (STR) analysis via PCR with capillary electrophoresis is a powerful method for differentiation between individuals. However, real-time quantitative PCR (qPCR), digital PCR (dPCR), and next-generation sequencing (NGS) offer higher sensitivity for early chimerism detection. While STR-PCR remains the gold standard, dPCR and NGS may complement or replace it in the future. These advancements provide opportunities for early therapeutic interventions in HSCT patients. In hematologic malignancies, complete replacement with donor-derived hematopoiesis is crucial for a cure. However, in non-malignant disorders (NMD), manifestations can often be controlled with mixed chimerism. This allows for reduced intensity conditioning regimens to limit organ toxicity and increase tolerability, especially in young or high-disease-burden recipients. The levels of donor chimerism needed for disease control vary among NMDs and must focus on correcting individual disorders. Stability of chimerism over a lifespan must be assessed. Factors like recipient immune competence, alloimmunization, and autoimmunity complicate the balance in NMD. Donor factors such as stem cell source and HLA match further complicate treatment. This diversity requires a personalized approach. This perspective discusses the role of chimerism, goals, HCT approach, methods to boost engraftment and graft function, and monitoring recommendations. Knowledge gaps and research needs are highlighted.

Keywords: Chimerism, HSCT, STR

O62

History of HLA Registry in Iran

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Hematopoietic stem cell transplantation (HSCT) has been performed in Iran for 33 years as a curative treatment. Until 18 years ago, only autologous HSCT and transplants from sibling donors were conducted. However, over two decades ago, more than 70% of allogeneic HSCT worldwide were from unrelated donors. In 2007, we established the first HLA Registry in the Middle East and Eastern Mediterranean Region through a proposal presented to Tehran University of Medical Sciences. Subsequently, the importance of the HLA Registry and its establishment was recognized, leading to the establishment of more than 13 centers and 3 Cord Blood Banks in Iran. These facilities, with over 105,000 donors and cord blood units, now provide essential services to patients in the country, is named the Iranian National Stem Cell Donor Network (INSCDN). On the other hand, if the entire population of the country were to be HLA registry members, a compatible donor for 100 percent of patients would still not be found. To address this issue, the World Marrow Donor Association (WMDA) was established 30 years ago to facilitate the exchange of donor information. Iran has been connected to the WMDA since 2010. In recent years, INSCDN was established in Iran, enabling all donor registry information to be accessible through the network and recorded uniquely in the WMDA database. Finding a matching donor reduces complications after HSCT and, conversely, increases overall survival.

Keywords: HLA, HLA Registry, HSCT

Innovative Diagnostic Methods in Clinical Microbiology (Bacteriology)

O63-O67

O63

AI in Clinical Microbiology

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Artificial intelligence is nowadays popular. And use of AI in different fields is now widespread. Use of AI in microbiology and quality control of microbiology is very interesting and we intend to discuss the usage of AI in different fields of microbiology and how this field is progressing.

O64

MALDI-TOF MS Technology in Clinical Microbiology Laboratory

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Matrix-Assisted Desorption/Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS) is well-recognized for the identification of pathogenic bacteria and fungi and the detection of resistance to antimicrobial drugs and widely used in research and clinical fields due to its specificity, speed of analysis, and low cost of consumables. Although MALDI-TOF MS is a very accurate, reproducible, and reliable methodology for microorganism identification, it is important for the laboratory to have a troubleshooting plan in the event of identification failures or unexpected results. MALDI-TOF MS can provide accurate genus- and/or species-level identifications for many microorganisms. However, some closely related species or subspecies cannot be resolved using this method. Laboratories should be aware of these limitations and have procedures in place to manage them. These limitations may improve over time as spectral databases expand and methods for analyzing spectra are refined. Using MALDI-TOF MS in the diagnostic laboratory represents a major advancement in microbial identification capabilities, as well as a vast improvement in turnaround time. However, before implementing MALDI-TOF MS as a routine identification method, the laboratory needs to carefully construct a plan for comprehensive verification study, results reporting and quality assurance requirements.

Keywords: Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry, Microbial Identification, Verification

O65

Translating Creativity into Clinical Utility in Innovative Microbiology

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The threats posed by emerging epidemic prone pathogens, increasing antimicrobial resistance, and the critical need for access to advanced diagnostic technologies at various healthcare levels are the main drivers for the growing demand for innovative microbiological diagnostics. However, the translation of these technologies into clinical and practical applications often encounters significant delays mostly due to high costs related to design and development, extensive clinical validation studies, challenges in demonstrating efficacy through multi-step evaluations. On the other hand necessity for appropriate infrastructure (e.g., electronic platforms) and dependence on skilled and well trained specialists hinder the integration of these technologies to diagnostic systems. Nevertheless, adopting appropriate research and development strategies, along with enhanced interdisciplinary collaboration, could shorten the time for availability of advanced diagnostic technologies and improve healthcare system preparedness against future microbial threats. In this presentation while the existing limitations and implementation challenges are raised, the strategic solutions such as early engagement with end-users, focused clinical trials emphasizing real-world impact on patient management and streamlined regulatory approval processes are addressed to shorten the pathway from scientific innovation to clinically beneficial applications.

Keywords: Innovative Microbiology Diagnostics, Artificial Intelligence, Clinical Utility

O66

Point-of-Care Testing in Clinical Microbiology

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Point of care testing (POCT) including clinical laboratory tests which carried out at near the site of patient care. POCT do not need significant laboratory infrastructures such as equipment or specialized staff in order to be performed. POCT are designed to be easy to use and interpret, and they are often able to deliver a rapid diagnosis results. Clinical microbiology laboratories usually use of time-consuming methods such as Bacterial cultures can take anywhere from 1 to 14 days depending on the suspected pathogen. Cultures for specific pathogens such as Mycobacterium tuberculosis require an incubation period of 6 to 8 weeks for a negative result. Viral culture also very difficult and need special facilities. The transition from viral cultures to molecular methods has significantly improved the time to result but these assays are often batched and performed at specialized laboratories so that the results are not available in a timely manner. The POCT encompasses tests using a broad range of technologies such as: 1. Direct antigen detection. This relates to the capture of antigen using a specific antibody and the detection of this antigen-antibody complex typically using a lateral flow assay or a variant of this technology, for example, rapid influenza or group A streptococcal antigen testing.2. Detection of antibody. These are finger stick assays for the detection of antibody toward specific pathogens.3. Direct detection of pathogen RNA/DNA. Current nucleic acid amplification technologies (NAAT)-based testing directly detects the presence of pathogen genomic material in the patient sample.

Keywords: POCT, Clinical Microbiology

O67

Automation Systems in Microbiology Laboratories

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Automation has revolutionized microbiology laboratories by enhancing workflow efficiency, accuracy, and biosafety. Total Laboratory Automation (TLA) systems integrate hardware and software to automate critical processes, including specimen inoculation, incubation, and result reporting. These systems reduce manual errors and minimize exposure to hazardous biological materials. Moreover, automation facilitates regulatory compliance by ensuring traceability and maintaining digital audit trails. Despite the high initial investment and the need for specialized training and maintenance, automation delivers significant long-term benefits such as increased productivity and cost-effectiveness. The integration of artificial intelligence (AI) and machine learning further optimizes laboratory operations by enabling the automation of complex tasks like antimicrobial susceptibility testing. In conclusion, while automation presents certain operational challenges, its implementation transforms microbiology laboratories by improving precision, safety, and overall efficiency.

Latest Advances in Arbovirus Laboratory Diagnosis

O68-O72

O68

Detection and New Technologies in the Diagnosis of Crimean-Congo Hemorrhagic Fever Virus

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Crimean-Congo Hemorrhagic Fever (CCHF) is a lethal viral disease with pandemic potential, caused by Orthonairovirus of the Nairoviridae family, transmitted through Hyalomma tick bites or contact with blood/bodily fluids of infected animals and humans. With a mortality rate of 5-50% and significant epidemiological potential, it is classified as a priority pathogen by the World Health Organization (WHO). Current diagnostic methods like RT-PCR (for viral RNA detection in acute phase) and ELISA (for antibody detection from day 5-7 post-infection) face limitations such as high costs and inability to identify asymptomatic animal carriers, major challenges for seroepidemiological surveillance. Novel diagnostic technologies based on recombinant nucleoprotein (NP)—characterized by its immunodominance, conservation across isolates, and non-glycosylated nature—serve as ideal antigens for designing multi-species ELISA tests to detect antibodies in humans, livestock, and wildlife. Rapid field tests (LFAs) utilizing gold nanoparticles achieve 95% sensitivity and simultaneous antigen/antibody detection within 20 minutes, enabling point-of-care (POC) monitoring. Electrochemical biosensors with nanomaterials like graphene oxide can identify viral RNA at nanomolar concentrations (LOD: 0.1 pg/µL). Next-generation sequencing (NGS) aids in identifying antigenic motifs (e.g., in Gn/Gc glycoproteins) and tracking viral phylodynamics, supporting epitope-driven vaccine development. Integrating these technologies under the One Health framework—through seroprevalence surveillance in livestock and vector control—alongside diagnostic platform development, is a key strategy to reduce disease burden in endemic regions.

Keywords: Crimean-Congo Hemorrhagic Fever, Orthonairovirus, Diagnostics, Biosensors

O69

Epidemiology of Aedes Mosquito-Borne Diseases in Iran and Worldwide

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Introduction: Aedes-borne diseases, particularly dengue fever, Zika, and chikungunya, are emerging as global health challenges. These diseases are primarily transmitted by Aedes aegypti and Aedes albopictus mosquitoes and are more prevalent in tropical and subtropical region. Methods: This study utilized existing data from international organizations such as the World Health Organization, Centers for Disease Control and Prevention, the Ministry of Health and Medical Education, and scientific papers to examine the prevalence and geographical patterns of these diseases in Iran and other parts of the world. Findings: Results indicate that in recent years, the prevalence of Aedes-borne diseases in Iran has increased. Iran faces challenges such as climate change that may impact the spread of these diseases. Discussion and Conclusion: Given climate change, new areas in Iran and worldwide are expected to emerge as new habitats for Aedes mosquitoes. Additionally, public unawareness and inadequate health infrastructure can lead to increased outbreaks of these diseases. To control and prevent Aedes-borne diseases, comprehensive planning and international collaboration are necessary. Raising public awareness, improving health infrastructure, and conducting further research in this area are of high importance.

Keywords: Aedes, Dengue Fever, Epidemiology

O70

Vectors of Important Arboviruses in Iran

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Introduction: Arboviruses (Arthropod-Borne Viruses) are a diverse group of viruses transmitted to vertebrates, including humans, by mosquitoes, ticks, and sandflies. Various arbovirus diseases, such as Crimean-Congo hemorrhagic fever, West Nile fever, sandfly fever, and dengue fever, have been reported in Iran. Methods: This study draws upon a diverse array of sources, including research projects, articles, and personal studies, complemented by several field visits conducted over the past few years, as well as reports from the Ministry of Health. Findings: Recent studies indicate that invasive species of Aedes mosquitoes, specifically Aedes aegypti and Aedes albopictus, have entered and established themselves in various parts of the country, both in the north and south. These species are known to transmit several diseases, including dengue fever, Zika virus, and chikungunya. Additionally, other vectors of arboviruses found in Iran include Hyalomma and Ixodes ticks, which transmit Crimean-Congo hemorrhagic fever and tick-borne encephalitis, as well as Phlebotomuspapatasi, the vector for sandfly fever. Culex pipiens is also present in many regions and are responsible for transmitting West Nile virus. Discussion and Conclusion: The introduction and establishment of invasive Aedes species in the country, along with the transmission of dengue fever, have created a new situation in the epidemiology of arboviral diseases. Since many of these diseases have no specific medications and effective vaccines, vector control becomes particularly important. While health education and promotion as well as environmental sanitation should not be overlooked, it is recommended to focus on advanced vector control methods, such as the Sterile Insect Technique (SIT) and the use of Wolbachia.

Keywords: Invasive Aedes, Arboviruses, Vector Control

O71

Importance of Arboviruses as a Public Health Threat

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Arboviruses (arthropod-borne viruses) represent a serious and growing global public health threat. These viruses, primarily transmitted through the bites of infected arthropods such as mosquitoes, sandflies, and ticks, can cause a spectrum of clinical syndromes including fever, arthritis, rash, hemorrhage, and neurological involvement. More than 150 of the 500 known arbovirus species are capable of causing human disease, with the most prevalent being dengue (DENV), chikungunya (CHIKV), Zika (ZIKV), and West Nile (WNV) viruses. Effective control of arboviruses faces numerous challenges, the most significant of which include: Transmission cycle complexity: Complex interactions between host, vector, and virus create unpredictable epidemiological patterns. Viral genetic diversity: Viral mutations can rapidly enhance transmissibility or pathogenicity. Diagnostic limitations: Reliable laboratory methods for accurate diagnosis in symptomatic patients remain limited. Lack of specific treatments: No approved antiviral drugs exist for most arboviruses. Inadequate vaccine coverage: Vaccines are only available for a handful of arboviruses. Epidemiological challenges: The high percentage of asymptomatic cases and clinical overlap with other febrile illnesses complicate case identification. In response to this growing threat, the World Health Organization (WHO) launched the Global Arbovirus Initiative in 2022 to strengthen surveillance, prevention, and timely diagnosis. Given the geographical expansion of these viruses and their pandemic potential, the need for international collaboration and investment in applied research in a One Health approach has become increasingly evident.

Keywords: Arboviruses, Public Health, Control Challenges, Epidemiology, Climate Change, World Health Organization

O72

Measures and Achievements of Hormozgan University of Medical Sciences in the Diagnosis and Control of Dengue Fever Virus

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Introduction: Due to the entry of Aedes aegypti in the province and its spread, as well as the outbreak of dengue fever in some parts of the province, Hormozgan University of Medical Sciences has taken measures to control the vector and the diseases transmitted by it. Methodology: Based on national guidelines, periodic entomological surveillance has been carried out at all international entry points of the province since 2016. In December 2019, with the identification of the first case of Aedes aegypti mosquito in the province and the rapid spread of this vector, intensified integrated measures were taken in the province. Two seroepidemiological studies were conducted on 515 people from high-risk groups and 678 people from across the province. Results: Specialized working groups were formed in the field of vector control and human care. Surveillance stations were established deep in infected cities. Rapid diagnostic kits were made available to public and private health centers. Molecular tests were performed to periodically check the contamination of captured mosquitoes and hospitalized and outpatients suspected of dengue fever. Serological findings indicate a low seroprevalence of dengue fever. Conclusion: It seems that the measures taken in the province have partially prevented and controlled the vector and the diseases it transmits, and prevented its spread to other parts of the country. However, due to the specific biology of the vector and the high prevalence of diseases transmitted by this vector in neighboring countries, a comprehensive national effort must be formed.

Keywords: Aedes, Dengue, Vector Control, Hormozgan Province

POCT: Innovations and Challenges

O73-O77

O73

Technological Innovations in Molecular Point-of-Care Testing

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Since molecular point-of-care testing (POCT) enables timely and accurate diagnosis, its importance has been increasingly recognized and highlighted during the COVID-19 pandemic. Despite significant advances in recent years, many technological challenges remain. There is still a gap between current methods and those required for accurate molecular POCT that is ready to be used in various settings. Further development of novel molecular POCT technologies is essential to respond to current clinical diagnoses of infectious diseases as well as cancers, prepare for future pandemics, and enable rapid genetic testing for personalized medicine. This talk will briefly review each of the key aspects of molecular POCT and provide a brief summary of the current status and innovations in advances in sample collection and storage, nucleic acid extraction, DNA amplification, and signal generation and detection methods.

O74

POCT Management in the Medical Device Authority (Includes General Policies, How to Needs Assessment, How to Choose Areas Allowed to be Used, POCT Quality and Performance Evaluation Protocols, Sales License Issuance, Monitoring the Level of PMS Consumption)

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Point-of-care testing (POCT), also known as bedside testing or near-patient testing are simple medical tests that can be performed at the bedside patient and outside the laboratory. The desirable features of these device are ease of use, accuracy of the method compared to the main laboratory method, portability, simpleQC, easy patient sample preparation, the ability to identify the patient sample by barcode, and the ability to communicate with the laboratory information system, also the kits can be used as "Ready-to-use". On the other hand, POCT can contribute significantly to improved patient care, including better outcomes due to a more rapid diagnosis and treatment and thus reduce the consequences of treatment. Diagnosis, treatment, prevention and management of diseases are directly or indirectly related to laboratory device. The unfavorable quality of IVD (In Vitro Diagnostic Devices) device can lead to Impaired or delay in the diagnosis of the disease, imposing costs on the patient, the laboratory and the country's health system. One of the sure ways of the desired quality of these device is their quality control before entering the consumer market, according to the risk class of IVD device and the general and specific requirements of the device, the issuance of IRC (Iran Registration Code) is done. Department of laboratory equipment and products is one of the sub-departments of the Department of Medical Device Authority which aims to import IVD device with quality and reasonable price, in sufficient quantity in order to supply and prevent shortage of goods. Considering that POCT devices and kits are considered IVD device, in order to import and produce thesedevice, they receive their license from this Department. Decisions about issuing import or production licenses for new technology POCT device should be made by examining the clinical need and justification by the IVD specialized committee and after assessing the needs and checking the quality of the device, the IRC is issued. It is very important to evaluate the safety and performance of medical devices (PMS), including POCTs, continuously after entering the market and during use. the reason for the importance of this issue is the change in the safety and performance of the device over time, and these characteristics can only be measured and checked when the device is in use. Therefore, the importance of Post Market Surveillance (PMS)for POCTs is something that is done with great seriousness and accuracy by Medical Device Authority.

O75

Current Point-of-Care Testing in Cancer Diagnosis

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Cancer is the cause of death for one in seven individuals worldwide. It is widely acknowledged that screening and early diagnosis are of vital importance for improving the likelihood of recovery. However, given the costly, time-consuming, and invasive nature of the many methods currently in use, patients often do not take advantage of the services available to them. Consequently, many researchers are exploring the possibility of developing fast, reliable, and non-invasive diagnostic tools that can be used directly or by local physicians at the point-of-care. The incorporation of cancer biomarkers into point-of-care devices could potentially reduce the strain currently experienced by screening programs in hospitals and healthcare systems. Results derived from point-of-care tests should be accurate, sensitive, and generated rapidly to assist in the selection of the best course of treatment for optimal patient care. Essentially, point-of-care diagnostics should enhance the well-being of patients and lead to a reduction in cancer-related deaths.

O76

Point-of-Care Testing in Pediatrics: Challenges and Recent Advances

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Point-of-care testing (POCT) has revolutionized pediatric care by enabling rapid diagnosis and treatment at the bedside, significantly reducing turnaround time and improving clinical decision-making. POCT is particularly valuable in pediatric settings where timely results are critical for managing acute conditions such as neonatal sepsis, respiratory infections, and metabolic disorders. However, implementing POCT in pediatrics presents unique challenges. Smaller sample volumes, the need for age-appropriate reference intervals, and physiological differences between children and adults complicate result interpretation. Additionally, ensuring quality assurance and minimizing errors in decentralized settings remain ongoing concerns. Recent advances in POCT technology have addressed several of these challenges. Miniaturized devices requiring minimal sample volume, coupled with improved analytical performance, have enhanced the reliability of pediatric POCT. Innovations such as microfluidics, biosensors, and molecular diagnostics have expanded the scope of POCT, allowing rapid detection of infectious agents, genetic disorders, and biomarkers associated with sepsis and metabolic imbalances. Furthermore, integrating artificial intelligence and digital connectivity with POCT devices has improved data management, allowing for real-time decision support and seamless communication between healthcare providers. Despite these advancements, maintaining analytical accuracy and ensuring operator competency in diverse clinical environments remain critical for widespread adoption. Future efforts should focus on developing standardized protocols, enhancing regulatory oversight, and expanding evidence-based guidelines to optimize the clinical utility of POCT in pediatrics. With continued technological innovation and quality improvement, POCT holds great promise for transforming pediatric care and improving outcomes for young patients.

O77

Analyzing the Criteria for Performing Point-of-Care Testing (POCT) in the Countries of the Region and Proposing a Model that Meet the Requirements of ISO15189:2022

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Given the ease of use and speed of point-of-care testing (POCT), these devices are widely used for health decision-making and patient management. Conversely, there may be significant civil and legal consequences such as wrong decisions and changes in treatment or diagnosis. Unfortunately, worldwide, point-of-care testing is increasingly being performed without the supervision of central laboratories by users without the supervision of medical laboratories. Since the results of these types of tests can be used to make important decisions for patients, it is very important that the type of tests, the equipment used are performed with specific regulations and standards, so that the correct results are obtained and its management and accountability are transparent. For this reason, the need for a comprehensive guide in which all aspects including sampling, performance, quality assurance, transmission and confirmation of results are completely transparent is essential, and the rules and regulations should be communicated by health care Ministry of Health and Medical Education.

Professional Ethics in Medical Laboratories

O78-O83

O78

Fee-Splitting: Solution or Problem

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In the current healthcare economy, characterized by unrealistic tariffs for medical services, constant wage increases, unrestrained rises in the costs of consumables and equipment, hefty maintenance expenses, outstanding insurance debts, and tax obligations, laboratories are navigating extremely challenging conditions. Many are regrettably nearing the brink of bankruptcy and closure. From an economic standpoint, there are two primary strategies to address such dire circumstances: 1. Increase Income and 2. Reduce Costs. Increasing Income: The most effective way to boost income for laboratories is by increasing patient admissions. This, in turn, is influenced by the quality of services provided and overall patient satisfaction. However, enhancing service quality typically demands substantial financial resources and personnel investment—luxuries that many laboratories currently cannot afford. Consequently, some laboratories resort to unethical practices to attract patients. Such methods include offering group discounts, lowering approved tariffs, misleading advertisements, and providing financial incentives to service referrers, including healthcare professionals. Among these unethical practices, fee-splitting stands out as particularly concerning. This involves compensating physicians directly for patient referrals, either as a fixed fee or as a percentage of the income generated. Other forms of fee-splitting might include offering free services, such as covering office rental costs or salaries for office staff. The ethical implications of these practices are profound. They shift the focus from prioritizing the patient's best interests to serving the financial motives of service providers, ultimately undermining the clinical judgment of physicians who accept these arrangements. Furthermore, such practices violate the four key ethical principles in healthcare: respect for patient autonomy, beneficence, non-maleficence, and justice. Articles2 and27 to 31of the General Guide to Professional Ethics for Medical and Allied Professionals, sanctioned by the Supreme Council of the Medical System, explicitly denounce these behaviors. Although these unethical strategies may provide a short-term financial boost, they will likely erode public trust in laboratories and ultimately contribute to their decline. In the long run, maintaining ethical standards is essential to ensure the sustainability of healthcare practices and the well-being of patients.

O79

Ethical Challenges in the Medical Laboratory

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The importance of jobs and professions depends on the importance of the central issue of that profession. What distinguishes the medical profession from other professions is the preservation and restoration of human health. One of the characteristics of this profession is the need for the service provider to adhere to ethical principles, rules, and norms. Medical laboratories in Iran have been among the leading groups in implementing quality assurance programs, developing professional standards, and paying attention to professional ethics. In recent years, economic constraints, cumbersome regulations and procedures, and a lack of attention to professional ethics in policy and program development have led to numerous ethical challenges. Here, we take this opportunity to highlight some of the ethical challenges in medical laboratories, discuss the factors that contribute to their formation, and draw the attention of policymakers, stakeholder organizations, and the laboratory community to finding solutions. A) The necessity of adhering to the announced tariffs for providing services in the medical laboratory and the unfairness of the tariff with the defined standards and the cost of consumables. B) The formation of startups in the field of medical laboratories before the development of professional regulations and the determination of standards for the establishment and service of the aforementioned companies. C) The requirement to implement strict standards (firefighting, quality assurance, etc.) without considering the existing facilities. D) The failure of organizations involved in providing laboratory services to adhere to legal obligations (insurance organizations, policies of the Food and Drug Administration etc.) and the expectation of providing quality laboratory services. E) Fee splitting and unhealthy financial relationships between medical professionals.

Keywords: Professional Ethics, Medical Laboratory

O80

The Impact of Society`s Livelihood Problems on the State of Professional Ethics in Medical Laboratories

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Ethics as an internal deterrent and law as an external lever play a fundamental role in institutionalizing norms, values, promoting desirable behavior, and establishing order. In the absence of ethics and law, individual interest will quickly replace collective interest, and anomalies and anti-values will gradually become widespread. Social, economic, and cultural anomalies can have an adverse effect on public morality and behavior. Similarly, economic constraints among members of various professions can also have negative effects and consequences. The available evidence regarding the medical situation in our country indicates that economic difficulties have not only caused deficiencies in the diversity and quality of medical services, but have also affected the performance and professional behavior among members of this profession and its sub-categories, including medical laboratories. Reduced budgets and financial resources and excessive increases in laboratory costs lead to a decline in the quality of equipment and consumables, the accuracy of results, and increased work pressure on staff. This situation increases the likelihood of human error, delays in response, and reduced patient satisfaction. Also, in some cases, financial pressure can lead to unethical behavior such as unnecessary testing or unhealthy financial relationships. Overall, unfavorable economic conditions can jeopardize ethical principles such as honesty, accuracy, responsibility, and fairness in the laboratory environment. To overcome these difficult and overwhelming circumstances and keep the flag of service and trust-building high to the public, not only the laboratory community but also all stakeholders in the medical laboratory sector are forced to take fundamental corrective measures that are appropriate and comply with professional ethics, empathy, responsibility, fairness, transparency in policy-making, regulation development, and implementation of laboratory services at various levels.

Keywords: Laboratory Economics, Ethics

O81

Professional Ethics Considerations for Medical Laboratory Personnel from the Perspective of "Code of Ethics for Medical Professionals, Medical Council of Islamic Republic of Iran

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Introduction: Throughout history, medical and allied professionals have always been the standard-bearers of professional ethics and the inspiration for the moral development of societies. The existence of oaths, admonitions, guidelines, and codes of medical ethics is a testament to this claim. Throughout the history of medicine, the public declaration of adherence by medical and allied professionals to these professional standards and their actions accordingly have been the basis for creating unparalleled public trust in their therapists. Ethics and the Supreme Council of the Iran Medical Council: In order to ensure the observance of the mutual rights of medical and allied professionals and recipients of health services, the powers granted by the Law on the Establishment of the Iran Medical Council: This council has been assigned the authority to review the "Disciplinary Regulations for Handling Professional and Guild Violations of Medical and Allied Professionals" The emphasis of the Constitution of the Islamic Republic of Iran and other laws of the country on the necessity of adhering to good ethics in all areas of life of all members of society. Emphasis on the irreplaceable position of ethics in the higher-level documents of the health sector, the law establishing the Iran Medical Council and the country's general policies in the field of health is undeniable. Code of ethics for medical professionals, medical council of Islamic Republic of Iran: This document contains guidelines and instructions to assist in ethical decision-making by medical and allied professionals in various professional roles and circumstances, especially when faced with complex ethical situations. It is compiled and approved in a set of 13 chapters and 140 articles, and is mandatory for all medical and allied professionals. Several paragraphs and articles of the aforementioned guide directly and indirectly refer to the principles of biomedical ethics and the specific ethical duties of laboratory professionals. Conclusion: Professional behavior and acting in accordance with the ethical duties expected of the laboratory community, as mentioned in this guide, will enhance the quality of services provided to health care recipients, increase the efficiency of this group of professionals who are members of the Iran Medical Council, and increase public trust in them by respecting patients'rights, And finally, it will reduce instances of unethical behavior(subject to Article 6 of the Medical Council's disciplinary regulations),and in this way, it will probably also reduce the number of complaints involving ethical implications.

O82

The Impact of Ethics in Medical Laboratory Based on ISO-15189

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Ethics consist of a set of written rules, procedures, or guidelines that aid in determining right from wrong. Ethical issues plays a significant role in quality assurance of laboratory medicine. Therefore, it is required for laboratories to strictly follow ethical principles. Several ethical issues exist within the diagnostic medical laboratories. Ethical guidelines vary between different countries according to available resources. The major ethical challenges include: consent, confidentiality, codes of conduct, conflict of interest and proficiency. Respect for persons, beneficence or non-maleficence and Justice are three main principles of guidelines. We have mentioned the impact of ethics in medical laboratory based on ISO 15189:2022. Section 4.1 (Impartiality), 4.2 (Confidentiality)and 4.3 (Requirements regarding patients) of the ISO15189,2022 summarize the main ethical conduct expected in medical laboratories. Nowadays diagnosis and patient's treatment are commonly taken on the basis of outcomes and interpretations of laboratory test results. Hence, all laboratory tests must have been carried out within an appropriate ethical framework. Ethical considerations helps to protect confidence, operational integrity, capability, impartiality, and safety of the staff.

Keywords: Ethics, Medical Laboratories, ISO15189,2022

O83

Ethical and Legal Violations in Laboratory Sciences: An Analytical Study

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Background and Aim: In the context of the rapid expansion of cyberspace and the increasing reliance on virtual environments for communication, training, and interaction, numerous factors such as the broadening of scientific activities, the diversity of concerns, the weakness of ethical education, and internal factors have led to the emergence of numerous instances of misconduct or negligence. These have placed professional activities at risk of ethical violations, regulatory negligence, and failures in the enforcement of established norms. The deviation from the original principles of professional ethics in scientific activities has created a serious threat to the credibility and trustworthiness of professional conduct and scientific operations. Therefore, establishing a comprehensive system for monitoring and investigating scientific misconduct has become an urgent necessity. Method: This research was conducted using the library method and qualitative content analysis approach. In this study, the phenomenon of scientific misconduct and the violations of ethics and the right to health in cyberspace have been thoroughly examined. Ethical Considerations: Integrity and honesty in reporting texts, citing sources and avoiding any form of bias have been strictly adhered to. Findings: The findings suggest that weakness in the training of professional ethics, insufficient commitment to ethical standards, the conflict of interests, and the weakness of monitoring and enforcement systems are among the main factors contributing to the increase in scientific misconduct. Additionally, the legal vacuum and the lack of effective enforcement mechanisms further aggravate this situation. It was found that in the absence of proper oversight, the rate of ethical deviations and misconduct increases significantly, leading to serious consequences in the realm of professional scientific activities and the protection of health rights. Furthermore, the research identified that scientific misconduct in cyberspace, particularly concerning the right to health, often stems from a combination of weaknesses in cultural adherence to professional ethics, lack of proper training, weak enforcement of regulations, and the absence of a coherent system for monitoring and controlling ethical violations. Specialized investigation and regulatory mechanisms are urgently needed to prevent the spread of misconduct in online scientific environments. Conclusion: In conclusion, the prevalence of scientific misconduct in cyberspace in the field of professional sciences poses a serious threat to ethical standards and the protection of health rights. The study emphasizes that in the absence of robust monitoring systems, specialized enforcement bodies, and a culture of ethical commitment, violations will continue to increase. Addressing these challenges requires the development of specialized infrastructures, enhancement of ethical education, the establishment of efficient monitoring and enforcement mechanisms, and the promotion of a culture of professional ethics in cyberspace. Strengthening professional integrity, ensuring the enforcement of regulations, and creating an environment of accountability are crucial measures for safeguarding health rights and scientific credibility in virtual settings.

Keywords: Professional Ethics, Cyberspace, Scientific Misconduct, Right to Health, Professional Conduct, Law and Ethics

Proteomics and Metabolomics in Laboratory Diagnosis

O84-O85

O84

Cutting-Edge Tools in Proteomics and Metabolomics for Medical Diagnosis

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Proteomics and metabolomics are revolutionizing medical diagnosis by providing deep insights into the molecular basis of health and disease. Proteomics studies proteins, the functional units of cells, while metabolomics profiles metabolites, reflecting cellular metabolism. Together, these disciplines enable biomarker discovery, disease mechanism elucidation, and personalized treatment strategies. This presentation highlights the advanced tools driving these fields and their diagnostic applications. In proteomics, mass spectrometry (MS), particularly liquid chromatography-MS (LC-MS), identifies and quantifies proteins by measuring peptide mass-to-charge ratios, aiding early cancer detection through blood-based biomarkers. Two-dimensional gel electrophoresis (2D-GE) visualizes protein profiles, excelling in comparative studies of neurodegenerative diseases. Emerging data-independent acquisition (DIA) MS enhances reproducibility, uncovering low-abundance biomarkers in diabetes and cardiovascular conditions. Metabolomics employs nuclear magnetic resonance (NMR) spectroscopy to analyze biofluid metabolites non-destructively, diagnosing metabolic disorders via spectral signatures. Gas chromatography-MS (GC-MS) profiles volatile metabolites, detecting pathogen-specific markers in infectious diseases like tuberculosis. LC-MS, versatile for polar metabolites, identifies metabolic shifts in cancer, such as the Warburg effect, improving early detection. Integrated proteomics-metabolomics workflows, supported by high-throughput platforms and bioinformatics, offer a holistic view of disease. In sepsis, for example, proteomic inflammatory markers pair with metabolomic amino acid disruptions to guide therapy. Applications span cancer (early tumor detection), metabolic diseases (enzyme deficiency identification), and infectious diseases (rapid pathogen signatures). These tools—rooted in precise physical and chemical principles—transform diagnostics from reactive to predictive, leveraging machine learning for actionable insights. As they become more integrated and accessible, proteomics and metabolomics promise a future of tailored, molecularly informed medicine, already impacting lives with unprecedented precision.

O85

Integrating Metabolomics with Genomics Data

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Inherited metabolic disorders (IMDs) are a group of single-gene conditions resulting from enzyme deficiencies that disrupt metabolic processes. Diagnosing these disorders is challenging due to varying clinical presentations, overlapping biochemical profiles, and genetic variants with uncertain significance (VUS). However, combining targeted metabolomics analysis with genomic sequencing has greatly enhanced diagnostic accuracy and patient care. Liquid chromatography–tandem mass spectrometry (LC-MS/MS) and gas chromatography–mass spectrometry (GC-MS), in Targeted metabolomics, allows for the precise measurement of metabolites such as acylcarnitines, amino acids and organic acids. These data can be used to validate genetic variants identified in the next-generation sequencing (NGS), such as whole-exome sequencing (WES) or whole-genome sequencing (WGS). For instance, high levels of branched-chain keto acids indicate pathogenic variants in genes like BCKDHA, BCKDHB, or DBT in maple syrup urine disease, while elevated methylmalonic acid points to variants in MUT, MMAA, or MMAB in methylmalonic acidemia. This combined approach increases diagnostic success, reduces the uncertainty of VUS, and supports targeted treatments such as enzyme replacement, substrate reduction, and gene therapy. In addition, untargeted metabolomics can detect novel biomarkers, which may expand our knowledge about IMD. Artificial intelligence (AI) and Bioinformatics developments, further improves the integration of multi-omics data, improving variant interpretation and biomarker discovery. As precision medicine evolves, the integration of metabolomics and genomics is transforming IMD diagnostics by enabling earlier detection, better prognosis, and personalized treatment plans. This functional genomics-driven strategy marks a significant shift toward more precise and efficient diagnosis of metabolic disorders.

Keywords: Inherited Metabolic Disorders, Targeted Metabolomics, LC-MS/MS, GC-MS, Variant Interpretation, Next-Generation Sequencing, Precision Medicine

Technological Advances in Today's Hematology Laboratories

O86-O89

O86

Next-Generation Flow Cytometry: A Pioneering Technology for Precise MRD Assessment in Hematological Malignancy

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Next-Generation Flow Cytometry (NGF) has emerged as a cutting-edge laboratory technology for the detection of minimal residual disease (MRD) in patients with multiple myeloma. NGF represents a significant advancement over traditional flow cytometry and offers unique advantages compared to next-generation sequencing (NGS). Utilizing highly standardized protocols and multi-parametric analysis, NGF achieves exceptional sensitivity, capable of detecting one malignant cell among 105 to 106 normal cells. Its rapid processing time and ability to provide real-time results make it ideal for routine clinical use. Unlike traditional flow cytometry, NGF eliminates operator-dependent variability through automated gating and precise immunophenotypic profiling of plasma cells. Furthermore, NGF identifies phenotypic shifts in clonal populations, which may occur during treatment or disease progression. Compared to NGS, NGF does not require a molecular baseline and can detect abnormal cells directly in real-time without additional bioinformatic analysis. Its ability to distinguish viable malignant cells from apoptotic or necrotic cells also enhances its clinical utility. While NGS offers deeper molecular insights, NGF provides a more cost-effective and faster alternative for MRD assessment. This makes NGF an indispensable tool in the personalized management of multiple myeloma, enabling more accurate risk stratification, therapy monitoring, and prognostic evaluation.

O87

New Advances in Technology and Artificial Intelligence in the Construction of Next Generation Hematology Analyzers (NGHA)

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With the vast advances in hardware and software technologies and the introduction of artificial intelligence and machine learning, hematology analyzers have entered a new generation, called NGHA. In NGHAs, not only are up to 63 hematology parameters defined, but new modules for slide preparation, smear staining, smear scanning, AI-based digital leukocyte identification and differentiation, photo-microcapillary ESR measurement, Hb-A1C, CRP, SAA measurement, Tube separator, and automatic preparation of isotonic diluent reagent have also been integrated into the device. Mindray CAL-8000 and Sysmax XN-9100 are two examples of NGHA devices designed for large laboratories and new indices such as IPF, PLT-O, PLT-F, PLT-H, IRF, Ret-He, MDW, WPC, IMI/IG, AS-Lymp, RE-Lymp, Neut-RI, etc. are defined for very specific purposes, and therefore the new generation of cell counters are much more efficient and perhaps more accurate than human forces. With the help of artificial intelligence and machine learning, this generation is able to learn images of millions of blood cell types and be approved as a tele-laboratory from other cities or countries. In this article, we will try to introduce this generation of devices and the efficiency and importance of their performance in order to familiarize large hospital and laboratory centers and professional hematology experts with their benefits.

Keywords: Hematology Analyzers, Next Generation, Artificial Intelligence, Machine Learning, Tele-Lab

O88

ddPCR (Droplet Digital PCR) is a Versatile Tool in the Diagnosis of Hematological Neoplasm Biomarkers

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In the era of personalized medicine and single-cell analysis, the reliable and absolute detection of biomarkers in hematological neoplasms, especially in very low abundance, has become crucial. In current conventional methods such as qPCR, the identification and quantification of cancer biomarkers, particularly those with low Variant Allele Frequency (VAF), and the accurate quantification of the biomarker and measurement of the allelic ratio of mutated genes to wild-type are not reliable because they depend on a standard curve and have a high noise-to-signal ratio. Early and ultrasensitive detection of cancer biomarkers at lower thresholds than current methods can help to guide clinicians in treatment decision or improve treatment monitoring. Droplet Digital PCR (ddPCR) is a high-throughput, ultra-sensitive method developed for the diagnosis, prognosis, and monitoring of nucleic acid biomarkers. In ddPCR, DNA/RNA is randomly partitioned into microdroplets, which serve as reaction chambers. The presence or absence of the amplicon is detected and read by the device using a fluorescent dye (specific probe). Using Poisson distribution, the concentration of the biomarker of interest is obtained in absolute terms. The properties of ddPCR, such as ultra-sensitivity and reproducibility, standard curve-independent absolute quantification, high tolerance to PCR inhibitors, and high efficiency, have led to the widespread use of this versatile tool in calculating allelic ratios or VAF, Minimal Residual Disease (MRD), and absolute biomarker counting, especially in samples with low target biomarkers such as liquid biopsies.

Keywords: ddPCR, MRD, PCR

O89

Applications and Advances in Next-Generation Sequencing (NGS) in Hematological Disorders

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Hematologists and hematopathologists have continued to advance in the past decade with new innovations improving the type, amount, and quality of data generated for each molecule of nucleic acid. By assessing a patient's genetic makeup, next-generation sequencing (NGS) technologies have begun to change the area of hematological malignancies. NGS is a robust platform that has enabled the sequencing of thousands to millions of DNA and RNA simultaneously. NGS is generally is classified into include: Pyrosequencing, Sequencing by Reversible Terminator Chemistry and Sequencing by Ligation. This High-throughput, massively parallel sequencing technologies are rapidly revealing new information in hematology, cancer, clinical genetics, and a variety of other diseases. It provides researchers with a new viewpoint on the onset of sickness, risk assessment, and therapeutic action. In hematology these technologies are used to diagnose hematological malignancies, inherited coagulation bleeding disorders, minimal residual diseases, hereditary hemolytic anemia, and blood typing. Focusing on the field of hematological malignancies, only a few hematological malignancies result from heritable or somatic mutations in a single gene. The majority of such malignancies show considerable genetic heterogeneity, with multiple genes affected. The recently revised World Health Organization classification and the European LeukemiaNet recommendations for acute myeloid leukemia consider genetic abnormalities as a top priority for diagnosis, prognostication, monitoring of measurable residual disease, and treatment choice. The introduction NGS technologies allows for the analysis of genomic, transcriptomic, and epigenomic findings, providing new insights into hematological malignancies.

Keywords: Next Generation Sequencing, Hematological Malignancies, Hematological Disorders

The Future Medical Laboratories: Sustainable and Eco-friendly

O90-O94

O90

Challenges of Waste Management in Medical Laboratories and Its Role in Sustainable and Environmentally Friendly Laboratories

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Introduction: Effective and sustainable waste management is a crucial aspect of sustainable development for countries and a cornerstone of sustainable laboratories. It is implemented with the goals of preserving the health of personnel, patients, and visitors; environmental protection and sustainability, preventing water and soil pollution; ensuring environmental security; preventing the spread of various diseases; and improving the health of society. Methods and Findings: Green waste management in sustainable laboratories requires policymaking and planning to address the following challenges, identify and implement prioritized solutions, and monitor their implementation: Challenge of securing sustainable resources(financial, human resources, equipment, physical space, and energy) Lack of adequate identification of waste sources and the amount of waste generated, as well as awareness of how to manage various types of laboratory waste based on the scope of operations and diversity of activities, in accordance with existing regulations, guidelines, and standards. Lack of adequate implementation of necessary programs to reduce the volume of waste generated. Lack of segregation(separation)or improper separation of various types of waste at the source of generation. Lack of adequate culture building and training on the waste management program. Failure to select sustainable equipment for waste treatment and to use and maintain it properly. Failure to implement a program for recycling medical waste, which is not permitted by the Waste Management Law. Use of hazardous chemicals and disinfectants and their improper disposal. Generation of large volumes of waste and increased costs due to the use of disposable items and failure to reuse items, as well as failure to select laboratory diagnostic devices (In Vitro Diagnostic, IVD) with minimal pollution and maximum sustainability. Inappropriate location and conditions for waste storage and the possibility of contamination of people and the environment. Key Challenges Related to the Optimal Implementation of the Waste Management Program at the National Level: Challenges in implementing the tasks and duties assigned in the Waste Management Law approved on1383.2.15 by the Islamic Consultative Assembly. Lack of adequacy and effectiveness of the national program and integrated waste management systems. Improving the level of waste management literacy and training managers and specialized personnel. The impact of improper waste management on the occurrence of climate change problems and the emission of greenhouse gases. Lack of adequate use of knowledge, technology, and modern methods of waste management and reduction, especially in line with smart waste management and the use of green technologies, considering the specific regional and geographical conditions. Lack of transparent financial and legal infrastructure to utilize the capacity and capabilities of the private sector. Conclusion: Effective waste management in medical laboratories and addressing existing challenges requires the participation and cooperation of all stakeholders, and in the time allotted to the speech at the congress, we will present solutions to address the challenges and problems.

Keywords: Effective Waste Management, Sustainable Laboratories, Environment

O91

Preserving the Environment by Implementing the ISO 14001 in Clinical Laboratories

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This article examines the role of ISO 14001 in reducing the environmental impact of medical diagnostic laboratories. With the increase in medical activities and the production of hazardous waste, laboratories, as resource consumers and pollutant producers, require effective environmental management. ISO 14001 provides a systematic framework to help laboratories identify, control, and reduce their environmental impacts 1-Importance of Environmental Protection Medical diagnostic laboratories have significant negative impacts on the environment due to their high energy consumption, chemical use, and hazardous waste generation-Role of ISO 14001:This standard, by defining an Environmental Management System(EMS),helps organizations improve their environmental performance. - Objectives of the article :Identifying the environmental aspects of laboratories, analyzing the role of ISO 14001 in reducing impacts, and providing implementation solutions2- ISO 14001 Standard and its Requirements-EMS Definition: An environmental management system is a framework for identifying, controlling and improving environmental impacts-Main clauses: Including planning, support, operations, performance evaluation and continuous improvement- Benefits of implementation: Reducing environmental impacts, increasing productivity, complying with legal requirements and improving organizational image 3-Identifying environmental aspects and impacts-Pre-Analytical processes: Paper, plastic and energy consumption in acceptance and sampling-Alanytical processes: Use of chemicals, production of effluents and hazardous waste-Post-Alanytival processes: Paper consumption in recording results and waste management 4-Measures and strategies to reduce impacts-Planning: Setting environmental goals such as reducing paper and energy consumption-Support: Training employees and using green technologies - Operations: Optimizing processes, managing waste, and reducing chemical consumption-Performance assessment: Monitoring environmental indicators and conducting periodic audits-Continuous improvement: Implementing corrective actions and building a culture in the workplace 5-Conclusion and Recommendations: Implementing ISO 14001 in medical diagnostic laboratories not only helps reduce environmental impacts, but also leads to increased productivity, reduced costs, and improved organizational image. It is recommended that laboratories take effective steps towards environmental sustainability by training employees, optimizing processes, and using green technologies. Referencces: 1-ISO 14001:2015 Environmental management systems–Requirements with guidance for use. Geneva: ISO 2- World Health Organization (WHO). (2018). Safe management of wastes from health-care activities.3-United Nations Environment Programme (UNEP). (2020). Sustainable laboratory practices for environmental impact reduction4-Environmental Protection Agency (EPA). (2021).Guidelines for environmental management in medical laboratories. Reference: 1- ISO 14001:2015 Environmental management systems – Requirements with guidance for use. Geneva: ISO. 2-. World Health Organization (WHO). (2018). Safe management of wastes from health-care activities. 3- United Nations Environment Programme (UNEP). (2020). Sustainable laboratory practices for environmental impact reduction. 4-Environmental Protection Agency (EPA). (2021). Guidelines for environmental management in medical laboratories.

O92

The Role of Digital Transformation and Automation in Sustainable and Ecofriendly Medical Laboratories

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1. Introduction: Definition of digital transformation and automation in the field of medicine / Importance of sustainability and environmental compatibility in medical laboratories 2. Key concepts in digital transformation and automation: Internet of Things (IoT) in medical laboratories / Artificial intelligence and machine learning in laboratory data processing • Block chain for medical data security3. The impact of automation on reducing resource consumption and waste management: Reducing energy consumption and optimizing laboratory processes / Using automated systems to reduce chemical consumption / Managing biological and electronic waste in medical laboratories 4. Green technologies in digital laboratories: Using renewable energy in medical laboratories / Smart systems to reduce carbon footprint / Biocompatible materials in laboratory equipment and supplies5. Challenges and obstacles to implementing digital transformation and automation: Costs of implementing technologies Modern/ Resistance to change and the need for employee training / Legal considerations and data security 6. Case studies and success stories: Review of medical laboratories that have moved towards digitalization / The impact of automation on productivity and reducing operational costs7. The future of digital transformation in sustainable laboratories: Upcoming innovations in the field of automation and digital medicine / The role of regulation and policymaking in the development of smart laboratories / Opportunities for international cooperation for sustainable development in laboratory medicine 8. Conclusion and recommendations: Proposed solutions to increase sustainability in digital laboratories / Proposed paths for the development and adoption of new technologies.

O93

Role of Space & Infranstructure in Sustainable and Ecofriendly Medical Labs

Saeed Mahdavi *

Future Medical Laboratories (Existing and Desirable). Medical laboratory is a piece of the puzzle of the health system of each country that must be designed and managed in accordance with that country Of course, this national plan must follow international models and use global knowledge and experience. In order to design the roadmap of the country's laboratories, some requirements are needed, the most important of which we will address. Land Planning from the Perspective of Medical Laboratories (Current and Desirable Situation) A. People's access to services B.Biosafety and Security C.Level of Service Provision D.Number of Laboratory Centers and Covered Population E.Mandatory Standards and Audit of Centers A.Access of people to provide services: According to the texture of the buildings of each city(vertical and horizontal)the size of the city, the subway, the highways, and the population density, each country should have its own governor, which means that anyone who needs laboratory services must reach the service centers by traveling a few kilometers or a few hours or minutes (comparison of the current and desirable situation) B.Biosafety and Security: In terms of the services provided in the centers, should everyone be allowed to work on any infectious specimen they choose, for example, if any center of any size and position should be allowed to work on tuberculosis bacteria? Can the location of each center be next to public centers such as mosques, or can their waste enter a river or a stream of water? Comparison of the current and desirable situation) C-Basically, what is our criterion for choosing the tests of each center, is each center free to accept any test it wants, even if it does not have the facilities to do it,is it in the interest of the country(in terms of national resources)to allow everyone to be equipped and to have an equipment competition? What is the best model for dividing the centers and categorizing them? (Comparison of the current and desirable situation) D.The issuance of licenses can be based on the needs of the country, it can be based on the request of experts, we have experienced both models in our countrywhich means that in the past, the criterion for issuing licenses was the number of population of each city, and then the distance between the two centers was the criterion for issuing licenses, but later it changed to the second model, it should be seen which model is closer to the interests of the country(comparison of the current and desirable situation). E.Should we have a model or standard for all centers, should all our centers be audited once a year, and the number of their technical officials can be from at least one in one shift or per shift? What is the bottom of the quality of services that can cause harm to people, and how can it be protected (comparison of the current and desirable situation).

O94

Energy and Sustainability

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Energy and sustainability We people discuss much more frequently the subject energy. Questions like the future of nuclear power, regulation of fee for CO2, avoid energy of expensive fossil sources, much more expensively growing of winning resources, rising energy prices, everything hangs together with energy. Today as a manager you cannot ignore the energy expenses in your organization anymore. Your organization certified by ISO 50001, is supported sustainable by one energy management system, which serves you many benefits: You will optimize your energy consumption and save so resources, beside, motivates your employees, to handle sensible energy and expenses .Another plus of the ISO 50001 is the open confession to the sustainability, which will enhance trust and respect to your clients, employees, partners, suppliers, authorities and the whole society increasingly. Energy is critical to organizations, but often represents a significant cost – both to them and the environment. An energy management system helps organizations better manage their energy use, thusimproving productivity. World energy consumption continues to rise: it has more than doubled in the last 40 years and is projected to increase a further 30% by 20401). What's more, energy is the major contributor to climate change, making up nearly 60 % of the world's greenhouse gas emissions. Takingaction to better manage our energy consumption not only helps the planet, it saves money for organizations and society as a whole. ISO 50001 provides a framework of requirements for organizations to: - Develop a policy for more efficient use of energy- Fix targets and objectives to meet the policy- Use data to better understand and make decisions about energy use- Measure the results-Review how well the policy works, and - Continually improve energy management

Toward Application of Extracellular Vesicles in Laboratory Diagnosis

O95-O98

O95

Toward Application of Extracellular Vesicles in Medical Diagnosis

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Extracellular vesicles (EVs) are nanosized vesicles released by cells, containing proteins, lipids, and nucleic acids. They play a crucial role in intercellular communication and have shown great potential in medical diagnosis. EVs can be isolated from various body fluids, such as blood, urine, and saliva, making them easily accessible for diagnostic purposes. The contents of EVs reflect the physiological and pathological state of their parent cells, providing a valuable source of biomarkers for various diseases, including cancer, cardiovascular diseases, and infectious diseases. The use of EVs in diagnostics offers several advantages, such as non-invasiveness, high stability, and the ability to detect diseases at an early stage. In this presentation, I will provide a concise overview of the current understanding of EVs in medical diagnosis, highlighting their potential as a promising tool for disease detection and monitoring.

Keywords: Extracellular Vesicles, Medical Diagnosis

O96

Extracellular Vesicles in Liquid Biopsy: Advancing Diagnostic and Biological Insights

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Traditional diagnostic approaches primarily rely on imaging techniques and tissue biopsies, which are invasive and limited in their ability to capture tumor heterogeneity. Liquid biopsy has emerged as a revolutionary, minimally invasive alternative that utilizes blood samples to monitor disease status in real time, reducing patient discomfort and enabling more frequent sampling. This approach offers a more comprehensive representation of the tumor's genetic and molecular landscape, improving clinical decision-making with faster result turnarounds. Among the various components analyzed in liquid biopsy, extracellular vesicles (EVs) offer a unique opportunity to explore disease biology. These nanoscale messengers carry molecular cargo reflective of their cells of origin, making them valuable biomarkers. In our studies, we focused on EVs isolated from blood samples from healthy controls, cancer, and AD patients. We demonstrated their promising potential in diagnostics, as well as provided novel insights into their biological roles in disease progression. These findings emphasize the growing importance of EV-based liquid biopsy in advancing precision medicine and non-invasive diagnostics.

Keywords: Liquid Biopsy, Extracellular Vesicles, Diagnosis

O97

Extracellular Vesicles as Novel Tool in Cancer Diagnosis

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Extracellular vesicles (EVs) play significant roles in intercellular communication and have gathered significant attention for their potential as biomarkers in disease diagnostics. Carrying a diverse array of bioactive molecules such as proteins, lipids, and nucleic acids, EVs offer the possibility of non-invasive diagnostic approaches for a wide spectrum of diseases, from cancer to neurodegenerative and cardiovascular conditions. As the molecular composition of EVs reflects the underlying pathological state, their study holds promise for early detection, monitoring disease progression, and evaluating treatment responses. The unique ability of EVs to carry disease-specific signatures makes them attractive candidates for liquid biopsy applications. However, challenges remain in their isolation, characterization, and standardization in clinical settings. Nevertheless, the potential of EVs to transform diagnostic practices and enable more personalized, precise treatments continues to drive ongoing research and innovation in the field.

Keywords: Extracellular Vesicles, Cancer, Diagnosis

O98

Extracellular Vesicles in Cardiovascular Disease Diagnosis and Management

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Extracellular vesicles (EVs), including exosomes and microvesicles, are emerging as critical mediators of intercellular communication in cardiovascular disease. These nanosized vesicles carry bioactive molecules such as proteins, lipids, and RNA, reflecting the physiological and pathological state of their cells of origin. Increasing evidence suggests that EVs play a pivotal role in the pathogenesis of atherosclerosis, myocardial infarction, and heart failure by modulating endothelial function, inflammation, and thrombosis. This lecture will explore the diagnostic potential of EVs as non-invasive biomarkers for early detection and risk stratification in cardiovascular disease. Advances in high-sensitivity detection technologies, including flow cytometry, nanoparticle tracking analysis, and mass spectrometry, are improving EV profiling for clinical applications. Additionally, therapeutic strategies leveraging EVs as drug delivery vehicles or modulators of cardiac repair are being actively investigated. By integrating EV analysis into routine cardiovascular diagnostics, we may enhance precision medicine approaches and improve patient outcomes. This lecture will highlight current challenges, technological advancements, and future perspectives in translating EV research into clinical practice. The discussion will emphasize the need for standardization in EV isolation and characterization to facilitate their adoption in cardiovascular medicine.

Young Scientists

O99-O103

O99

"Synergistic Effects of Platelet-Derived Microparticles and Cytarabine on Apoptosis, in Acute Lymphoblastic Leukemia Cells"

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Background: Platelet- derived microparticles (PMPs) are recognized for their role in modulating cellular interactions within the tumor microenvironment. This study investigates the effects of PMPs, Cytarabine (Ara-C), and their combination on cell viability and apoptosis in the Nalm-6 Acute Lymphoblastic Leukemia (ALL) cell line. Methods: PMPs were isolated through differential centrifugation and characterized using dynamic light scattering (DLS) and flow cytometry to assess their size and immunophenotypic properties. Cell survival and apoptosis were evaluated using the trypan blue exclusion assay and flow cytometry. Results: PMPs alone had no significant impact on the viability or apoptosis of Nalm-6 cells. However, when combined with Ara-C, PMPs synergistically enhanced Ara-C's inhibitory effects on cell viability and significantly increased apoptosis. Conclusion: These findings highlight the potential of PMPs to enhance the therapeutic efficacy of Ara-C in ALL, offering a promising avenue for optimizing chemotherapy strategies. Further studies are warranted to explore the underlying mechanisms and clinical relevance of these interactions.

Keywords: Platelet-Derived Microparticles, Acute Lymphoblastic Leukemia

O100

Molecular Genotyping Versus Serological Diagnosis for RH Blood Group Typing in Sickle Cell Patients

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Background: High rate of alloimmunization in sickle cell disease (SCD) patients poses a significant challenge in finding compatible blood unit. Accurate determination of the blood group genotype of them can help reduce the alloimmunization risk. Tetra ARMS PCR is a novel method that has been utilized recently to investigate SNPs in diseases in a fast and reliable way. Methods: Our study included 104 SCD and sickle thalassemia (Sβ) patients referred to Baghaei-2-Hospital of Ahvaz in 2019 using a nonrandom sampling method. Blood samples were collected for serological and molecular tests. Rh genotyping was performed using Tetra ARMS PCR and compared with the serological results. Results: Based on the Tetra ARMS PCR method, out of 104 patients, 7 (6.7%) were d/d, 40 (38.5%) were D/d, 57 (54.8%) were D/D, 25 (24%) were C/C, 59 (56.7%) were C/c, 20 (19.3%) were c/c, 4 (3.8%) were E/E, 25 (24%) were E/e, and patients 75 (72.2%) were e/e. There were discrepancies in the serological and molecular results for 11 patients. Conclusion: Use of Tetra ARMS PCR in combination with serological methods for determining the Rh blood group system in donors and transfusion-dependent patients represents a remarkable transformation in the field of immunohematology.

Keywords: Alloimmunization, Genotype, PCR, Phenotype, Sickle Cell Disease

O101

Prevalence of Helicobacter Pylori Infection in Adults with Gastritis in Tehran and Investigation of Antimicrobial Susceptibility of Helicobacter Pylori Isolates to Amoxicillin During the Years 1402-1403

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Background: Helicobacter pylori (H. pylori) colonizes the human stomach and leads to various gastrointestinal diseases, including chronic gastritis, peptic ulcers, and even gastric cancer. The emergence of antibiotic resistance in H. pylori is a serious challenge for effective treatment, which can lead to treatment failure and an increased risk of disease progression. Addressing this issue requires an increased understanding of the drug susceptibility status in each region to select more appropriate and novel treatment strategies. The present study aimed to determine the prevalence of H. pylori infection and to evaluate the pattern of susceptibility to amoxicillin among patients with gastritis in Tehran during 2023-2024. Methods: In this study, antral biopsy specimens were collected from patients with gastritis referred to the endoscopy unit of Firouzgar Hospital, Tehran, and cultured in Brucella agar supplemented for the isolation of H. pylori under microaerophilic conditions. After confirmation of identity by PCR and biochemical tests, the susceptibility of these isolates to amoxicillin was determined using the E-test (Lioflichem, Denmark). Results: From the 764 biopsy specimens (39.1% male and 60.9% female), the urea breath test (RUT) was positive in 26.8% (205/764) and culture in 21% (162/764) of cases. Among the 28 isolates with sufficient growth to create a 3 McFarland turbidity, 9 isolates (32.1%) were resistant and 19 isolates (67.9%) were sensitive to amoxicillin (the MIC range of resistant isolates to amoxicillin was between 0.19 and 1.5 µg/mL and for amoxicillin-sensitive isolates was 0.016 to 0.125 µg/mL). Discussion: These results collectively showed a relative decrease in the prevalence of H. pylori infection and a relative increase in resistance to amoxicillin compared to the previous decade among adults in Tehran. However, it appears that amoxicillin can still be used in treatment regimens for H. pylori infection.

Keywords: Helicobacter pylori, Prevalence, Infection, Antimicrobial Resistance, Amoxicillin

O102

Co-Delivery of Streptomycin and Hydroxychloroquine by Labeled Solid Lipid Nanoparticles to Treat Brucellosis: An Animal Study

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Can brucellosis-related biochemical and immunological parameters be used as diagnostic and treatment indicators? The goal of this project was to look at biochemical parameters, trace elements, and inflammatory factors in the acute and chronic stages of brucellosis after treatment with streptomycin and hydroxychloroquine-loaded solid lipid nanoparticles (STR-HCQ-SLN). The double emulsion method was used for the synthesis of nanoparticles. Serum levels of trace elements, vitamin D, CRP, and biochemical parameters were measured in rats involved in brucellosis. The therapeutic effect of STR-HCQ-SLN was compared with that of free drugs. In both healthy and infected rats, serum concentrations of copper, zinc, iron, magnesium, potassium, and biochemical parameters of the liver were significantly different. By altering the serum levels of the aforementioned factors, treatment with STR-HCQ-SLN had a positive therapeutic effect on chronic brucellosis. Vitamin D levels declined (46.4%) and CRP levels rose (from 7.5 mg to less than 1 mg) throughout the acute and chronic stages of brucellosis. This study showed that by comparing the biochemical parameters and the levels of trace elements in the serum of healthy and diseased mice in the acute and chronic stages of brucellosis, it is possible to get help from other routine methods for diagnosis.

Keywords: Streptomycin, Nanoparticles

O103

Intracellular Delivery of Antiviral shRNA Using Penetratin-Based Complexes Effectively Inhibits Respiratory Syncytial Virus Replication and Host Cell Apoptosis

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Background Cell-penetrating peptides (CPPs) are effective for delivering therapeutic molecules with minimal toxicity. This study focuses on the use of penetratin, a well-characterized CPP, to deliver a DNA vector encoding short hairpin RNA (shRNA) targeting the respiratory syncytial virus (RSV) F gene into infected cells. RSV is known to cause severe lower respiratory infections in infants and poses significant risks to immunocompromised individuals and the elderly. We evaluated the antiviral efficacy of the penetratin-shRNA complex by comparing its ability to inhibit RSV replication and induce apoptosis with ribavirin treatment. Methods Penetratin- shRNA complexes were prepared at different ratios and analyzed using gel retardation assays, dynamic light scattering, and zeta potential measurements. The complexes were tested in HEp-2 and A549 cells for transfection efficiency, cytotoxicity, viral load, and apoptosis using plaque assays, real-time reverse transcription-polymerase chain reaction (RT-PCR), DNA fragmentation, propidium iodide staining, and caspase 3/7 activation assays. Results The gel shift assay determined that a 20:1 CPP-to-shRNA ratio was optimal for effective complexation, resulting in particles with a size of 164 nm and a zeta potential of 8.7 mV. Transfection efficiency in HEp-2 cells was highest at this ratio, reaching up to 93%. The penetratin-shRNA complex effectively silenced the RSV F gene, reduced viral titers, and decreased DNA fragmentation and apoptosis in infected cells. Conclusion Penetratin effectively delivers shRNA targeting the RSV F gene, significantly reducing viral load and preventing apoptosis without toxicity. This approach surpasses Lipofectamine and shows potential for future therapeutic interventions, especially when combined with ribavirin, against RSV infection.

Keywords: Human Respiratory Syncytial Virus, shRNA, Penetratin, Cell-Penetrating Peptides, Ribavirin, Fusion Gene, Apoptosis

Poster

Accreditation in Medical Laboratory Based on ISO 15189

P1-P10

P1

"Enhancing Diagnostic Accuracy in Medical Laboratories: A Novel Approach Using Machine Learning Models for Predicting Laboratory Results"

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Background: This paper explores the applications of Artificial Intelligence (AI) and Machine Learning (ML) in personalized medicine, focusing on disease diagnosis, medical trend prediction, and the development of therapeutic models. Given the complexity of biological and medical data, AI and ML-based predictive models are capable of simulating complex physiological processes and improving diagnostic accuracy. Method: We searched in databases including PubMed, Scopus, and Web of Science, along with Google Scholar search engine and included 20 relevant studies. The research introduces key innovations in utilizing advanced algorithms such as Deep Learning and Reinforcement Learning to analyze clinical and genetic data, leading to targeted and personalized treatments. Results: Additionally, predictive models are examined that can effectively simulate and assess the risk of diseases such as cancer, diabetes, and cardiovascular diseases. Conclusion: However, despite significant progress in this field, several challenges remain, including data quality, model interpretability, and ethical concerns. This paper, in addition to addressing these challenges, offers key recommendations for overcoming them. The findings of this study indicate that AI and ML have significant potential to transform therapeutic processes and medical predictions, but further model development and the collection of reliable data are required to achieve high efficiency.

Keywords: Artificial Intelligence, Machine Learning, Predictive Models, Personalized Medicine, Deep Learning

P2

Laboratory Hematology: Quality Assurance Approaches

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The clinical laboratory is central to patient care and about 80% of medical decisions are based on the critical diagnostic information it provides. This paper discusses quality assurance (QA) in laboratory operations as a vital component in the accuracy, precision and validity of the results obtained. Over the last five decades, external quality assessment (EQA) schemes have greatly enhanced laboratory reliability through follow up of anomalies in results. The QA measures are internal (IQA) and external quality assessment (EQA), where IQA is concerned with the day-to-day consistency of the results and the latter with the comparison of the results with the external reference values. The focus is therefore laid on the possible sources of preanalytical errors such as clotted or hemolyzed samples which account for the majority of laboratory errors. This article also discusses other QA measures including the Six Sigma method, Levey–Jennings chart, and internal controls for hematology analyzers. Additionally, it discusses the role of personnel, following international standards like ISO 15189, and comparing results between laboratories and instruments. These techniques lead to the development of better clinical laboratory practices and enhanced patient care.

Keywords: Quality Assurance, Quality Control, Laboratory Hematology, Pre-Analytical Errors, Internal Quality Assessment, External Quality Assurance

P3

External Quality Control in Laboratories of Educational Centers/Hospitals Affiliated with Mazandaran Medical Sciences Centers

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External quality control in laboratories of educational centers/hospitals affiliated with Mazandaran Medical Sciences Centers Mehrdad Jalalian. Mohammad Shokrzadeh, Azar Hasel Mehri, Somaieh Jani, Ahmad Tabrizi, Masoumeh Majidi, Reza Hashemi, Hossain Alee Background and objective: The external quality control program distributes similar control samples to different laboratories and evaluates the results obtained with a common criterion. The purpose of this work was to assess the accuracy of the performance of educational/hospital laboratories and prevent possible consequences in the performance of participating laboratories at Mazandaran University of Medical Sciences. Materials and methods: Serum samples free of hepatitis B, C, and HIV were collected and stored in a -20 freezer. Concentration groups were prepared based on the Bowers et al article using ethylene glycol and acetic acid. After stability, they were distributed throughout the province. The results were analyzed with SPSS software. The results were reported to hospitals as excellent, good, acceptable, warning, and unacceptable. Results: Results: The samples were tested at different concentrations. Sample A: Results in the excellent range 4.4%, good range 44.6%, acceptable range 25.2%, warning range 8.6%, and unacceptable range 17.2% and Sample B: Excellent range 7.4%, good range 42.2%, acceptable range 24.6%, warning range 9.8% and unacceptable range 15.8%. Sample C: Excellent range 10.7%, good range 45.8%, acceptable range 17.8%, warning range 13.7% and results in unacceptable range 11.9%. Conclusion: Verification and participation in proficiency testing are recommended to ensure the highest quality of laboratory results are reported.

Keywords: External Quality Control, Laboratories, Hospital

P4

Prevalence of Adenovirus-Associated Gastroenteritis in Pediatric Patients in Northwest Iran

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Background: Acute gastroenteritis (AGE) remains a significant cause of morbidity in children under five, with adenovirus being one of the important viral pathogens responsible for gastrointestinal infections. Adenoviruses are non-enveloped double-stranded DNA viruses that can cause a wide range of clinical manifestations, including respiratory, ocular, and gastrointestinal diseases. Among the various adenoviral serotypes, types 40 and 41 are primarily associated with gastroenteritis, particularly in young children. Despite its global burden, data on the prevalence, seasonal distribution, and demographic characteristics of adenoviral gastroenteritis in specific regions remain limited. This study aimed to investigate the prevalence, seasonal patterns, and demographic associations of adenovirus-induced AGE in pediatric patients in northwest Iran. Methods: A cross-sectional study was conducted in 2023 on 180 children under five years old presenting with acute gastroenteritis (AGE) at a referral hospital. Stool samples were analyzed using Real-Time PCR (RT-PCR) to detect adenovirus. Data were evaluated for seasonal distribution and demographic associations of adenoviral gastroenteritis. Results: Adenovirus was detected in 7.8% of pediatric gastroenteritis cases. The infection was more prevalent among older children, particularly those aged 19 to 26 months. Although no statistically significant association was found between adenovirus prevalence and seasons, most cases were detected during autumn and winter, the colder months of the year. Additionally, no significant association was observed between gender and adenoviral infection rates. Conclusion: Adenovirus is an important viral cause of pediatric acute gastroenteritis (AGE) in northwest Iran, particularly affecting older infants and toddlers. While no significant seasonal variation was observed, most cases occurred during the colder months, highlighting the potential role of environmental and behavioral factors in transmission. These findings emphasize the need for continued epidemiological surveillance, improved diagnostic strategies, and further research on preventive measures to mitigate the burden of adenoviral gastroenteritis in young children.

Keywords: Adenovirus, Acute Gastroenteritis, Pediatric Infections, Epidemiology, Real-Time PCR

P5

The Difference between Silicone Gel and Acrylate in Gelled Tubes

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In all medical diagnostic laboratories, gel tubes are used to separate the serum from the clot Companies offer different brands with different specifications and laboratories use them just because they have IMED. Since the author, as a technical consultant of a company that produces gel tubes, has been comparing these tubes with each other as well as foreign brands for several years, I have reached interesting results The components of gelled tubes include plastic tubes, chelating agents, and gels. There are two different types of gel used in the pipes: silicon oil and butyl acrylateor ethyl acrylate. Most of the imported gel tubes are silica van gel and have a higher price. Typically, the gel in the tube is separated from the bottom of the tube with 3000 centrifuge cycles and placed between the serum and the clot. The behavior of the gel in some tubes is irregular and does not fit completely between the serum and the clot, therefore, it causes a connection between the clot and the serum, which practically causes the laboratory to suffer from pre-analytical errors. Some of them have small, microscopic fragments that eventually fall into the needles of the auto-analyzer devices. But the important point in acrylate gelled tubes is the "cross-reaction" between some of the tests and the gel in the tube. The two errors obtained by the author in the comparison of the tests are errors in TIBC and urea. Compared to Van silica gel tubes, these changes were not observed. Since medical diagnostic laboratories are not aware of this issue, it is necessary to inform the doctoral association or other authorities about this issue, or not to specify the correction coefficients or prevent the distribution of these tubes. Certainly, more tests are needed to accurately determine the correction coefficients.

Keywords: Acrylate, Silicone, Gel Tube

P6

Urgent Alert: Potential Risk of Dengue Infection Transmission Through Blood Transfusion in Iran

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Dengue infection is an emerging public health issue in Iran, with about 149 confirmed newly infected cases. It can be transmitted by the bite of infected Aedes mosquitoes and even nosocomial routes. Due to the rapid replication and geographical spread of the mosquito, there is a potential risk of increased infected individuals. Given the possibility of the transmission of dengue infection through transfusion, it is important to implement policies to improve blood safety. Proper donor selection by utilizing appropriate blood donor questionnaires and performing general physical examinations, along with performing sensitive diagnostic tests on blood donor samples, utilizing pathogen reduction techniques, and implementing lookback programs, can be effective in reducing the risk of transfusion-transmitted dengue virus (TT-DENV).

Keywords: Dengue Virus, Transfusion-Transmissible Dengue, Dengue Viral Infections

P7

Effect of Different Mueller-Hinton Agar Brands on Antibiotic Susceptibility Testing of Staphylococcus aureus

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Introduction: With the increasing resistance of bacteria to antibiotics, conducting antimicrobial susceptibility testing (AST) in laboratory settings is essential. The disk diffusion method is widely used due to its standardization, simplicity, flexibility, and cost-effectiveness. Mueller-Hinton agar (MH agar) is the recommended medium by CLSI and EUCAST because its starch content absorbs bacterial toxins, preventing their interaction with antibiotics. Additionally, the ionic composition, particularly calcium and magnesium, plays a crucial role in antibiotic susceptibility. Objective: This study aimed to evaluate the effect of five different commercial Mueller-Hinton agar brands on the results of Staphylococcus aureus antimicrobial susceptibility testing. Methods: The antibiotic susceptibility of 20 clinical isolates and one standard strain (S. aureus ATCC 25923) was tested against vancomycin, gentamicin, ciprofloxacin, and methicillin using five different commercial Mueller-Hinton agar media. The diameter of the inhibition zone was measured using three methods: double-layer culture, pour plate, and swabbing, and the results were compared with the cation content of each medium. Results: The inhibition zone diameters in the double-layer culture method were smaller than those in the pour plate and swabbing methods, whereas the pour plate and swabbing methods produced more uniform and reproducible results. Analysis of the cation composition showed variation among the five commercial brands, with Quelab medium having the highest levels of essential cations. Additionally, Merck and Sigma MH agar provided more reliable and CLSI-compliant results for both standard and clinical strains. Conclusion: The ionic composition of Mueller-Hinton agar, particularly calcium and magnesium levels, significantly influences antibiotic susceptibility test results. Standardization of culture media is crucial to ensuring accurate and reproducible AST outcomes in clinical microbiology laboratories.

Keywords: Staphylococcus aureus, Antimicrobial Susceptibility Testing, Disk Diffusion, Mueller-Hinton Agar, Cation Concentration

P8

Improving Laboratory Test Validation in the Era of COVID-19: Statistical Approaches and Quality Assurance

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The COVID-19 pandemic highlighted the essential role of laboratory tests in diagnosing and managing the virus. Accurate and reliable laboratory tests are critical in ensuring public health measures, guiding treatment, and controlling the spread of the virus. Laboratory test validation, which ensures precision and consistency, is crucial for test effectiveness. This study investigates the statistical approaches and quality assurance methods used to improve test validation in the era of COVID-19, drawing on data collected from medical diagnostic tests, including PCR, ELISA, and other biomarkers. Our analysis focused on validating diagnostic tests by assessing key statistical metrics such as sensitivity, specificity, and predictive values. Descriptive statistics and correlation analysis were used to examine test results and their relationship with demographic factors such as age, gender, and underlying health conditions. Initial findings show that the sensitivity and specificity of PCR tests remain high, while variations in D-Dimer and CRP values suggest potential insights for diagnosing severe COVID-19 cases. Furthermore, predictive values were evaluated to assess the accuracy of rapid antigen and antibody tests in different patient populations. Quality assurance practices were also highlighted, emphasizing the importance of internal and external proficiency testing, adherence to standard operating procedures (SOPs), and maintaining reproducibility and repeatability of results across different labs. The study underscores the importance of rigorous validation frameworks, especially during public health emergencies, to maintain the reliability of laboratory results and improve overall diagnostic capacity.

Keywords: Laboratory Test Validation, COVID-19 Diagnostics, Statistical Methods, Sensitivity, Specificity, Quality Assurance, Predictive Values

P9

Revolutionizing Laboratory Quality Management: Integrating Six Sigma, Digital Twins, and AI for Virtual Audits and Enhanced Quality Assessment

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Introduction: The intricacies of contemporary procedures are sometimes overlooked by traditional approaches in the quickly changing field of laboratory quality management. This study looks at how Six Sigma, Digital Twins, and Artificial Intelligence (AI) can be combined to improve laboratory quality management. It focuses on virtual audits and improved quality evaluation. Method: This review article was performed within article published in PubMed, Google Scholar and Scopus. The focus on Six Sigma techniques, Digital Twin technology, and AI applications in lab settings led to the selection of pertinent publications. In order to collect actual data and case studies that illustrate the efficacy of these integrated techniques, data banks and repositories were carefully inspected. Result: Through the use of Digital Twin simulations and integrated Six Sigma approaches, the results show notable gains in laboratory efficiency, accuracy, and compliance. Predictive analytics is improved by artificial intelligence, which makes proactive quality evaluations and efficient virtual audits possible. According to laboratories that used this integrated framework, operational efficiency increased by 40% and mistake rates decreased by up to 30%. Conclusion: this study emphasizes how combining Six Sigma, digital twins, and artificial intelligence may revolutionize laboratory quality control. Labs can increase compliance, productivity, and adaptability in a more complex environment by enhancing quality evaluation procedures and enabling virtual audits. Incorporating these technologies is not only advantageous but also necessary for laboratory operations that are prepared for the future.

Keywords: Laboratory Quality Management, Six Sigma, Digital Twins, Artificial Intelligence, Virtual Audits

P10

Elevating Laboratory Excellence: Integrating Six Sigma and ISO 15189 Standards in the New ISO Structure for Enhanced Quality Control

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Introduction: Getting precise and trustworthy diagnostic results depends on maintaining laboratory excellence. This study looks at how Six Sigma techniques and ISO 15189 standards can be combined under the new ISO framework. Improving quality control procedures in medical labs is the goal. Method: This review article was performed within article published in PubMed, Google Scholar and Scopus. by searching this database, 11 articles were found and 5 were removed by reading titles and abtracts.6 articles were selected under the inclusion criteria. All article were chosen from English articles. the keywords were Six Sigma, ISO 15189, Quality Control, Medical Laboratories, Continuous Improvement. Results: Labs saw significant improvements in key performance metrics, such as shortened turnaround times, lower mistake rates, and higher patient satisfaction, by combining Six Sigma principles with ISO 15189 requirements. Both operational efficiency and quality compliance significantly increased as a result of the implementation of these approaches. According to statistical analyses, these combined methods fostered a lasting culture of continuous improvement within the laboratories. Conclusion: The integration of Six Sigma methodologies with ISO 15189 standards enhances laboratory performance and ensures diagnostic quality assurance. This study emphasizes the importance of these methodologies to achieve better clinical outcomes and improve laboratory services.

Keywords: Six Sigma, ISO 15189, Quality Control, Medical Laboratories, Continuous Improvement

Advanced Technologies in Blood Transfusion Practice from Donor Vein to Patient Vein

P11-P20

P11

Advancements in Transfusion Medicine: From Molecular Diagnostics to Blood Management

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Background: In recent decades, transfusion medicine has experienced remarkable progress, particularly in molecular diagnostics, blood management, and advanced technologies. Key topics include the application of artificial intelligence in blood banks, the development of cost-effective diagnostic methods for low-resource areas, and important regulatory changes. These advancements promise a bright future for transfusion medicine. Method: A review of articles from the Transfusion Today journal in 2024 was conducted. Results: In malaria-endemic regions, the RTS, S/AS01 vaccine has reduced severe anemia cases and improved blood resource management. In platelet management, new storage methods have extended shelf life, and techniques like Luminex and ELISA have helped address platelet resistance. In molecular diagnostics, tools like next-generation sequencing (NGS) and cell-free DNA (cfDNA) testing enable accurate blood group identification and detection of rare antigens. Furthermore, advancements in laboratory automation have enhanced precision and safety. Conclusion: Despite challenges such as high costs and the need for specialized training, emerging technologies like artificial intelligence and Raman spectroscopy hold the potential to revolutionize diagnostics and personalized treatments. To further progress, focusing on the development of cost-effective technologies, international collaborations, and big data analytics can make blood transfusion services safer and more accessible.

Keywords: Transfusion Today, Artificial Intelligence, Platelet, Laboratory Automation

P12

Platelet Concentrates from Apheresis and Pooled Platelet-Rich Plasma: Comparative Analysis of Platelet-Derive Microparticles

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Background: Therapeutic platelet transfusions in adults typically require 4-6 units of platelets from whole blood or single unit of apheresis platelets. The count of platelet-derive microparticles (PMPs) may be affected by methods of preparation and storage of the platelet concentrates (PCs). This study aimed to assess the effect of the production process of apheresis-Pcs and leukoreduced pooled-PCs collected from platelet-rich plasma (PRP), along with their storage, on the generation of PMPs and platelet activation. Methods: Four apheresis-PCs were collected using the Haemonetics MCS+ device and four pooled platelet concentrates were prepared by integrating six individual platelet units from PRP, followed by leukofilteration. We evaluated P-selectin expression (as a marker of platelet activation), and platelet microparticle countswere measured on days 1, 3, and 5 using flow cytometry. Results: The PMPs count was significantly higher on day 5 compared to day 1 in the pooled PRP-PCs. For the apheresis-PCs, the PMPs count was higher on day 3 and day 5 compared to day 1. Additionally, the PMPs count in the apheresis-PCs was significantly higher than the pooled PRP-PCs on day 3. The P-selectin expression on the first day in the apheresis-PCs was significantly higher than that of the pooled PRP-PCs, but this difference disappeared during storage. Conclusions: The pooled PRP-PCs exhibited better preservation of platelet activation and lower PMPs count during the initial days of storage compared to apheresis-PCs.

Keywords: Platelets, Apheresis, Microparticle, Pooled

P13

A Comprehensive Analysis of Immunological Mechanisms Underlying Adverse Reactions Regarding Fresh Frozen Plasma Infusion

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Background: Fresh frozen plasma (FFP) infusion is a vital and dynamic therapeutic intervention in patient care, yet it is associated with potential adverse effects. This study aimed to explore the adverse reactions following FFP infusion in patients admitted to Hafez Hospital and to elucidate the underlying immunopathological mechanisms and molecular pathways involved. Methods: The study analyzed data from patients who received blood products over an eight-year period. Adverse effects observed post-infusion were systematically recorded. Using the GSE104107 dataset and R Software, key genes exhibiting significant changes in mononuclear cells after FFP infusion were identified. Bioinformatics tools were employed to analyze biological pathways and immunological mechanisms contributing to adverse reactions. Results: Adverse effects were reported in 0.39% of patients, with allergic reactions being the most prevalent. FFP was identified as the primary trigger for these allergic responses. Gene expression analysis revealed significant alterations in genes associated with TNF and IL-17 signaling pathways. These genes were implicated in molecular functions related to cytokine and chemokine receptors, enhancing myeloid and leukocyte chemotaxis. The findings suggest that FFP may activate host immune cells, leading to allergic reactions. Conclusion: This study highlights the necessity of closely monitoring patients receiving FFP infusion and underscores the importance of further research to improve FFP safety by understanding immune-mediated pathways. By identifying key molecular and immunological mechanisms, this work provides a foundation for developing strategies to mitigate adverse reactions associated with FFP transfusion.

Keywords: Fresh Frozen Plasma, Adverse Effects, Allergic Reaction, TNF Signaling, IL-17 Signaling

P14

The Application of Microfluidics and 3D Bioprinting in Artificial Blood Production and Blood Transfusion Optimization

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Background: Artificial blood refers to substances designed to mimic the oxygen-carrying capacity of natural blood, often used in situations where blood donations are scarce or not feasible. In recent years, 3D bioprinting has achieved widespread recognition and had an enormous effect on healthcare. In this review we attempt to explores the convergence of microfluidics and 3D bioprinting as enabling technologies for revolutionizing artificial blood production and optimizing blood transfusion strategies and objectively evaluate the state-of-the-art, difficulties, and potential future possibilities of integrating these technologies. Methods: In this review we demonstrated searches with PubMed, Google Scholar, and medical journals identifying articles relevant to our topic. Results: The production and characterization of nanoscale oxygen carriers are made achievable by the outstanding control over fluid dynamics provided by microfluidic platforms. For improved erythropoiesis, 3D bioprinting enables the production of complicated, three-dimensional structures that closely resemble the natural bone marrow microenvironment. Additionally, the production of in vitro models for assessing the immunological response, hemocompatibility, and possible toxicity of artificial blood replacements is made simplified by the combination of microfluidics and 3D bioprinting. Conclusions: There is great potential for developing artificial blood production and enhancing the results of blood transfusions as a result of the combination of microfluidics and 3D bioprinting. The potential of these integrated technologies to address important issues in regenerative medicine and transfusion medicine is highlighted in this study. With its capacity to produce useful components with a variety of characteristics, polymer 3D printing is constantly advancing and pushing beyond the boundaries of engineering and medicine.

Keywords: Microfluidics, 3D Bioprinting, Artificial Blood Production, Blood Transfusion

P15

Artificial Intelligence: A Novel Approach for Blood Donation Management

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Artificial intelligence: a novel approach for blood donation management Diba Rezapour1, Mehdi Jahedi Zargar2* 1.Student in Laboratory Sciences, Student Research Committee, School of Allied Medicine, Alborz University of Medical Sciences, Karaj, Iran 2.Department of Medical Laboratory Sciences, school of Allied Medicine, Alborz University of Medical Sciences, Karaj, Iran Introduction: Providing an adequate blood supply in healthcare systems is essential to saving patients' lives and improving the quality of treatment. Artificial intelligence (AI) can optimize blood donation processes. It is particularly important to use data-driven tools to recruit and retain donors and predict demand. Methodology: In this review study, 2,850 articles were identified by searching for the keywords "blood donation," "artificial intelligence," and "machine learning" in the scientific databases Google Scholar, Scopus, PubMed and Cochrane. Subsequently, 52 articles were reviewed using EndNote software, and 20 outstanding articles were selected for in-depth analysis. Findings: This review study highlights the significant role of artificial intelligence in improving blood donation processes. Key applications include donor selection, identifying factors influencing blood donation, predicting donor behavior patterns, and managing seasonal variations. Machine learning and data mining algorithms assist in identifying potential donors, recruiting in emergency situations, and designing incentive programs to boost participation from underrepresented groups, such as women. Additionally, this technology aids in predicting seasonal fluctuations and enhancing the donor experience. A major focus is optimizing processes to reduce blood wastage due to expiration and manage blood shortages effectively. Conclusion: Artificial intelligence enhances the blood donation process by analyzing data and predicting demand. Identifying blood donation patterns and implementing targeted solutions, such as smart advertising campaigns, optimizing scheduling, and providing tailored incentives, increase donor participation. This technology helps reduce blood wastage, improve resource allocation, and ensure that patients have access to sufficient, high-quality blood during critical periods. Keywords: Artificial intelligence (AI), Machine learning (ML), Blood donation.

Keywords: Artificial Intelligence (AI), Machine Learning (ML), Blood Donations

P16

The Immunogenic Feature of KLH-Conjugated Peptide of RhD as a Blood Group Antigen in Culture Medium

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Background: Immunization against each antigen such as RhD blood group antigen is done to produce antibodies in various ways. One of the effective methods is in vitro immunization (IVI). For the immunization of B lymphocytes, both complete protein and specific peptide sequence can be utilized. synthetic peptides have advantages as they can target specific regions of the target protein and do not require antigens derived from humans or animals. Despite these benefits, synthetic peptides necessitate conjugation with a larger protein known as a carrier for the effective immunization. Methods: The synthetic peptide used for immunization was designed against the amino portion of the Rh protein, consisting of 30 amino acids. To enhance the immunogenicity of the peptide in question, it was conjugated with KLH protein known as a carrier. PBMCs were separated from the whole blood of an O-blood donor by density gradient centrifugation and using Ficoll reagent. Then the cells were cultured with the conjugated peptide together with IL-4 and INF-γ cytokines in a cell culture plate with RPMI medium. After 5-7 days of immunization, the cell culture supernatant was collected and examined for antibody production. Results: To assess antibody production in the culture medium, two types of ELISA plates were designed: one coated with AHG and the other with a BSA-peptide conjugate. This approach aimed to evaluate total antibody production without regard to specificity, as well as to identify peptide-specific antibodies. The optical density readings at 450 nm confirmed the presence of antibodies on both types of coated plates. Additionally, the influence of cytokines; particularly IL-4 was shown during the immunization process by the increased antibody production. Furthermore, the efficacy of the peptide-KLH for immunization was highlighted when compared to the whole RhD protein. Conclusion: using the KLH-conjugated peptide for IVI against the RhD antigen is a feasible approach.

Keywords: Synthetic Peptide, Antibodies, Immunization, RhD Antigen

P17

Nanotechnology in Blood Preservation: Enhancing Stability of Blood Components with Nanoparticles

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Background: The stability of blood components, such as red blood cells, platelets, and plasma, is critical for their therapeutic applications, especially during storage and transportation. Blood components are susceptible to degradation, which affects their efficacy. Traditional methods to extend stability, like refrigeration, often fail to prevent oxidative damage and clot formation. Recent advancements in nanotechnology, particularly the use of nanoparticles, have opened new avenues for improving the stability of blood components. Methods: The data were collected by searching PubMed, Scopus databases, and Google Scholar search engine. The advanced search keywords were: “Blood products,” “nanoparticles,” “Nanodiamonds,” “Stability” and, “Blood Preservation.” The search was limited to English studies and accessible full texts. Review, duplicate, and non-relevant articles were excluded. Results: In this review, 70 articles were initially retrieved from database searches, and 46 articles met the inclusion criteria after preprocessing and screening. Nanoparticles, particularly lipid-based, polymeric, and metal nanoparticles, have been extensively studied for their potential to stabilize blood components. These nanoparticles are designed to interact with blood cells and plasma proteins, protecting them from oxidative damage, preserving cellular integrity, and maintaining their functionality over time. Conclusion: Nanoparticles represent a promising approach to enhance the stability of blood components. Their application could revolutionize blood storage and transfusion practices, offering longer shelf life and improving therapeutic outcomes. Further studies are needed to refine nanoparticle formulations and evaluate their clinical safety and efficacy.

Keywords: Blood Products, Nanoparticles, Nanodiamonds, Stability, Blood Preservation

P18

Enhancing Blood Donation: Challenges, Motivations, and Future Strategies

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Background: Blood donation is a critical component of modern healthcare systems, ensuring a stable and adequate blood supply for patients in need. However, donor recruitment and retention remain significant challenges worldwide. Understanding the factors influencing blood donation, as well as strategies to enhance donor participation, is essential for improving blood supply sustainability. Methods: This review synthesizes recent literature on blood donation, focusing on donor motivation, barriers to donation, and strategies for increasing donor participation. Studies from various regions and healthcare settings were analyzed to provide a comprehensive understanding of the global landscape of blood donation. Results: The review identifies key motivational factors, such as altruism, social responsibility, and incentives, alongside barriers, including fear, lack of awareness, and logistical constraints. Effective strategies for improving donation rates include targeted awareness campaigns, enhanced donor care, and innovative recruitment methods leveraging digital platforms. Conclusion: Addressing the challenges associated with blood donation requires a multifaceted approach involving education, policy changes, and technological advancements. By implementing evidence-based strategies, blood donation systems can be optimized to ensure a stable and sustainable blood supply.

Table 1: Factors Influencing Blood Donation and Strategies for Improvement

Factor	Description	Improvement Strategies
Motivational Factors	Altruism, social duty, personal satisfaction	Awareness campaigns, recognition programs
Barriers to Donation	Fear of needles, misinformation, inconvenience	Education, improved donor care, flexible donation hours
Recruitment Strategies	Digital platforms, mobile donation units, incentives	Social media campaigns, workplace donations, community outreach
Retention Strategies	Positive donor experience, follow-up communication	Donor appreciation programs, personalized engagement

Keywords: Blood Donation, Donor Motivation, Healthcare Systems, Recruitment Strategies, Transfusion Medicine, Public Health, Donor Retention

P19

Determining the Frequency of Hemoglobin Above 18 g/dL in Donors Referred to the Iranian Blood Transfusion Organization

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Background: The high quality blood and blood products has always been a primary concern for the Blood Transfusion Organization, necessitating the improvement of donor selection systems that Consider comprehensive and standard criteria for selecting donors, as it should not only maintain the health of donors and recipients but also prevent a reduction in blood reserves High hemoglobin is one of the limitations in the preparation of products. The aim of this study was to examine the hemoglobin levels above 18 in blood donors in Iran. Methods: This study was conducted in 21 provinces of Iran with a total of 12,504 donors. The questionnaires completed by the donors included demographic information, history of diseases related to high hemoglobin, family history of hemoglobin-related diseases in first-degree relatives, history of tobacco and cigarette use and its quantity, use of specific medications, residence at high altitudes and occupation. the number of individuals who had high hemoglobin levels in the initial capillary method (Hemocue) was re-confirmed by the venous method (Cell counter). Results: Out of the 12,504 questionnaires, we confirmed that 558 donors had hemoglobin levels above 18 gr/dl. the highest percentages belong to Alborz with 13.7% and Isfahan with 10.3%, while the lowest percentage is in Zanjan with 1% There is also a significant relationship between the number of donors with hemoglobin levels above 18 gr/dl and their living conditions in large industrial and polluted cities, as well as the frequency of tobacco use, especially cigarettes, altitude above sea level. Conclusion: In this study, the importance of determining the maximum hemoglobin limit for blood donation across the country is highlighted. high hemoglobin concentrations in routine blood transfusion centers can lead to issues with product quality, the plasma from these individuals is often unusable and the red blood cells produced have a high concentration, leading to problems during blood transfusions

Keywords: Hemoglobin, Donors, Quality Control

P20

Role of Erythropoiesis-Stimulating Agents in Transfusion Management for Thalassemia Patients

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Background: In recent years, innovations in transfusion medicine have introduced erythropoiesis-stimulating agents (ESAs) such as erythropoietin, Epoetin alfa, Epoetin alfa-epbx, and Retacrit to manage thalassemia. These agents, used alongside red blood cell transfusions, aim to reduce the need for frequent transfusions in some thalassemia patients. This study evaluates the role of ESAs in decreasing transfusion frequency and improving patient management. Methods: A comprehensive search was conducted using specific keywords in PubMed and Google Scholar to gather relevant scientific literature. Results: The findings indicate that ESAs stimulate red blood cell production in the bone marrow, reducing the need for frequent transfusions and helping maintain stable hemoglobin levels. This minimizes complications such as iron overload and alloimmunization. Epoetin alfa, a synthetic form of erythropoietin, requires regular dosing due to its shorter half-life. Epoetin alfa-epbx, a biosimilar to Epoetin alfa, is used similarly for anemia treatment. Erythropoietin, the natural hormone regulating red blood cell production, is mimicked by recombinant forms like epoetins. Retacrit, another biosimilar to Epoetin alfa, increases red blood cell production in anemia-causing conditions. ESAs can improve quality of life by alleviating anemia symptoms such as fatigue and weakness. However, they may also cause side effects like high blood pressure, blood clots, and an increased risk of certain cancers. Additionally, combining ESAs with blood transfusions may elevate the risk of iron overload in some patients, despite efforts to reduce transfusion frequency. The high cost of ESAs and limited accessibility, depending on healthcare coverage and insurance, further complicate their use. Conclusion: In conclusion, it is crucial to discuss the potential benefits and risks of ESAs with healthcare providers to determine the most appropriate treatment approach for thalassemia. Treatment plans should be individualized based on factors such as disease severity, iron overload status, and patient response to therapy.

Keywords: ESAs, Erythropoiesis-Stimulating Agents, Thalassemia Major, Transfusion

Advances in Viral Hepatitis Multi-omics Research

P21

P21

Prevalence of Various Hepatitis C Genotypes among Chronic HCV Patients in Golestan Province

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Background: Hepatitis C virus (HCV) has different genotypes throughout the world. Based on its genetic variability, HCV is classified into at least six genotypes and a series of subtypes. HCV genotyping is important for prediction of clinical outcome and therapy of HCV infection. so recent studies have focused on determination of HCV genotypes. The purpose of this study was to determine the distribution of HCV genotypes among HCV positive patients in Golestan province, Iran. Methods: In this cross-sectional study, 90 patients with anti-HCV-positive specimens were enrolled. Following extraction of viral RNA of the serum, HCV-RNA was detected using polymerase chain reaction (PCR) and then HCV genotypes performed by AB-Anaitica kit according to the specified protocol assay. Results: The highest frequency was noted for subtype 3a (51.85%) followed by subtype 1a (29.65%), 1b (7.40%), 4 (5.55%), 2 (3.70%) and 6 (1.85%). Subtype 3a was the most frequent genotype in patients over 40 years of and subtype 1a was the most frequent in patients under 40 years. Conclusions: Genotypes 3a was predominant in HCV positive patients in Golestan province. These variations in the epidemiology of HCV reflect differences in the routes of transmission, status of public health, lifestyles, and risk factors in different groups and geographic regions of Iran.

Keywords: Hepatitis C, Genotype, Iran

Cancer Screening Tests: Evaluating the Evidence

P22-P46

P22

Investigating the Frequency of rs1569686 (-579G>T) Polymorphism of DNMT3B Gene in Patients with Acute Myeloid Leukemia

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Acute myeloid leukemia (AML) is the most frequent type of leukemia among adults, accounting for almost 80% of all cases. Epigenetic changes, including methylation, significantly impact the reduction of gene expression and are generally considered as “cancer hallmark”. The DNMT3B gene is responsible for denovo methylation. Different polymorphisms can significantly impact the function of the DNMT3B gene. AML heterogeneity based on DNA methylation can improve clinical diagnosis and prognosis. The current study was conducted to investigate the frequency of the rs1569686 polymorphism in the DNMT3B methyltransferase gene in fifty newly diagnosed AML patients and fifty healthy controls. The relationship between the frequency of this polymorphism and mutation of FLT3 and NPM genes, as well as age, gender, and hematological factors of patients, was evaluated. The frequency of the rs1569686 polymorphism was determined by Tetra primer ARMS PCR. The results were analyzed using SPSS software and logistic regression tests and Fisher's exact test. According to the findings, There was no significant difference in the frequency of rs1569686 polymorphism between healthy individuals and AML patients. Also, no significant correlation was observed between these results and FLT3 and NPM gene mutation, age, gender, and hematological factors of the patients. Although the mutant state was more frequently observed in patients, it was not statistically significant (p-value>0.005). Further investigations could pave the way for discovering a novel method for cancer screening and early diagnosis.

Keywords: Acute Myeloid Leukemia, DNMT3B, Polymorphism, Methylation

P23

Diagnostic Value of Tumor Biomarkers in the Detection and Treatment of Gastric Cancer

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Gastric cancer is a significant cause of cancer-related mortality worldwide, necessitating advancements in diagnostic and therapeutic strategies. Tumor biomarkers have emerged as pivotal tools for early detection, prognosis, and treatment monitoring. Among the widely studied biomarkers, carcinoembryonic antigen (CEA), carbohydrate antigen 19-9 (CA19-9), and carbohydrate antigen 72-4 (CA72-4) are prominent, with CA72-4 demonstrating superior sensitivity and specificity for gastric cancer diagnosis. Additional biomarkers, such as CA125 and lactate dehydrogenase (LDH), contribute valuable prognostic information, particularly in advanced cases. Emerging molecular markers, including circulating tumor DNA (ctDNA) and methylated septin 9 (mSEPT9), further enhance the diagnostic landscape by offering non-invasive approaches for disease monitoring and the detection of minimal residual disease. This study synthesized data from the literature to evaluate the diagnostic accuracy and clinical utility of these biomarkers in gastric cancer. The findings reveal that combining CA72-4 with CEA and CA19-9 significantly enhances diagnostic sensitivity and specificity, while ctDNA holds promise for precise tracking of disease progression and therapeutic efficacy. Biomarker-based surveillance enables the earlier detection of recurrence and facilitates tailored treatment approaches, ultimately improving patient outcomes. Integrating traditional biomarkers with advanced molecular technologies could revolutionize gastric cancer management, providing a robust framework for personalized medicine. These advancements underscore the critical role of tumor biomarkers in improving survival rates and quality of care for patients with gastric cancer. Future research should focus on standardizing biomarker applications and further exploring their integration into routine clinical practice to address existing challenges.

Keywords: Gastrointestinal Cancer, Colorectal Cancer, Tumor Markers, Biomarker

P24

Innovative Cancer Screening and Detection Methods for Reducing Turnaround Time: A Systematic Review

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Introduction & Objective: Advancements in cancer detection methods have significantly redefined diagnostic capabilities, emphasizing precision, accessibility, and reduced turnaround time (TAT). This systematic review explores cutting-edge technologies in cancer screening and detection, highlighting innovations that integrate microfluidics, biosensors, and artificial intelligence (AI) to enhance diagnostic workflows. Emerging methods, focusing on minimally invasive techniques for detecting circulating tumor cells (CTCs), extracellular vesicles (EVs), and microRNAs. Methods: Following the PRISMA guidelines, PubMed, Embase, Web of Science, were systematically searched using keywords including “Cancer Biomarker”, “Point of care test” and “Microfluidic”, “Biosensor”, and “turnaround time” covering studies and innovations from 2019 to 2025. Two independent authors screened the results, with a third resolving conflicts. Observational studies assessing novel methods in cancer general biomarker analysis for TAT reduction were included, while review articles, editorials, and conference papers were excluded. Results: Out of 132 initial studies, 28 met the inclusion criteria after removing 45 duplicates and 59 irrelevant articles this review highlight innovations such as CRISPR-powered systems and surface plasmon resonance (SPR) biosensors, which reduce TAT from hours to minutes, with methods like paper-based devices providing cost-effective solutions for low-resource settings. Conclusion: emerging cancer detection technologies, combined with the transformative potential of digital pathology, are poised to address key challenges in traditional workflows, offering scalable and efficient solutions. These advancements hold promise for integrating real-time, patient-centered diagnostics into routine clinical practice, ultimately improving early detection and patient outcomes.

Keywords: Cancer, TAT, Biomarker, POCT

P25

Effect of Oral Silymarin on Liver Function in Pediatric Acute Lymphoblastic Leukemia During the Maintenance Phase: A Double-Blind Randomized Trial

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Introduction: Liver dysfunction is a prevalent condition among patients with acute lymphoblastic leukemia (ALL). This study examines the impact of oral silymarin on liver function in pediatric patients with acute lymphoblastic leukemia (ALL). Methods: In the present double-blind clinical trial study, 121 patients, all over 5 years of age, were enrolled in this double-blind clinical trial. They were randomly assigned to either a silymarin treatment group or a placebo group. The silymarin group received either 70 mg of silymarin in capsule form twice daily or 5 ml of silymarin syrup three times a day (equivalent to 50 mg of silymarin per 5 ml). Liver function was monitored monthly for 9 months, measuring alanine aminotransferase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP), gamma-glutamyl transferase (GGT), bilirubin, albumin, and cholesterol. Results: The findings indicated that the silymarin group experienced a significant reduction in ALT, AST, GGT, and bilirubin levels ($p < 0.05$), suggesting a protective effect on the liver. However, no significant changes were observed in ALP, albumin, or cholesterol levels ($p > 0.05$). The authors attribute the liver-protective effects of silymarin to its potent antioxidant properties. Discussion: this study suggests that silymarin may be a promising treatment to improve liver function in pediatric patients with ALL, offering a potential therapeutic benefit alongside standard treatment for liver dysfunction.

Keywords: Acute Lymphoblastic Leukemia, Pediatrics, Liver Function Tests, Silymarin, Liver Toxicities

P26

Differential Expression of Long Non-Coding RNA LINC01611 in Patients with Colorectal Cancer

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Background: Colorectal cancer (CRC), a prevalent malignancy with high recurrence and poor prognosis, involves long non-coding RNAs (lncRNAs) as key diagnostic and prognostic biomarkers. The current study evaluated lncRNA (LINC01611) expression in CRC tissues versus adjacent margins. Methods: The study involved 96 tumor tissues and adjacent margins that were collected from 48 patients with CRC from a single ethnic group. LINC01611 was identified using GEO microarray data and R/BioConductor as the selected lncRNAs with higher fold change and less P value. Paired tumor and margin tissues were collected from each patient and RNA was extracted. lncRNA expression was analyzed by real-time with GAPDH as the internal control. Data was analyzed using multivariable regression and Wilcoxon signed rank with significance set at $P<0.05$. Results: Most patients were males (58.3%) with a mean age of 59.5±3.53 years. The majority of patients exhibiting lymph node metastasis (60.4%), moderate to well-differentiated tumors (58.3%,) and 20.8% had stage IV tumors. The findings showed that LINC01611 expression level was significantly lower in tumor tissues compared to adjacent margins ($P<0.001$). LINC01611 expression was significantly associated with tumor differentiation ($P<0.05$). Multivariable regression analysis showed that a family history of CRC significantly influenced LINC01611 expression by regression coefficient (b) of (b=1.03; 95% CI: 0.30, 1.76, P=0.007), while other variables were not significantly associated ($P>0.05$). Conclusion: The findings illustrated that LINC01611 expression was significantly reduced in CRC tumor tissue compared to the tumor's margin, suggesting its potential roles in CRC pathogenesis and as biomarker for tumor progression.

Keywords: Colorectal Cancer, LINC01611, Long Non-Coding RNAs

P27

Use of Iron Nanoparticles in Detecting PSA Antigen with Luminometry Techniques

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Use of Iron Nanoparticles in Detecting PSA Antigen with Luminometry Techniques Mahsa Kalantari 1*, Bahram Amini2 Background Prostate-specific antigen (PSA) is a critical biomarker for the diagnosis and monitoring of prostate cancer. Traditional detection methods often lack the necessary sensitivity and specificity, necessitating innovative approaches. Recent advancements in nanotechnology, particularly the application of iron nanoparticles (FeNPs), have emerged as promising solutions for enhancing PSA detection through luminometric techniques. Methods A comprehensive literature search was conducted using databases such as PubMed, Scopus, and Google Scholar, focusing on studies published between 2018 and 2024. The keywords included "iron nanoparticles," "PSA detection," "luminometry," and "biosensors." The inclusion criteria focused on studies that utilized FeNPs for PSA detection through luminescence-based methods. Results The reviewed studies consistently reported that FeNPs significantly enhance the specificity and sensitivity of luminometric detection of PSA through improved signal amplification. For instance, iron nanoparticles functionalized with antibody conjugates demonstrated increased sensitivity, enabling PSA detection at picogram levels. Comparative analyses showed that these nanoparticle-modified luminometry techniques outperform traditional methods in terms of detection limits and response times. Additionally, the integration of FeNPs into luminometric systems improved signal intensity and reduced background noise, leading to more accurate quantification of PSA levels from complex biological samples. However, challenges such as nanoparticle aggregation, reproducibility, and scalability remain. Conclusion Iron nanoparticles represent a transformative approach to PSA detection, significantly improving the sensitivity and specificity of luminescent assays compared to conventional methods. The integration of FeNPs not only enhances signal output but also facilitates rapid and cost-effective testing methodologies. Future research should focus on optimizing the synthesis and functionalization of FeNPs to further improve assay performance and explore their clinical applicability in prostate cancer diagnostics.

Keywords: Iron Nanoparticles, PSA Detection, Luminometry, Biosensors

P28

Correlation between C-MET Expression at Protein Level and Different Stages of Colorectal Cancer in Iranian Patients

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Background: colorectal cancer is one of the most common. The cancer begins from adenoma and if it isn't removed in the early stages, it will be progress to carcinoma due to mutation enhancement. Biomarkers Can be used for diagnosis, prognosis and prediction of cancer and play a critical role in the clinical management of the patients. CMET is one of the cell surface receptors that plays an important role in the invasion of cancer cells. Therefore, we investigated the CMET expression in different stages of colorectal cancer to evaluate its potential prognostic significance in different stages of colorectal cancer. Methods: after preparation of 45 paraffin tissue sections, protein expression level was investigated by using immunohistochemistry technique. Results: The CMET was statistically correlated with TNM- stage. There was a significant difference in protein expression between Stage I and Stage III, IV and also Stage II with Stage III, IV. Also, there was no significant difference between normal tissue and Stage I and II, but compared to Stage III and IV, difference was significant. Conclusion: The higher expression of CMET in advance stage is probably contributed to the invasive nature of tumor cells and metastases. Therefore, CMET could be able to distinguish higher stages from normal and early stages, but it is unable in determining the exact stage of the disease.

Keywords: Colorectal Cancer, CMET, Biomarker, Immunohistochemistry

P29

Examining the Prevalence of Papilloma Virus in the Samples of Patients with Symptoms Referred to the Laboratories of Mazandaran Province in 1402

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Background and purpose: HPV is the most common sexually transmitted virus that causes cervical cancer, which is the fourth most common cancer in women. In this study, samples from patients referred to laboratories in Mazandaran province in 2013 were collected with the aim of determining the frequency of the virus in men and women, its frequency in 4 age groups, and high- and low-risk genotypes, and cytology slide examination was performed. Materials and methods: The study population included patients suspected of HPV referring to private and government laboratories in Mazandaran province in 1402. In this study, samples were taken from 5240 patients and examined using an RT-PCR kit. Findings: In this study, out of a total of 5240 samples, 1971 positive cases (37.61%) were positive, of which 92.8% were women and 7.2% were men. The majority of samples were from the age group of 30-40 years (58.20%) and over 50 years of age, the lowest (3.40%). The highest frequency of high-risk genotypes was H16, H52, H53, and low-risk genotypes were L6, L11, L42, respectively. And the highest frequency among high-risk and low-risk genotypes was L6, H16, H52, and... genotypes, respectively. In cytology slide examination, (16.66%) was HSIL, (58.42%) was LSIL, and (24.92%) was Ascus. Conclusion: With timely and rapid diagnosis, especially of high-risk genotypes, using RT-PCR molecular methods, the patient can be saved from death.

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

P30

EZH2 Upregulates Notch Signaling Pathway Genes and Increases Cell Migration in Gastric Cancers

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Aims and background: Gastric cancer, faced different therapeutic imperfections such as chemoresistance, dangerous side effects, and non-specificity of the treatments. Our aim in the present study was to investigate the potential of the Enhancer of Zeste Homolog 2 (EZH2) gene as a therapeutic target through analyzing its role in cell migration and regulation of Notch signaling pathway in gastric cancer. Material and methods: The overexpression and silencing studies of EZH2 gene were performed in MKN-45 and AGS gastric cancer cell lines using pCMV3-ORF-HA and RNAi-Ready p SIREN-Retro Q Retroviral vectors, respectively. The cell migration was assessed using wound healing and closure assays. The effect of EZH2 overexpression and silencing on the Notch signaling pathway was evaluated using real-time PCR in the cells. Results: The EZH2 expression is directly correlated with an increase in rate of cell migration. Furthermore, EZH2 increased expression of the majority of the Notch signaling pathway genes including MAML, HES5, NOTCH1, NOTCH2, NOTCH3, HEY1, and HES1 in MKN and AGS cells. Conclusion: EZH2 enhances the cell migration capacity in gastric cancer, and modulate expression of Notch signaling pathway gene as an upstream regulator. EZH2 can be considered as a proper target for the treatment of gastric cancer.

Keywords: Enhancer of Zeste Homolog 2, EZH2, Gastric Cancer, Notch Signaling Pathway, Cell Migration

P31

The Role of Circulating Tumor DNA in Oncology

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Background: New methods for molecular diagnosis are now available in oncology thanks to the discovery of circulating tumor DNA molecules in the plasma of cancer patients. By utilizing blood samples, clinical practice is on the verge of new discoveries from the analysis of cell-free DNA (cfDNA). The method, known as a “liquid biopsy”, consists of analyzing therapeutic targets and drug-resistant conferring gene mutations in circulating tumor cells and cell-free circulating tumor DNA (ctDNA). Methods: Our review's findings were derived from analyzing publications in the PubMed, Scopus, and WOS databases using keywords cell-free DNA, circulating tumor DNA, diagnosis and cancer. Results: Studies have shown that ctDNA extracted after the completion of curative therapies can act as an indicator of patients who have evidence of residual, radiographically occult cancer. Tracking ctDNA mutations with ddPCR can identify MRD in patients with breast cancer, allowing for earlier identification of patients at risk of tumor relapse. Chaudhuri et al. demonstrated that detecting ctDNA prior to radiographic progression is possible in patients treated for localized lung cancer. This was extended to ctDNA mutation profiles associated with positive responses to TKIs or immune checkpoint blockades, with similar findings in stage II colorectal cancer patients. Conclusion: Liquid biopsies are becoming more popular in cancer research as a non-invasive, rapid and simple method for tracking the progression of diseases. In both clinical trials and, potentially, in routine clinical management, real-time ctDNA analysis has promise as a useful tool in precision oncology.

Keywords: Cell-Free DNA, Circulating Tumor DNA, Diagnosis, Cancer

P32

Mycoplasma Hominis as One of the Potential Causes of Prostate Cancer…?

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Background: Mycoplasma hominis, an opportunistic pathogen in human genitourinary tract, can cause chronic infection in the prostate. Intracellular survival of M. hominis leads to a prolonged presence in the host cells that can affect the cell's biological cycle. In the present study, we aimed to evaluate the frequency of M. hominis DNA in prostate tissue of Iranian patients with prostate cancer (PCa) in comparison to a control group with benign prostatic hyperplasia (BPH). Methods This research was a retrospective case-control study using 61 archived formalin-fixed paraffin-embedded (FFPE) blocks of prostate tissue from patients with PCa and 70 FFPE blocks of patients with BPH. Real-time PCR, targeting two different genes, 16S rRNA and yidC, in the M. hominis genome was performed for all specimens. Results Out of 61 blocks of prostate biopsy from patients with PCa, eight samples (13%) were positive for M. hominis, while the bacterium was not detected in any of the 70 blocks of patients with BPH (P value, 0.002). Conclusions The high frequency of M. hominis in patients with PCa likely shows a hidden role of the organism in prostate cancer during its chronic, apparently silent and asymptomatic colonization in prostate.

Keywords: Real-Time PCR, Prostate, Prostatitis, Benign Prostatic Hyperplasia, Carcinogenic, yidc

P33

Elevated SOX-9 Expression as a Biomarker for Lung Cancer Progress and Chemotherapy Response: A Combined Analysis of PBMC and Tissue Levels

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Background: SOX-9 has been involved in many malignancies, including lung cancer. Nevertheless, its role in disease progression, metastasis, and chemotherapy response is not yet determined. In the present study, expression level and diagnostic significance of SOX-9 in lung tissue and in peripheral blood mononuclear cells (PBMCs) in lung cancer cases and healthy controls have been examined for its association with clinicopathologic factors. Methods: 60 subjects (30 cases and 30 controls) have been included in a case-control study. Immunohistochemistry (IHC) analysis evaluated expression of SOX-9 in lung tissue samples, and real-time PCR evaluated gene expression of SOX-9 in PBMCs. Associations between expression of SOX-9, stage of the tumor, metastasis, smoking, chemotherapy, and disease prognosis have been evaluated with statistics. Results: Lung cancer cases exhibited increased expression of SOX-9 when compared with healthy controls ($p < 0.05$). Higher expression of SOX-9 exhibited a positive association with increased stage of the tumor, metastasis, and with a positive history of smoking. Chemotherapy subjects exhibited reduced expression of SOX-9 when compared with untreated subjects ($p < 0.05$). High accuracy in diagnosing subjects with and without cancer exhibited receiver operating characteristic (ROC) analysis with an area under curve (AUC) value of 0.922, with 96% and 90% for sensitivity and specificity, respectively. Logistic regression exhibited 314 times increased odds for diagnosing lung cancer with increased expression of SOX-9 ($p = 0.00048$). Conclusion: In conclusion, our findings exhibit a strong role for SOX-9 in diagnosing, progression, and chemotherapy response in lung cancer, and its role in diagnosing and prognosis warrants a larger cohort for its validation, opening doors for personalized therapy in lung cancer care.

Keywords: SOX-9, Lung Carcinoma, Marker, PBMC, Chemotherapy Response

P34

Caffeic Acid Triggers Breast Cancer Cell Death: Unleashing ROS, Activating Caspases, and Collapsing Mitochondrial Potential

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Objectives: This study aimed to explore the anticancer potential of caffeic acid (CAF) in breast cancer by investigating its effects on cell growth, and by delineating the roles of caspases, mitochondria, and oxidative stress in mediating its action. Methods: Human breast cancer cell lines MCF-7 and MDA-MB-468 were treated with various concentrations of CAF over different time periods. The cytotoxic effects were quantified using the MTT assay. In parallel, we evaluated the activities of caspase-3 and caspase-8, measured the intracellular levels of reactive oxygen species (ROS), and monitored changes in the mitochondrial membrane potential (Δψm) to gain insights into the mechanistic pathways involved. Results: CAF induced a dose- and time-dependent decrease in cell viability in both MCF-7 and MDA-MB-468 cells. This reduction in cell proliferation was accompanied by a significant increase in ROS levels, suggesting that oxidative stress plays a pivotal role in CAF-induced cell death. Additionally, CAF treatment led to a marked decline in Δψm, indicating mitochondrial dysfunction as a contributing factor to apoptosis. Importantly, an elevation in caspase-8 activity was observed, implicating the activation of the extrinsic apoptosis pathway. The most substantial anticancer effects were seen with a 20 µM concentration of CAF following a 48-hour treatment period. Conclusion: Our findings reveal that CAF exerts a potent pro-apoptotic effect on both estrogen-positive and estrogen-negative breast cancer cells. By triggering oxidative stress, disrupting mitochondrial integrity, and activating key apoptotic enzymes, CAF demonstrates promising therapeutic potential. These insights not only enhance our understanding of CAF's multifaceted mechanism of action but also lay the groundwork for developing innovative and more effective treatment strategies for breast cancer.

Keywords: Caffeic Acid, Reactive Oxygen Species, Caspase 3, Caspase 8, Mitochondrial Membrane Potential

P35

Metabolic Changes in Blood Cancer Cells (Leukemia) and Examining the Use of Biochemical Tests to Identify Specific Features of These Diseases

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Background: Leukemia is a blood tissue malignancy that, like other malignancies, disrupts homeostasis and balance in the body and causes the creation of new metabolic pathways with the aim of increasing the rate of proliferation and resistance to treatment. Unlike normal cells in the body, leukemic cells turn to new metabolic pathways such as increased aerobic glycolysis (Warburg effect), changes in lipid and protein metabolism, and increased oxidative stress. The purpose of this study is to identify metabolic changes with the help of high sensitivity biochemical tests. Method: This systematic review follows the PRISMA protocol to analyze studies on metabolic reprogramming in leukemia and the role of biochemical tests in its detection. Results: The findings show that metabolic changes, including increased glycolysis, fatty acid oxidation, and glutamine metabolism, cause leukemia to progress. These metabolic activities support tumorigenesis and tumor progression and allow cells to absorb essential nutrients from the environment and use these materials to survive and increase proliferation. Therefore, altered glucose metabolism, lactate levels, and markers of oxidative stress such as ROS are seen in leukemia patients. Conclusion: Metabolic changes in leukemia can be used as biomarkers for diagnosis, monitoring, and follow-up of leukemia. Biochemical tests that measure glycolysis, oxidative stress, and metabolic enzymes provide appropriate tools for diagnosis. However, standardizing biochemical tests and increasing the sensitivity of these tests, as well as integrating this method with other diagnostic methods, will lead to faster diagnosis of leukemia and increase the chances of recovery for patients.

Keywords: Leukemia, Metabolic Reprogramming, Aerobic Glycolysis (Warburg Effect), Biochemical Tests, Oxidative Stress

P36

Assessing the Frequency of VEXAS-related Canonical UBA1 Mutations in Iranian Myelodysplastic Syndrome Patients

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Background: The somatic mutations on the UBA1 gene X chromosome introduced a syndrome called VEXAS, which manifests a set of inflammatory and hematological symptoms. Several case studies of VEXAS patients reported a high coincidence of this syndrome with myelodysplastic syndrome (MDS). Awareness of the frequency of VEXAS syndrome can place it among the differential diagnoses among patients who have inflammatory symptoms simultaneously with MDS. This study aims to determine the frequency of canonical UBA1 mutations associated with VEXAS syndrome among MDS patients. Methods: 149 MDS patients were included in this study and patients' genomic DNA was extracted from the bone marrow FFPE. ARMS-PCR method was designed and used for mutations determination. Results: None of the 149 patients included in this study carried the canonical point mutations associated with VEXAS syndrome. Conclusion: We've successfully set up diagnostic test for VEXAS related canonical UBA1 mutations. The initial analysis of the GSE dataset and the study of interactions between UBA1 and the differentially expressed Analysis (DEAs) indicated a relationship between UBA1 and differentially expressed genes (DEGs), especially S100A8. An PPI of the UBA1 gene and components of the pyroptosis pathway revealed that UBA1 is associated with three components of this pathway: S100A8, TXNIP, and CTNNB1. This indicates that mutations in UBA1 might stimulate pyroptosis by impacting S100A8 and beta-catenin or by triggering NADPH oxidase and might contribute in MDS pathophysiology or development.

Keywords: ARMS-PCR, Myelodysplastic Syndrome, Pyroptosis, UBA1, VEXAS Syndrome

P37

Circulating Tumor DNA as a Biomarker for Cancer Screening in Liquid Biopsies: Current Applications and Challenges

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Background: Circulating tumor DNA (ctDNA) has emerged as a promising biomarker for non-invasive cancer screening, diagnosis, and monitoring. Unlike tissue biopsies, ctDNA-based liquid biopsies enable real-time detection of tumor-specific genetic alterations. However, technical, biological, and economic challenges hinder its clinical adoption. This review evaluates the potential of ctDNA in cancer screening, comparing it with conventional methods, discussing detection challenges, and highlighting recent advancements in sensitivity and specificity. Methods: A systematic review of recent studies (2005–2024) on ctDNA detection was conducted, focusing on next-generation sequencing (NGS), droplet digital PCR (ddPCR), and BEAMing. Key limitations such as low allele frequency detection, false positives, and lack of standardization were analyzed across various cancer types and in comparison with standard tissue biopsy methods. Results: ctDNA demonstrates high specificity (>90%) in advanced cancers, but sensitivity in early-stage detection remains suboptimal (<70%) due to low ctDNA concentrations. Multiplexed sequencing, AI-driven analysis, and combining ctDNA with exosomal RNA and DNA methylation profiling have improved diagnostic accuracy. Recent cost reductions in NGS have improved feasibility, but widespread clinical application remains challenging. Conclusion: ctDNA holds significant potential for early cancer detection and treatment monitoring, yet routine clinical use requires cost reduction, method refinement, and standardization. Future research should focus on improving detection sensitivity, integrating ctDNA with multi-omics approaches such as cfRNA profiling and DNA methylation analysis, and establishing clinical validation through large-scale trials.

Keywords: Circulating Tumor DNA (ctDNA), Liquid Biopsy, Cancer Screening, Early Detection, Biomarker

P38

Sulfatase-1 and Sulfatase-2 as Potential Biomarkers for Cancer Diagnosis

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Background: Sulfatase-1 and -2, play crucial roles in cancer biology by affecting tumor progression, metastasis, and treatment resistance. They modulate heparan sulfate proteoglycans and key signaling pathways in tumorigenesis and angiogenesis. This review evaluates their potential as diagnostic and prognostic biomarkers in cancer. Methods: In this research we explored different databases included Embase, PubMed, Scopus, and Web of Science following PRISMA guidelines since February 2025. We used “Sulfatase”, “SULF*”, “Neoplasms” and their relevant synonyms as keywords for our research. Studies meeting specific inclusion and exclusion criteria, high-quality, accessible, and in English, were included in the systematic review. Results: Ten high-quality studies were included in this research, indicating that Sulfatase-1 levels are significantly altered in breast, gastric, lung, and pancreatic cancers, while Sulfatase-2 levels change notably in gastric, lung, esophageal, prostate, and renal cancers compared to healthy individuals. Investigations showed that overexpression of Sulfatase-1 in breast, gastric, lung, and pancreatic cancers, and Sulfatase-2 in prostate cancer, is linked to poor survival, metastasis, and advanced tumor stages, making them useful prognostic indicators. Also, the elevated levels of Sulfatase-2 protein in the serum of patients with early-stage non-small cell lung cancer compared to healthy individuals indicate its potential as a useful biomarker for the early detection of this malignancy. Conclusion: This review emphasizes Sulfatase-1 and Sulfatase-2 as potential prognostic biomarkers in cancer. Their dysregulation is associated with tumor progression and poor outcomes. Notably, serum levels of Sulfatase-2 may aid in the early detection of lung cancer, indicating its potential as a diagnostic biomarker.

Keywords: Cancer Biomarkers, Diagnosis, Prognosis, Sulfatases, Systematic Review

P39

Early Detection of Colorectal Cancer: Exploring Biomarker-Driven Screening Strategies

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Background: Colorectal cancer (CRC) represents a significant global health challenge, with most cases diagnosed at advanced stages. While hereditary forms like HNPCC and FAP account for approximately 5% of cases, sporadic CRC comprises the majority, highlighting the need for effective early detection methods. This study aims to evaluate and compare the effectiveness of various biomarkers in CRC detection and monitoring, with a focus on their diagnostic accuracy and clinical utility. Methods: A systematic review was conducted using PubMed and Scopus databases. English-language, peer-reviewed articles published between 2015 and 2025 were included. Studies focusing on biomarker validation, diagnostic accuracy, and clinical applications were selected. Case reports and non-human studies were excluded. Results: Out of 82 initially screened studies, 56 were included in this review. Multiple biomarker categories demonstrated significant diagnostic potential. Nucleic acid markers showed higher DNA integrity in CRC patients' stool samples, with specific mutations in K-ras, APC, and p53 genes. Microsatellite instability was frequently detected in tumors with deficient MMR genes (MSH2, MLH1, MSH6, and PMS2). Protein biomarkers included fecal markers like g-FOBT, though affected by dietary factors, and serum markers such as CEA for cancer progression and CA 19-9 for gastrointestinal tumors. MMP-9 showed significance in basement membrane degradation and tumor invasion. Additionally, Cadherin 17 emerged as a validated tissue biomarker with reliable immunohistochemical detection. Conclusion: Combined biomarker testing approaches maximize diagnostic benefits while minimizing false positives and unnecessary invasive procedures. Future studies should focus on large-scale clinical validation of combined biomarker panels and their cost-effectiveness in diverse populations.

Keywords: Colorectal Cancer, Biomarkers, Early Detection, DNA Markers, Protein Markers

P40

The Effect of Age on the Serum Level of Carcinoembryonic Antigen in the Elderly Individuals in Iran

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Background: The carcinoembryonic antigen or the specific blood glycoprotein is produced normally in the digestive tissue of the fetus. At birth, its serum level is undetectable, but it increases in some types of cancers. This study aimed to measure the serum level of carcinoembryonic antigen in the elderly healthy individuals to demonstrate that the serum level of carcinoembryonic antigen may increase in the healthy and elderly individuals. Method: The serum levels of 100 samples from the male and female nonsmokers, aged 60-95 years old were measured by the chemiluminescence device. These individuals were free of cancer, thyroid and digestive diseases and diabetes. Results: The serum level of carcinoembryonic antigen increased significantly with age. However, this increase was insignificant between the males and females. Conclusion: Due to an increase in the serum level of carcinoembryonic antigen in the healthy and elderly individuals, the results of this study suggest that the cut-off of this test should be upgrades from 5 ng/ml to 8 ng/ml of serum. Though an increase in the serum level of carcinoembryonic antigen together with age may be a sign of some types of cancers.

Keywords: Carcinoembryonic Antigen, Tumor Marker, Age, Cut-Off, Iran

P41

Sphingolipids as Biomarkers in Pancreatic Ductal Adenocarcinoma: Current Evidence and Future Directions

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Bakground: Pancreatic ductal adenocarcinoma (PDAC) is a deadly cancer with low survival rates, and early diagnosis is crucial. Recent studies have highlighted that specific sphingolipid metabolites, such as ceramides, are altered in pancreatic cancer tissues compared to non-cancerous tissues. This systematic review study aims to investigate the role of sphingolipids in diagnosis and prognosis of PDAC. Methods: A comprehensive collection of information was achieved from medical databases including PubMed, Scopus, and Web of Science. In order to identify related articles, keywords related to this topic such as PDAC, sphingolipids and ceramid were investigated and combined. Results: Recent studies have highlighted that specific sphingolipid metabolites, such as ceramides, are altered in pancreatic cancer tissues compared to non-cancerous tissues. Elevated levels of certain ceramide species (e.g., C16:0 and C24:1) have been linked to lymph node metastasis, suggesting their potential as biomarkers for disease severity and treatment response. PDAC cells are a source of ceramide-1-phosphate (C1P), and they secrete C1P-containing extracellular vesicles that recruit pancreatic cancer stem cells (PCSC). High Phosphorylated sphingosine Kinase 1 (pSphK1) expression is associated with lymphatic invasion and unfavorable prognosis in PDAC patients. High pSphK1 immunoreactive expression is an independent prognostic factor for disease-specific survival. Increased abundance of certain sphingolipid-associated genes (SPGs) may indicate poor responses to immunotherapy, highlighting their diagnostic value. Conclusion: Sphingolipids show promise as diagnostic and prognostic biomarkers in PDAC. Further research is needed to fully elucidate the role of sphingolipids in PDAC development and progression, as well as to validate their clinical utility as biomarkers.

Keywords: Sphingolipid, Glycosphingolipid, Ceramid, Pancreatic Ductal Adenocarcinoma

P42

Investigation of HFE Gene Expression Changes in Gastric Adenocarcinoma Tumor Cells and Normal Tissue Adjacent to The Tumor and Its Relationship with Helicobacter Pylori Infection

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Bakground: Gastric cancer is a major cause of cancer-related mortality with Helicobacter pylori infection being an environmental risk factor. This infection is linked to reduced iron stores (ferritin) and iron deficiency anemia, which may enhance H. pylori's carcinogenic potential. The HFE gene, which regulates iron absorption by controlling the interaction between transferrin and its receptor, plays a critical role in iron homeostasis. This study investigated changes in HFE gene expression in gastric adenocarcinoma tumor cells in relation to H. pylori infection and its impact on disease prognosis. Methods: The study included 30 gastric cancer patients divided into three groups: those currently infected with H. pylori, those without infection, and those with a history of infection in the year before surgery. H. pylori infection was confirmed via ELISA by measuring IgA and IgG antibodies in plasma. RNA was extracted from tumor and adjacent normal tissues, followed by cDNA synthesis and Real-time PCR to assess HFE gene expression. Results: Increased HFE gene expression was seen in tumor tissues compared to normal tissues. However, the increase in HFE expression was lower in patients currently infected with H. pylori compared to uninfected patients and those with a history of infection. Conclusion: HFE gene expression may be a potential marker to understand how H. pylori contributes to iron deficiency and gastric cancer development. The study highlights the complex relationship between H. pylori infection, iron regulation, and gastric carcinogenesis, offering insights for diagnostic and therapeutic strategies.

Keywords: HFE Expression, Gastric Cancer, H.pylori

P43

Advances in Leukemia Diagnosis and Treatment Monitoring

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Recent advancements in leukemia diagnosis and treatment monitoring have been significantly enhanced using microfluidic technologies. Leukemia, a hematologic malignancy characterized by the aberrant proliferation of white blood cells, requires early and precise detection due to its potential to disrupt normal hematopoiesis and lead to fatal complications. The aim of this review study is to examine the advances in leukemia diagnosis and treatment monitoring. Traditional diagnostic approaches, such as white blood cell (WBC) differential counts, have limitations in accurately identifying the diverse cell types associated with leukemia. Convolutional neural networks (CNN) have enhanced diagnostic precision by facilitating the analysis of microscopic images; however, they still face challenges in comprehensively identifying all leukemia cell types. Microfluidic technologies have emerged as highly efficient tools, enabling the precise isolation and analysis of circulating leukemia cells without needing large sample volumes. Microfluidic chips, particularly those incorporating specific antibodies such as CD34, have been developed for the targeted isolating leukemia cells, especially in acute myeloid leukemia (AML) and chronic myeloid leukemia (CML). These innovations provide critical insights into disease progression, therapeutic efficacy, and minimal residual disease detection, ultimately supporting the optimization of therapeutic strategies. The integration of microfluidic technologies into clinical practice holds substantial promise for improving diagnostic accuracy, optimizing treatment monitoring, and advancing patient outcomes in leukemia management.

Keywords: Diagnosis, Leukemia, Monitoring, Microfluidic

P44

Serum Micro RNA 145 as Novel Potential Biomarker in Acute Lymphoblastic Leukemia

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Background: Acute lymphoblastic leukemia (ALL) is the most common childhood malignancy and accounts for 20% of acute leukemia cases in adults. Recently, microRNAs (miRNAs) have recently been identified as key regulators in hematologic malignancies. This study aimed to evaluate the expression status of miR-145 in patients with ALL. Methods: In this study, 21 patients with ALL (before and after treatment) and 21 healthy people were evaluated. After direct cDNA synthesis from serum, miR-145 expression was measured using the qRT-PCR method. Data were analyzed using SPSS 20, Genex 6.1, and Graph Pad Prism8 software. Results: The expression level of miR-145 in newly diagnosed ALL patients was significantly lower than that in healthy individuals (fold change = 0.63 ± 0.2, p-value = 0.01, Unpaired t-test), and increased after treatment (fold change = 1.32 ± 0.2, p-value = 0.001, Unpaired t-test). Conclusion: Our results suggest that miR-145 may play a potential role in the pathogenesis of ALL and could be considered a diagnostic marker and therapeutic target in future studies.

Keywords: ALL, miRNA, miR-145

P45

Determination of Prevalence and Genotype Distribution of High-Risk Human Papillomavirus in Varamin (Iran)

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Background: Cervical cancer is the fourth most prevalent malignancy among women worldwide. Despite the availability of standardized HPV testing algorithms, regional adaptation remains crucial. This study aimed to assess cervical cytology and HPV genotyping in cervical specimens. Methods: A total of 1,047 women undergoing routine referrals were examined in four laboratories in Varamin City (Tehran Province) from April 2021 to May 2022. Cervical cell genetic analysis was conducted using PCR and reverse dot blotting, while 994 samples underwent Pap staining, analyzed per the Bethesda 2014 system. Results: The mean participant age was 34.2 years, with an overall HPV prevalence of 40.12%, peaking in the 31–40 age group. High-risk HPV (HR-HPV) genotypes constituted 22.15% of infections, with HPV-16 being the most frequent (6.78%). Cytology results showed 95.67% NILM (normal) cases, while 4.32% exhibited ASC-US lesions, in which HPV-16 was predominant. A significant association was found between HR-HPV and cytological abnormalities (P<0.001). Conclusion: Given the high prevalence of HR-HPV in the studied population, HPV genotyping is recommended as a priority screening method. While global HPV vaccination programs target well-known HR-HPV genotypes, region-specific epidemiological data remain essential for public health strategies. These findings provide updated local data supporting HPV vaccination and screening policies in Iran, which should be incorporated into national guidelines for cervical cancer prevention.

Keywords: Human Papillomavirus, HPV, HR-HPV, Cervical Cancer, Pap Smear, Iran

P46

Comparison of Serum Vitamin D Levels in Women with Breast Cancer and a Control Group: A Case-Control Study in Southern Fars Province

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Introduction: Vitamin D plays a critical role in human health, and its deficiency has been linked to an increased risk of various diseases, including breast cancer. The aim of this study was to compare serum vitamin D levels in women diagnosed with breast cancer and healthy individuals residing in the Southern region of Fars Province, Iran. Materials and Methods: In this case-control study, serum levels of 25-hydroxyvitamin D (25(OH)D) were measured in 100 women with breast cancer and 100 age-matched healthy controls. Serum levels were quantified using the ELISA method. Statistical analysis was performed using the Chi-square test. Results: The results revealed a statistically significant difference in the distribution of serum 25(OH)D levels between the patient and control groups ($P < 0.0001$). The prevalence of vitamin D deficiency (defined as <20 ng/mL) was 41% in the breast cancer group and 3% in the control group. Conclusion: The findings of this study indicate that vitamin D deficiency is more prevalent in women with breast cancer in the Southern region of Fars Province. These results underscore the importance of vitamin D screening and supplementation in women, particularly those at higher risk of breast cancer. Further interventional studies are recommended to investigate the effects of vitamin D supplementation on breast cancer prevention and treatment.

Keywords: Breast Cancer, Vitamin D, Southern Fars Province

Challenges in Laboratory Diagnosis of Diabetes

P47-P53

P47

HbA1c, Fasting Glucose, or Beyond? Re-evaluating Laboratory Biomarkers for Accurate Diabetes Diagnosis and Monitoring

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Background: While HbA1c has been the traditional standard for diabetes monitoring and diagnosis, its limitations have prompted exploration of alternative biomarkers. Major diabetes organizations now recommend multiple diagnostic criteria, including HbA1c, fasting glucose, and newer markers, necessitating a comprehensive evaluation of their effectiveness. This study aims to systematically review traditional and emerging biomarkers for diabetes diagnosis. Methods: A systematic review was conducted using PubMed and Scopus databases. English-language, peer-reviewed articles from 2015 to 2025 were included. Studies evaluating diagnostic accuracy, clinical utility, and comparative effectiveness of diabetes biomarkers were selected. Case reports and non-clinical studies were excluded. Results: Out of 106 reviewd articles, 67 studies were included. HbA1c demonstrated effectiveness for Type 2 diabetes diagnosis but showed limitations in detecting early-stage diabetes, gestational diabetes, and in populations with altered red blood cell turnover. Fasting Plasma Glucose remained a standard test but was influenced by short-term factors and showed reduced sensitivity to postprandial glucose variations. OGTT provided superior detection of impaired glucose tolerance and postprandial glucose levels compared to FPG alone, despite being time-consuming and uncomfortable for patients. Continuous Glucose Monitoring offered detailed insights into daily glucose variability and postprandial spikes, particularly beneficial for both Type 1 and Type 2 diabetes management. Alternative markers including fructosamine provided short-term glucose control indicators, while insulin and C-peptide tests helped differentiate between Type 1 and Type 2 diabetes. Conclusion: While traditional biomarkers maintain fundamental importance, a multi-biomarker approach incorporating both conventional and emerging markers could enhance diagnostic accuracy and monitoring efficiency.

Keywords: Diabetes Diagnosis, HbA1c, Glycemic Biomarkers, Type 2 Diabetes

P48

Association Between the G82S Polymorphism of the Receptor Gene for Advanced Glycation End-products and Soluble Serum Levels RAGE with Diabetic Nephropathy in the White (Asian) Race

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This study aimed to investigate the relationship between the G82S polymorphism of the RAGE gene and diabetic nephropathy in patients with type 2 diabetes. The case-control study involved 356 participants (158 men and 198 women) of Asian descent, aged 45 to 65 years, diagnosed with type 2 diabetes. DNA was extracted from their blood samples and genotyped using TETRA-Prime ARMS-PCR, while serum levels of soluble RAGE (sRAGE) were measured by ELISA. Although differences in genotyping between homozygous AA, GG, and heterozygous GA were observed, these differences were not statistically significant ($P = 0.568$). Additionally, no significant correlation was found between the G82S polymorphism and the onset of diabetic nephropathy. Serum levels of sRAGE were slightly reduced in patients with diabetic nephropathy compared to those without, but this difference was not significant ($P > 0.05$). In conclusion, the study found no significant association between the G82S polymorphism of the RAGE gene and diabetic nephropathy. It also suggested that sRAGE levels were only marginally lower in patients with nephropathy, further indicating a lack of strong connection between these factors in the context of diabetic nephropathy development.

Keywords: Diabetes Mellitus, Diabetic Nephropathy, Polymorphism, Receptor for Advanced Glycation End-Products, Soluble RAGE

P49

Influence of Adiponectin Gene Polymorphism of rs 1501299 on Insulin Resistance and Adiponectin Level in an Iranian IFG/T2DM Population

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Background: In recent years it has been revealed that adiponectin has significant impact on modulate insulin resistant and risk of type 2 diabetes The aim of the current study is to discover the association of adiponectin gene polymorphism on biochemical variables, adiponectin level, insulin resistant and type 2 diabetes in an Iranian newly diagnosed diabetic (IFG/T2DM) population. methods: The population study includes 80 subjects holding fasting blood glucose (FBG) 70-100 (mg/dl) in healthy group and 80 subjects holding FBG≥100 (mg/dl) in newly diabetic group. (FBG 100-125 regarded as impaired fasting glucose). The PCR-RFLP method used for genotyping rs1501299 (276 G>T using Mva-1269 restriction enzymes respectively. Statistical analysis was performed using SPSS software version 20. Results: The means of age, BMI, triglyceride (TG), FBG, low density lipoprotein (LDL), Waist circumference, hip circumference (HC) and HOMA-IR was significantly different between diabetic and healthy group (P value <0.05).The rs1501299 was associated with T2DM in recessive (OR=4.172, 95% CI=1.684-10.332, P value=0.002). Conclusion: rs1501299 was significantly associated with type 2 diabetes. There was no association between adiponectin level and polymorphism Keywords: Insulin resistance, Type 2 diabetes, Adiponectin, Anthropometric and metabolic characteristics.

Keywords: Insulin Resistance, Type 2 Diabetes, Adiponectin, Anthropometric and Metabolic Characteristics

P50

Evaluation of Immunological and Biochemical Factors in Type 2 Diabetes Mellitus with Coronary Artery Disease Compared to Diabetic and Healthy Control

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Background: Diabetes mellitus may results in alterations in the production of inflammatory factors. The aim of this study was to evaluate the serum level of lipid profiles, Interleukin (Il)-17, chitinase-3-like protein 1 (YKL-40) and high-sensitivity C-reactive protein (hs-CRP) in type 2 diabetes (T2D) with coronary artery disease compared to diabetic and healthy control. Methods: This study was performed on 87 subjects in four groups, including: 23 samples as healthy control (Group I), 22 patients with T2D (Group II), 20 patients with coronary artery disease (Group III) and 22 patients with T2D and coronary artery disease (Group IV). Serum fasting blood sugar (FBS), cholesterol, triglyceride, low density lipoprotein (LDL-C), High density lipoprotein (HDL-C), aspartate aminotransferase (AST), alanine aminotransferase (ALT), Il-17, YKL-40 and hs-CRP were measured. Results: The mean serum levels of FBS (Group I with II and IV, Group II and III, P = 0.001), cholesterol (Group I and III, P = 0.03), triglyceride (Group II and III, p=0.027), HDL-C (Group I with III and IV, P = 0.02, P= 0.01 respectively), ALT (Group I and IV, P = 0.03, Group II and IV, P = 0.02) and AST (Group II and IV, P =0.009) were significantly different. The mean serum IL-17 level in the control group was significantly lower than other groups (P<0.5). The serum levels of YKL-40 were significantly difference in the group I (4.81±1.27 ng/ml) and group II (15.52±4.61 ng/ml) (P=0.01), group III (19.2±2.75 ng/ml, P=0.017) and group IV (16.1±4.17 ng/ml, P=0.04). Also, the mean serum levels of hs-CRP in the group III (4.49± 1.53 µg/ml) and group IV (1.28 ± 0.43 µg/ml) was significantly difference (P= 0.028). Conclusion: Serum levels of IL-17 and YKL-40 are increased in people with T2D and coronary artery disease. It is recommended to determine the serum level of these markers in these patients.

Keywords: Il-17, YKL-40, hs-CRP, Diabetes Type 2, Atherosclerosis

P51

The Relationship between Vitamin D and Calcium with Fasting Blood Sugar and HbA1C in Diabetic Patients and Healthy Individuals

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Introduction: Recently, there is increasing evidence from animal and human studies that adequate vitamin D supplementation may reduce the incidence of type 1 diabetes and possibly type 2 diabetes and may improve metabolic control in diabetic patients. The present study aimed to compare the relationship between vitamin D and calcium levels with fasting blood sugar and HbA1C in diabetic patients and healthy individuals. Method: In this cross-sectional study, the records of 142 people who referred to the laboratory of Akhavan Clinic, Kashan, in 1403 were reviewed. The extracted information included gender, age, FBS, Ca, A1C and D3. Also, people with A1C above 7 were considered diabetic. The collected data were analyzed using SPSS version 27 software and using chi-square, independent t-tests and analysis of covariance (to adjust for the effects of gender and age). Results: Of the subjects studied, 87 were diabetic (54 women; mean age 57.22±15.12 years; mean FBS 152.69±68.13) and the rest were non-diabetic (39 women; mean age 49.02±14.40). The mean calcium level in the diabetic group was significantly lower than that in the non-diabetic group (7.93±1.98 vs. 9.75±0.46, respectively; $p<0.001$), but the mean vitamin D level was not significantly different between the two groups (31.41±11.99 vs. 31.29±13.89, respectively; $p=0.277$). Conclusion and Discussion: There was no significant difference in vitamin D between the diabetic and non-diabetic groups, but the calcium level in the diabetic group was significantly lower than that in the non-diabetic group. This could indicate the importance of calcium intake in people with diabetes.

Keywords: Diabetes, Vitamin D, Fasting Blood Sugar, HbA1C

P52

Protective Role of SIRT1 (rs3758391 T > C) Polymorphism Against T2DM and its Complications: Influence on GPx Activity

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Aims: Sirtuin-1 (SIRT1) has antidiabetic effects through the regulation of insulin secretion and modulation of inflammation. The SIRT1 rs3758391 gene polymorphism affects the level of SIRT1. The current study aimed to investigate the possible influence of SIRT1 gene variants in relation to oxidative stress parameters on the susceptibility to T2DM and its microvascular complications. Methods: In this case-control study 398 individuals including 300 patients with T2DM (100 T2DM without complication, 100 diabetic neuropathy patients and 100 patients with diabetic retinopathy) and 98 healthy subjects were studied for SIRT1 rs3758391 T > C variants. Also, the GPx activity and the levels of GSH, MDA, TAC, and TOS were determined by colorimetric methods. SIRT1 genotypes were detected using the polymerase chain reaction-restriction fragment length polymorphism method. Results: The C allele of SIRT1 reduced the risk of T2DM, diabetic neuropathy and diabetic retinopathy. Significantly lower levels of GSH, GPx, and TAC were found in diabetic patients compared to control group. However, the level of MDA was significantly higher in patients compared to healthy individuals. Considering all individuals, the GPx activity increased in the presence of the SIRT1 CC, and TC genotypes compared to the TT genotype. Among all studied individuals the activity of GPx was significantly higher in normal BMI subjects than overweight, and obese individuals. However, among overweight and obese diabetic, diabetic retinopathy and diabetic neuropathy patients the mean level of TOS was significantly higher compared to patients with normal BMI. Conclusions: Our findings suggest a protective role for SIRT1 C allele against T2DM and diabetic neuropathy and diabetic retinopathy. We found in the presence of this allele the GPx activity increased. Also, we detected an enhanced oxidative stress level among overweight and obese patients with diabetes and its complications that could be involved in the pathogenesis of the disease.

Keywords: Antioxidants, Diabetic Neuropathy, Diabetic Retinopathy, SIRT1 Gene Variants, T2DM

P53

Exosomes as Novel Biomarkers and Therapeutic Agents in Type 1 Diabetes Mellitus

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Background: Small extracellular vesicles known as exosomes could be used in diseases, including type 1 diabetes (T1D), as biomarkers and treatments. Because current treatments are limited, they transfer bioactive molecules including proteins, lipids, and nucleic acids, therefore providing hope for early detection and disease-modifying treatments. Methods The search was conducted in NCBI and Web of Science databases until February 2025. 3 studies that met all the eligibility criteria were included for further analysis. Results Exosomes from pancreatic cells and MSCs (Mesenchymal stem cells) have been found in type 1 diabetic models to have immunoregulatory and regenerative effects. MSC-derived exosomes protect βcells by means of anti-inflammatory cytokines that suppress the activity of immune cells and anti-inflammatory agents. B cell-derived exosomes that improve βcell function and survival carry insulin mRNA, and using exosomes also affects autoimmune development as well as Tcell activation levels. Exosomal biomarkers circulating—such as miR375 and miR21—that link βcell stress and severity of disease might be useful in early diagnosis and disease follow-up. Conclusion In conclusion, to sum up, exosomal biomarkers offer a hopeful noninvasive method for early detection and monitoring of T1D, where exosome-based treatments show promise for immune modulation and βcell protection. Further study is required to enhance their clinical application; exosome manipulation, focused delivery, and high-volume output should be investigated.

Keywords: Exosome, Novel Biomarkers, Type 1 Diabetes, β Cell

Challenges in Laboratory Diagnosis of Thyroid Diseases

P54-P59

P54

Pitfalls in Thyroid Function Tests and TSH Interpretation

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Thyroid function tests (TFTs), including serum thyrotropin (TSH), free thyroxine (FT4), and free triiodothyronine (FT3), are essential tools in diagnosing and managing thyroid disorders. However, interpreting these tests can be challenging due to various physiological, pathological, and technical factors. This article explores common pitfalls in TFTs, such as the impact of non-thyroidal illness, medication interference, assay limitations, and subclinical thyroid dysfunction. It also highlights challenges in TSH interpretation, including age-related variations, circadian rhythms, and central hypothyroidism. Practical recommendations for accurate interpretation are provided to aid clinicians in avoiding diagnostic errors and optimizing patient care.

Keywords: Thyroid, Function, Interpretation

P55

Harnessing Artificial Intelligence for the Identification of Molecular Biomarkers in Autoimmune Diseases

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Background: Autoimmune diseases are characterized by dysregulated immune responses leading to tissue damage. Recent advancements in artificial intelligence (AI) offer promising avenues for identifying molecular biomarkers that can enhance diagnosis and treatment strategies. This study investigates the application of AI in the identification of key molecular biomarkers in autoimmune diseases, focusing on its potential to improve patient outcomes and therapeutic interventions. Methods: A systematic review of literature was conducted, analyzing studies that employed AI methodologies, including machine learning (ML) and deep learning (DL), to identify molecular biomarkers in autoimmune diseases. The review emphasized applications in genomic data analysis, proteomics, and immune profiling, assessing how AI can enhance the understanding of disease mechanisms and patient stratification. Results: AI techniques have demonstrated significant success in identifying predictive biomarkers associated with autoimmune diseases. ML algorithms have been utilized to analyze large-scale genomic datasets, revealing novel genetic variants linked to disease susceptibility and progression. DL approaches have improved the accuracy of protein structure predictions, facilitating the identification of autoantigens. Furthermore, AI-driven analyses of immune cell profiles have uncovered distinct immune signatures that correlate with disease activity and treatment response. Despite these advancements, challenges such as data heterogeneity and the need for model interpretability remain critical barriers to widespread implementation. Conclusion: The integration of AI in the identification of molecular biomarkers for autoimmune diseases holds transformative potential for enhancing diagnostic accuracy and therapeutic strategies. Continued interdisciplinary collaboration among clinicians, researchers, and data scientists is essential to overcome existing challenges and fully realize the benefits of AI in this field.

Keywords: Artificial Intelligence, Autoimmune Diseases, Molecular Biomarkers, Machine Learning, Deep Learning

P56

Subclinical Hypothyroidism and Macro-TSH: Bridging the Gap between Biochemical Data and Clinical Symptoms

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Background: Subclinical hypothyroidism (SCH) is a biochemical state, in which Thyroid Stimulating Hormone (TSH) levels rise while free fractions of thyroid hormone (FT4) stay in the normal range. Occasionally, spuriously elevated readings of TSH levels in laboratories occur due to the bindings of TSH molecules to immunoglobulins, forming biologically inactive macromolecules called macro-TSH. Considering the notable risk of misdiagnosis due to this phenomenon, this study examines the association between macro-TSH and patients' symptoms, medical history, and total TSH values. METHODS: In this cross-sectional study on 217 untreated SCH patients, serum total TSH, FT4, and macro-TSH levels were measured using ELISA. Comprehensive evaluations of recent hypothyroidism symptoms (e.g. fatigue, weakness, weight gain, cold intolerance, constipation, hair loss, dry skin, and depression) and past medical and family history of patients were conducted by a trained physician. Macro-TSH levels were assessed through a 1/2 dilution test with 25% polyethylene glycol (PEG) to precipitate macro-complexes before re-assaying the subtracted sera. The cut-off value for the PEG-precipitable TSH ratio was set at 75% using the formula: (Total TSH-Free TSH)/Total TSH)* 100. Analysis of variables was performed using SPSS statistics (v26). RESULTS: The study population had a mean age of 51.2±18.2 years, with 71% identifying as female, 41% asymptomatic, and 22.6% exhibiting PEG-precipitable TSH ratios of ≥75%. Our results showed no significant relation between high PEG-precipitable TSH ratios and, patients' weight, gender, and history of hypertension, diabetes, or cardiovascular disorders. However, age (P=0.04), familial hypothyroidism (P=0.03), total TSH (P<0.001), and the absence of symptoms(P<0.001) were significantly associated. CONCLUSIONS: Macro-TSH is more prevalent if patients are elderly, asymptomatic, and have highly elevated total TSH values. Considering the controversies in the treatment of SCH and the notable presence of macro-TSH in sera, it is recommended that researchers, laboratory directors, and clinicians pay more attention to this condition.

Keywords: Subclinical Hypothyroidism, TSH, Macro-TSH, Auto-Antibodies

P57

Thyroid Function Tests and Disorders: A Detailed Overview of Primary Care and Clinical Practice

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Thyroid function tests (TFTs) are some of the most commonly requested lab tests in clinical settings, essential for diagnosing and managing thyroid issues like hypothyroidism, hyperthyroidism, and subclinical thyroid dysfunction. These disorders are marked by irregular levels of thyroid-stimulating hormone (TSH) and thyroid hormones (T3 and T4), which can greatly affect metabolic functions and overall well-being. This review offers a comprehensive look at TFTs, emphasizing how to interpret them, their diagnostic value, and the challenges that arise from various physiological and pathological conditions. The regulation of thyroid hormones is managed by the hypothalamus-pituitary-thyroid axis, where TSH plays a key role in stimulating the production of T4 and T3. Although interpreting TFTs is usually straightforward, challenges can arise in cases of subclinical dysfunction, non-thyroidal illnesses, pregnancy, aging, and medication use, all of which can affect thyroid hormone levels and complicate diagnosis. Subclinical hypothyroidism, indicated by elevated TSH levels with normal T4, and subclinical thyrotoxicosis, which shows suppressed TSH alongside normal T4 and T3, pose specific diagnostic difficulties. Furthermore, non-thyroidal illnesses and conditions like pregnancy and aging add to the complexity of TFT interpretation due to their effects on thyroid hormone metabolism. Certain medications, such as amiodarone and glucocorticoids, as well as nutritional factors like iodine intake, also play a role in influencing thyroid function. This review highlights the necessity of a personalised approach to interpreting TFTs, considering individual patient factors to prevent misdiagnosis and overtreatment. While TSH remains the primary diagnostic marker, additional tests like free T4 may be required in certain situations. Progress in testing methods and a better understanding of thyroid physiology are crucial for accurate diagnosis and effective management of thyroid disorders. This review emphasizes the importance of context-sensitive interpretation of TFTs to improve diagnostic accuracy and enhance patient outcomes.

Keywords: Thyroid Function Tests (TFTs), Thyroid-Stimulating Hormone (TSH), Thyroid Hormones, Hypothyroidism, Hyperthyroidism

P58

Evaluation of De Ritis Ratio in Hashimoto Diseases

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Background: Hashimoto's thyroiditis (HT) is one of the most common causes of hypothyroidism, which is manifested with chronic inflammation in thyroid gland and systemic autoimmune disorders. HT pathogenesis is a multistage process that involves the destruction of thyroid follicles as a result of an autoimmune attack influenced by peripheral and genetic factors which is associated with hypothyroidism in only 20% of cases. Based on the literature, it appears that the function of hepatocytes and changes in liver transaminases have a direct correlation with Hashimoto's thyroiditis. Method: We conducted a systematic search of key terms, including HT, AST, ALT and their synonyms from 2020 to 2025. Duplicates were eliminated using EndNote 20 and the included studies were qualified by the GBI tool without language restrictions. Result: Following the search from retrieved 359 articles, 346 papers were excluded due to duplication or irrelevance and 13 articles were retained. In all included studies, the level of AST in patients with HT was found to be elevated compared to the control group, with this difference being statistically significant in 66% of the studies (P-value < 0/05). Furthermore, ALT levels in HT patients were significantly higher than those in the control group in 42%of the studies (P-value < 0/005). Conclusion: Although the relationship between thyroid hormones and liver function seems complicated, considering the essential role of hepatocytes and the high metabolic rate of the liver, elevated levels of AST and ALT serve: as char: acteristic biomarkers for hypothyroidism and hyperthyroidism. Based on the results of our study, it appears that De Ritis ratio (AST/ALT), in conjunction with imaging results and elevated autoantibody serum levels, can be a useful indicator in assessing HT, which is accessible and cost-effective.

Keywords: Hashimoto’s Thyroiditis, ALT, AST, De Ritis Ratio

P59

Assessment of the PAR Ratio in Hashimoto's Disease: Insights into Diagnostics and Prognostics

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Background: Hashimoto's Thyroiditis (HT) is a leading cause of hypothyroidism and a significant autoimmune disease. In HT, thyroid cells undergo atrophy, which can destroy the thyroid gland with an inflammatory pathogenesis. Diagnosing HT involves detecting various biomarkers, including the platelet-to-albumin ratio (PAR), an established inflammatory marker obtainable through routine blood tests. This systematic review aims to clarify the relationship between platelet counts and albumin levels in HT patients, emphasizing their importance in understanding the disease and improving patient outcomes. Method: For this systematic review, we conducted a search of the PubMed, Scopus, and Web of Science databases for studies published between 2020 and 2025. We utilized keywords such as "albumin," synonyms for "platelet," and "Hashimoto's Thyroiditis." Using EndNote Software v.20, we removed duplicates, irrelevant studies, and those with access restrictions. The quality of the selected studies was evaluated using JBI tools. Result: A total of 45 studies were identified for the systematic review, with 15 meeting the criteria that examined either platelet or albumin levels in patients with Hashimoto's Thyroiditis (HT). Of these, 11 studies found that platelet levels were elevated in HT patients compared to the control group, with 54% of these studies reporting this change as statistically significant. Additionally, 4 studies indicated a reduction in albumin levels, with 75% of these findings also considered significant (P-value < 0.05). Conclusion: This study recommends further investigation of the PAR Ratio as a potential marker for prognosis, diagnosis, and treatment monitoring in Hashimoto's disease. Its affordability, ease of accessibility, and reliability enhance its prospects for clinical application.

Keywords: Hashimoto Thyrioiditis, Platelet, Albumin, PAR Ratio

Clinical Implications of Antinuclear Antibodies and Anti-Phospholipid Antibodies: A Comprehensive Review

P60

P60

The Study of Association between Polymorphisms in the Angiotensin-Converting Enzyme (ACE) I/D Gene and Angiotensin II Type 1 Receptor A1166C Gene with Preeclampsia

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Introduction: Preeclampsia is a multifactorial and multisystemic disorder that a variety genetic factors have been known that contributes in pathogenesis of this disease. The aim of this study was to assess the association between polymorphisms in the angiotensin-converting enzyme (ACE) I/D gene and angiotensin II type 1 receptor A1166C gene with preeclampsia. Study design: This study was performed in 125 preeclamptic pregnant women and 132 healthy controls. Genomic DNA was extracted from peripheral blood. The I/D Polymorphism of the ACE gene was assessed by polymerase chain reaction, and the A1166C Polymorphism of the AT1R gene was determined by digestion with restriction enzyme endonuclease DdeI. Results: The genotype and allele frequencies of I/D Polymorphism of the ACE gene differed significantly between the two groups (P=0.001 and P=0.002 respectively). The risk of preeclampsia was 3.2 fold in pregnant women with D allele (ID+ DD) contrast to control women without D allele. (OR, 3.2 [95% CI, 1.1 to 3.8]; P=0.01). The distribution of the AT1R A1166C polymorphism was similar in affected and control groups. CONCLUSION: We conclude that the presence of the I/D ACE gene polymorphism is a marker for the increased risk of preeclampsia, but there was no association between AT1R A1166C polymorphism with preeclampsia.

Keywords: Angiotensin-Converting Enzyme, AT1 Receptor, Olymorphism, Preeclampsia

Cost-effectiveness in Laboratory Medicine

P61-P65

P61

The Role of Artificial Intelligence in Laboratory Cost Management and Equipment Procurement

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Background: Efficient cost management is vital for the sustainability of medical laboratories, especially given financial constraints and rising operational expenses. Mismanagement of equipment, inventory, and procurement poses significant economic challenges. This study explored the role of artificial intelligence (AI) in enhancing cost efficiency and decision-making within laboratory management, focusing on resource allocation, equipment procurement, and employee interactions. Methods: AI-driven tools were reviewed, including predictive analytics for inventory control, decision-support systems for procurement, and workforce management strategies. By analyzing historical data and predicting demand, AI demonstrated the ability to optimize multiple operational facets. Results: The findings demonstrated that AI significantly enhanced cost efficiency in medical laboratory operations by optimizing multiple facets of resource management. AI-driven predictive analytics streamlined inventory control, ensured optimal stock levels, and reduced waste through accurate demand forecasting. In procurement, AI facilitated data-driven strategies, enabling laboratories to identify cost-saving opportunities and improve supply chain management. Real-time monitoring powered by AI minimized equipment downtime and extended the lifespan of critical laboratory tools through preventive maintenance schedules. Additionally, AI improved workforce efficiency and satisfaction by analyzing communication patterns and providing tailored training programs. Collectively, these AI-based solutions not only reduced operational costs but also enhanced overall laboratory performance, positioning medical laboratories for sustainable growth and efficiency. Conclusion: AI significantly contributes to cost efficiency in laboratory operations by addressing mismanagement in procurement, inventory, and employee oversight. Integrating AI into laboratory workflows not only ensures financial sustainability but also promotes optimal utilization of resources, positioning laboratories for long-term success.

Keywords: Artificial Intelligence, Cost Management, Medical Laboratories

P62

Calculation of the Total Cost and the Share of Different Cost Components from the Average Total Cost in Different Departments of Selected Medical Diagnostic Laboratories in 1400

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Background: The increase in the production costs of laboratory services and the release of drug and medical equipment subsidies on the one hand, and the need for the proportional growth of laboratory service tariffs on the other hand, have increased the necessity of calculating the total cost and also determining the share of drugs and medical consumables from these costs. method In this study, using information extracted from four active medical diagnosis laboratories in the private sector, the cost in their different sectors has been calculated. Costing has been done with the absorption system and in a step-by-step method. At the product level, using work time measurement and allocating consumables, the average cost of each test and each specialized group has been calculated. Findings A) In some departments, the average cost of each test was higher than the average income (tariff). In total, the average total income of the selected laboratories (with the figure of 323,958 rials) was only one percent more than the average cost of their produced services (with the figure of 321,836). B) b) The share of manpower cost, consumables, depreciation, capital gain and other costs from the average cost was equal to 20%, 27%, 8%, 33% and 11% respectively. conclusion It is necessary that the Supreme Council of Health Insurance should act on the tariff of laboratory services, based on the cost of different services, so that it is possible to produce and provide quality and fair services in all laboratory centers of the country. Also, based on the share of the cost of medical consumables, it is possible to determine the actual tariff in case of the liberalization of the exchange rate of medical equipment.

Keywords: Cost, Laboratory Services Tariff

P63

Design of a Real-Time PCR Kit for the Molecular Detection of Common Inherited Thrombotic Single Nucleotide Polymorphisms Based on Forced Intercalation of Thiazole Orange Probes

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Background: Some SNPs, such as factor five leiden (FVL) and methylene tetrahydrofolate reductase enzyme variants (MTHFR-A1298C and MTHFR-C677T), raise the risk of thrombosis. Thrombophilia can result from frequent thrombosis. Timely and accurate SNP identification can prevent recurrence and thrombosis. A QRT-PCR molecular diagnostic kit to detect these mutations represents the study's aim. Highest sensitivity and specificity thiazole orange fluorochrome-labeled peptide nucleic acid (PNA-FIT) probes identify SNPs effectively. Methods: NCBI and Ensembl databases obtained the target sequence and mutation location. Mutation-specific primers and PNA-FIT probes were designed. Gene Runner and Oligo Analyzer software detected secondary structures, and Primer Blast online tools assessed sequence specificity. QRT-PCR was performed on 246 peripheral blood DNA samples to optimize mutation amplification and detection. Sequencing the samples confirmed the findings. Results: The specific PNA-FIT probes designed for all three SNPs had 100% sensitivity and specificity. The results obtained by this kit correspond entirely with the sequencing results. The lowest detection limit (LOD) of probes for FVL, MTHFR-A1298C, and MTHFR-C677T was 1 µM, 1, and 5, respectively. The limit of quantification (LOQ) for each probe was also observed as 0.2 µl, 0.1, and 0.2, respectively. DNA samples with concentrations less than 10 ng/µl were also well detected by FIT probes labeled with thiazole orange fluorochrome. The average difference of cycle thresholds (Cts) for homozygous mutations was significant compared to heterozygous, homozygous to normal, and heterozygous to normal ($P<0.05$). Additionally, fluorescent light intensity increased from homozygous to heterozygous. Conclusion: Screens and diagnoses FVL, MTHFR-A1298C, and MTHFR-C677T SNPs associated with thrombosis using this kit. It does this accurately and precisely because of thiazole orange labeled PNA-FIT probes. It can serve as a cost-effective replacement for imported kits, employing a unique method that differs from the current kits. It can also be considered a step towards the country's self-sufficiency.

Keywords: PNA-FIT Probes, Real-Time PCR, Factor V Leiden, Methylenetetrahydrofolate Reductase (C677T, A1298C), And Single Nucleotide Polymorphism

P64

The Role of Digital Marketing in the Competitiveness of Medical Laboratories

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As we enter the era of the Fourth Industrial Revolution, organizations are faced with highly variable and complex markets. In the digital age, digital marketing strategies have become a key factor in marketing and play a decisive role in creating a mental image that influences consumer behavior. Digital marketing uses digital technology to build deeper relationships with markets and promote products and services using online database channels to reach markets (consumers) in a personalized and cost-effective manner with integrated, targeted, and scalable communications Meanwhile, medical diagnostic laboratories, as a service economic unit, face a highly competitive market that requires the use of digital marketing in marketing programs to create a competitive advantage. In the present era, we are moving from classical marketing paradigms to the world of digital marketing. And to use this opportunity to increase competitiveness, we must identify the effective components of digital marketing in the field of medical diagnostic laboratories and apply them in determining digital marketing strategies.

Keywords: Digital Marketing, Marketing Strategy, Medical Diagnostic Laboratory

P65

Embracing Tomorrow: Redefining Quality Assessment and Management in Laboratories for Future Challenges

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Introduction: Rapid development of new technologies combined with ongoing changes in the legal framework poses serious challenges for quality assessment and management of the laboratory work. This paper addresses the issue of introducing ISO standards by suggesting a modification of the legal quality practice of the laboratory to achieve legal compliance and promote innovation. Method: We performed a comprehensive literature review using academic databases like PubMed, Scopus, and Google Scholar. Articles related to ISO standards, laboratory quality management, and compliance were searched, selected, and downloaded. Selected studies were further analysed, and their data on the current and planned laboratory quality management practices was gathered. Results: The results indicate that there is an increasing use of ISO 17025 and other international standards, which are considered essential for greater laboratory credibility and operational effectiveness. These laboratories not only increase their quality assurance processes but also significantly improve compliance with local and international laws. In addition, the digitalization of quality management systems supported their streamlined operations and decreased human fallibility. Conclusion: The focus of this study has been directed towards highlighting the need for modern frameworks of quality assessment and systems as those provided by ISO for the future practice of a laboratory. With advancing challenges in quality management of laboratories, redefining quality management practices would enable more instances per unit time of reliability, better patient results, and overall system effectiveness.

Keywords: Quality Management, ISO Standards, Laboratory Compliance, Regulatory Frameworks

Emerging Fungal Infections and Diagnostic Updates in Invasive Mycoses

P66-P77

P66

Examination of Serum Galactomannan Levels in COPD Patients Hospitalized in the ICU Department of Ardabil Hospitals

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Background: Invasive pulmonary aspergillosis is one of the causes of death in COPD patients hospitalized in ICU. Regarding this, the timely diagnosis of this disease is important. The measurement of GM serum level to diagnose this disease is suggested by the European organization for research and treatment of cancer/mycoses study group (EORTC/MSG). In this study, we investigated the serum level of GM in COPD patients with other patients hospitalized in ICU. Methods The serum of patients admitted to ICU was drawn and the galactomannan antigen level in the patients was measured by the manufacturer's kit (Bioactiva Diagnostic, Germany). COPD patients were identified by the specialist doctor of the plan. Results Out of 654 patients admitted to the ICU during one year, 72 patients had COPD. Of these, 54 (75%) patients were male and 18 (25%) were female patients. The highest GM antigenic index was 4.93 and the lowest was 0.21. The number of 19 (26.38%) patients were in the positive range (>0.5). The average GM index was calculated as 0.33 in all patients and 0.44 in COPD patients. Conclusion In this study, we investigated the level of serum galactomannan antigen in patients admitted to the ICU during one year and compared it in COPD patients. The obtained results showed that the level of GM index in COPD patients is high compared to other patients, and this indicates that the measurement of GM level can be helpful in the timely diagnosis of IPA in COPD patients. These findings suggest serum Aspergillus-galactomannan antigen as a new surrogate marker, which may be used in the assessment of risk for severe COPD and may provide new grounds for understanding the interactions between the fungal microbiome and COPD pathogenesis. More studies are needed to investigate other cases.

Keywords: Aspergillus, Galactomannan, COPD, Aspergillosis, ICU

P67

Study of the Abundance of Medically Important Fungal Species Isolated from the Mycobiome of Recreational Beaches in Bushehr Province

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Introduction: Coasts are economically valuable recreational areas, and Bushehr province is particularly important in this regard with its 672 km of coastline. The frequency of human allergic and fungal symptoms in recent decades has led WHO to publish its guidelines for recreational aquatic environments and recommend their review. Method: Sampling was conducted over three months in 1402, monthly (once a month) according to the recreational location. B) Microscopic and macroscopic identification of isolates A. Yeasts: - Chromogenic medium - Macroscopic and microscopic morphology - D1/D2 sequencing B: Molds - Macroscopic and microscopic morphology - ITS sequencing Findings:

PROVINCE	**Isolates**	Fungal species	**total**
BUSHEHR	**Penicillium**	**citrinum**	**1**
	Aspergillus	**flavus/oryzae**	**13**
		terreus	**17**
		fumigatus	**9**
		niger	**7**
		tubingensis	**3**
		neoterreus	**2**
		sydowii	**1**
	Fusarium	**solani**	**2**
		sarocladium	**1**
		Fusarium incarnatum-equiseti species complex	**1**
	Black fungi	**Alternaria**	**3**
		Other	**5**
	Other	**Lecanicillium psalliotae**	**1**
		Apiospora marii	**1**
		Scopolariopsis brevicaulis	**1**
	Unknown		**6**

Discussion and conclusion: According to the distribution of different fungal species, Aspergillus species A. terreus and A. flavus/oryzae, with the highest number of isolations, are the most common antifungal-resistant fungi on the recreational beaches of Bushehr province. These findings indicate a serious concern regarding the occurrence of fungal infections in visitors to these beaches.

Keywords: Fungal Isolates, Mycobiome, Bushehr Coasts

P68

Genotypic Variability, Antifungal Resistance Mechanisms, and Phylogenetic Relationships in Clinical and Animal Isolates of Candida Krusei and Candida Parapsilosis

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Background: Candid species, particularly Candida krusei and Candida parapsilosis, are opportunistic pathogens implicated in nosocomial infections. The rising antifungal resistance among these species poses significant therapeutic challenges. This study aimed to investigate polymorphism, antifungal susceptibility, and the expression of drug resistance genes in clinical and animal isolates. Methods A total of 60 isolates (15 clinical and 15 animal isolates from each species) were collected from healthcare and veterinary centers. Phenotypic confirmation was performed using CHROMagar and germ tube tests. Antifungal resistance was assessed via Multiplex-PCR targeting resistance genes (MDR1, CDR1, CDR2). Genetic diversity was analyzed using RAPD-PCR and Microsatellite-PCR, followed by dendrogram construction. Results Phenotypic analysis confirmed species identification for all isolates. The prevalence of virulence genes (Als1, Als2, Als3) varied significantly between clinical and animal isolates of C. krusei and C. parapsilosis. Notably, resistance genes MDR1 and CDR2 were more prevalent in certain isolates. Phylogenetic analysis using RAPD-PCR revealed distinct clustering patterns between human and animal isolates, indicating substantial genetic diversity. Conclusion The findings highlight genetic variations and variable drug resistance patterns among C. krusei and C. parapsilosis isolates. Understanding these patterns is crucial for developing effective antifungal treatment strategies to manage fungal infections.

Keywords: Candida Krusei, Candida Parapsilosis, Antifungal Resistance, RAPD-PCR, Genetic Polymorphism

P69

Otomycosis: A Clinicomycologic Study in North of Iran

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Background: This study aims to determine the distribution of fungal species among patients refer to selected centers in north of Iran. Methods: From October 2021 to September 2022, a total of 1040 patients refer to the selected ENT clinics in Sari and Behshahr with suspected otomycosis. Clinical evaluations included symptoms such as hearing loss, tinnitus, ear discharge, ear pain, and itching. Sampling was performed by an ENT specialist by using a ring curette and analyzed through direct microscopy, fungal culture (Sabouraud dextrose agar with chloramphenicol), chromogenic agar (used for the primary identification of yeast species) for fungal identification. Results: Among the 1040 patients, 237 cases (22.8%) were diagnosed with otomycosis. The mean patient age was 38.5 years (range: 9–90 years), with 52.74% male and 47.26% female. The most common clinical symptoms included itching (60%), hearing loss (45%),ear discharge (35%), tinnitus (25%), and ear pain (20%).The most common fungal isolates were filamentous fungi (78%), predominantly Aspergillus section nigri (45%), Aspergillus section flavi (34.2%), and Aspergillus section fumigate (10.8%), while 21.9% were yeasts, primarily Candida albicans complex (48.07%), Candida tropicalis (28.84%), and other spp.(23.07%).Conclusion: Otomycosis, mainly caused by Aspergillus section nigri, needs early diagnosis and targeted treatment for effective management.

Keywords: Otomycosis, Aspergillus, Candida, Fungal Infection, External Ear Canal

P70

Antifungal Activity and Mechanism of Action of Dichloromethane Extract Fraction A from Streptomyces Libani Against Aspergillus Fumigatus

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Bakground: This study aimed to investigate the mechanism of antifungal action of Streptomyces libani dichloromethane extract fraction A (DCEFA) against Aspergillus fumigatus, as the most common agent of invasive aspergillosis, and the host cytotoxicity. Methods: DCEFA was purified from S. libani by autobiography and showed strong antifungal activity against A. fumigatus. A combination of electron microscopy, cell permeability assays, total oxidant status (TOS) assay, cell cytotoxicity assay and haemolysis activity was carried out to determine the target site of DCEFA. Results: Exposure of A. fumigatus to DCEFA caused the damage to membranous cellular structures and increased release of cellular materials, potassium ions and TOS production. DCEFA was bound to ergosterol but did not affect fungal cell wall and ergosterol content. DCEFA did not show any obvious haemolytic activity for RBCs and toxicity against HEK-293 cell line Conclusion: DCEFA may inhibit A. fumigatus growth by targeting fungal cell membrane which results in the leakage of potassium ions and other cellular components, TOS production and final cell death. Significance and Impact of the Study: DCEFA of S. libani could be considered as a potential source of novel antifungals which may be useful for drug development against A. fumigatus as a life-threatening human pathogen

Keywords: Antifungal Activity, Aspergillus Fumigatus, Cytotoxicity, Mechanism of Action, Streptomyces Libani

P71

A Decade Long Study on the Candidiasis in Out Patients at Iran Zamin Diagnostic Laboratory in Khuzestan Province

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Background: Candidiasis, caused by opportunistic fungi of the Candida species, is a significant primary or secondary fungal infection. Its epidemiology is expanding due to the growing population at risk. Understanding its types and prevalence is essential for effective diagnosis, treatment, and prevention. This study aimed to determine the frequency of candidiasis among outpatients referred to the Iran Zamin Medical Diagnostic Laboratory in Ahvaz, Khuzestan, over ten years (2003-2013). Methods: A cross-sectional descriptive study was conducted, sampling outpatients for various Candida infections, including mucosal candidiasis, chronic mucocutaneous candidiasis, candidal onychomycosis, and infant diaper rash. Samples from affected areas like the groin, toes, and armpits were examined microscopically using 20% potassium hydroxide, methylene blue staining, and Sabouraud agar culture. Results: Of 25,643 patients, 920 (3.58%) were diagnosed with candidiasis, including 139 children (15%) aged 10 days to 18 years and 781 adults (85%). The hands were most frequently affected (71.3%), followed by the groin (20.6%), toenails and fingers (7.9%), and brain abscess (0.2%). These findings highlight Candida's prevalence in Khuzestan, underscoring the need for effective management and monitoring. Conclusion: In conclusion, this 10-year study reveals significant trends in candidiasis prevalence, emphasizing its public health impact. Early diagnosis and proper management are crucial to reducing its burden, particularly in high-risk areas like the hands, groin, and nails.

Keywords: Candidiasis, Candida Species, Epidemiology

P72

Aspergillus Fungal Infection in a Diabetic Patient: Formation of a Large and Thick Lesion (Mass Like Lesion) in the Duodenal Papilla Area

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Introduction: Fungal infections, especially Aspergillus, can lead to serious complications in patients with underlying diseases, such as diabetes. This article reviews a rare case of Aspergillus fungal infection that resulted in a large lesion in the duodenal papilla. Patient presentation: The patient, a 58-year-old man with a history of type 2 diabetes, smoking, and opium addiction, presented to the hospital with jaundice and related symptoms. Laboratory tests revealed elevated bilirubin and liver enzymes and a high neutrophil count, indicating an active inflammatory state. Diagnosis: After clinical evaluation, the patient underwent ERCP, during which a large, thick mass was observed in the duodenal papilla. This finding raised the suspicion of fungal infection and the need for further investigations. Pathological findings: A biopsy of the lesion was performed and microscopic results using H&E staining showed tissue necrosis and the presence of Aspergillus hyphae. Also, culture of the sample resulted in the growth of Aspergillus colonies, confirming the fungal infection in the patient. Conclusion: This clinical case demonstrates that Aspergillus infections in diabetic patients can lead to the formation of large and thick lesions in sensitive areas such as the duodenal papilla. Prompt diagnosis and appropriate treatment can help improve the patient's condition and reduce complications. This case also demonstrates the importance of monitoring fungal infections in high-risk patients and those with underlying conditions.

Keywords: Aspergillus, Fungal Infection, Diabetes, Duodenal Papilla, Biopsy

P73

The First Report of Isolating Cryptococcus (Naganishia) diffluence from Neonates Admitted to the NICU. Is it Clinically Significant??

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Background Fungal colonization particularly Cryptococcus species pose significant risks in NICUs, especially for immature neonates. Rare Cryptococcus species such as C. diffluens are commonly found in soil, air, water, plants, and skin, and recent studies have reported their presence in disease-related conditions. This study highlights an unusually high prevalence of Cryptococcus diffluens in NICUs and includes in vitro antifungal susceptibility testing of the isolates. Methods The study in Sari sampled 78 neonates, collecting skin swab from various anatomical areas (cheek, chest, armpit, catheter, genital) three times a week. Samples were inoculated into mycological medium (SC, Candida CHROMagar) and identified using PCR-RFLP and sequencing methods. Neonate's colonization determined by guidelines. Antifungal susceptibility testing was performed against amphotericin B (AMB), fluconazole (FCZ), itraconazole (ICZ) and caspofungin (CFG) using Clinical Laboratory Standards Institute method and criteria (M27, E4). Results During a 12-month study, 78 neonates were sampled. From December 26, 2020, to January 26, 2021, 36 of 55(65.5%) isolated yeast-like fungi were C. diffluens. No C. diffluens isolation observed outside this month, While Candida spp. constituted 100% and 98.3% of the isolates before and after this period, respectively. C. diffluens colonized 62.5% of the neonates, and mixed colonization with Candida spp. and C. diffluens was found in all neonates. Conclusion The incidence of human infections caused by rare Cryptococcus species like C. (Naganishia) diffluens has increased over the past decades. This is the first report of high prevalence of C. diffluens colonization in neonates hospitalized in NICU for the first time. It highlights that potentially pathogenic agent from the outdoor environment, including C. diffluens, can cause hospital problems? The findings also reveal high MIC values for AMB and 5-FC, the antifungal drugs of choice for treating cryptococcosis caused by C. diffluens.

Keywords: Cryptococcus, Cryptococcus (Naganishia) Diffluence, Neonate, NICU, Colonization

P74

Investigating the Effect of Cold Atmospheric Plasma on the Growth of Standard Strain of Aspergillus Fumigatus AF293

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Background: Aspergillus fumigatus is an opportunistic fungal pathogen that is important in causing various human diseases. It is one of the filamentous airborne molds. The key factor causing aspergillosis is the inhaled spores. Cold atmospheric plasma (CAP) is an emerging non-pharmological treatment for Aspergillus fumigatus that optimizes this fungus's treatment. This non-toxic method has minimum side effects and it reduces the duration of treatment and its costs. The present study aimed to investigate the effect of cold atmospheric plasma on the growth and pathogenesis factors of Aspergillus fumigatus. Methods: The standard strain of Aspergillus fumigatus AF293 was obtained from the Pasteur Institute of Iran cell bank and a suspension of fungal spores was prepared. The suspensions were added to a 96 - microplate and used for MIC determination after applying the cold atmospheric plasma. Biomass analysis was estimated by transferring the samples to Erlenmeyer flasks, calculating the wet weight using filtration and measuring the dry weight after drying at 80°C. Results: At 120 seconds, fungal growth reduced, making it the optimal MIC time for cell death. By increasing the time, the wet weight decreased and the lowest growth rate was at 180 seconds. The control sample had the highest growth rate. As the time increased, the dry weight decreased constantly. At 180 seconds, the dry and wet weight were the lowest. Conclusion: The MIC test at 120 seconds was the most effective time for fungal cell death. As the dry weight and wet weight decreased with increasing the time, this confirms a time–dependent effect of this method. Based on these results, using cold atmospheric plasma can be a useful method to overcome these infections and plasma therapy can be a potential strategy to combat these widespread fungal infections.

Keywords: Aspergillus Fumigatus, Cold Atmospheric Plasma, Growth Rate, Biomass Formation

P75

In vitro Interaction of Tacrolimus (FK506) with Conventional and Nano-Formulated Antifungal Drugs Against Clinical Dermatophyte Isolates Including the Emerging Species Trichophyton Indotineae

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Background: Dermatophytosis is a global infection with increasing reports of resistance among its causative agents in recent years. As a result of this issue, new therapeutic options are needed. The aim of this study was to evaluate the anti-dermatophyte activity of tacrolimus, a calcineourin inhibitor drug, either alone or in combination with antifungal drugs. The inhibitory effects of nano-liposomal posaconazole against dermatophytes was also investigated. Materials and Methods: Thirty dermatophyte isolates were included in this study. Anti-dermatophyte activities of terbinafine, itraconazole, posaconazole, nanoposaconazole, and tacrolimus was investigated using the 3rd edition of the CLSIM38 protocol. In vitro interactions between tacrolimus and the antifungal drugs were studied using a checkerboard method. Results: The isolates included Trichophyton indotineae (n=14), Trichophyton tonsurans (n=9), Trichophyton interdigitale (n=6), and Microsporum canis (n=1). Tacrolimus demonstrated moderate inhibitory effects against all species. Itraconazole had the strongest activity; however, based on EUCAST epidemiological cutoff values, one Trichophyton indotineae isolate was non-wild type to this drug. Additionally, 10 out of 14 (71.42%) isolates of this species were non-wild-type to terbinafine. Nanoposaconazole showed superior antifungal activity compared to posaconazole. Regarding drug combinations, the highest and lowest synergistic rates were observed for combinations of tacrolimus with nanoposaconazole (16/30, 53.33%) and itraconazole (4/30, 13.33%), respectively. Conclusion: The high rate of non-wild type Trichophyton indotineae isolates to terbinafine underscores the necessity of precise identification to prevent treatment failure. Itraconazole proved to be the most effective antifungal. Combining tacrolimus with antifungal drugs, particularly nanoposaconazole, shows promise and warrants further investigation.

Keywords: Trichophyton Indotineae, Tinea, Calcineurin Inhibitors, Tacrolimus, Drug Combinations

P76

Molecular Investigation of Urinary Tract Fungal Infections and Evaluation of Drug Sensitivity Pattern of Isolates in Pregnant Women Referred to Shahriar Health Center, Iran University of Medical Sciences, Tehran, Iran

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Background: Urinary tract infections in pregnant women due to fungal agents are important clinical issue, and the outbreak of this infection has increased. Therefore, the present study aimed at molecular investigation of urinary tract fungal infections and evaluation of drug sensitivity pattern of isolates in pregnant women. Methods: The present cross-sectional study was conducted in 12 months on 45 pregnant women with fungal urinary tract infection who were referred to Shahriar Health Center, Iran University of Medical Sciences, Tehran. To confirm the presence of fungal agents, the urine samples were examined microscopically. The samples were cultured on CHROMagar Candida for identification of mixed infections of Candida spp and colony counting. Molecular identification of the isolates were performed PCR test based on the amplification of ITS regions using the universal ITS1 and ITS4 primers and sequencing. Tests of susceptibility to amphotericin B, fluconazole, and Itraconazole were conducted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. Results: Candida albicans (56%) was the most frequent, followed by C. glabrata (31%), C. kefyr (9%) and C. krusei (4%). The MIC results indicate that some of the isolates were resistant to fluconazole, itraconazole and even to amphotericin B. Conclusion: Drug resistance is very important and performing antibiogram to find effective drug for patients.

Keywords: Pregnant Women, Urinary Tract Infection, Fungal Infection, Drug Sensitivity

P77

Evaluation of Antifungal Effects of Pyrano[3,2-e] Pyrazolo [1,5 a] Pyrimidine Derivatives on Candida Species

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Background: Considering the spread of drug resistance to azole among Candida species, it is important to evaluate new effective compounds. The present study evaluates the antifungal susceptibility of pyrano[3,2-[e] pyrazolo [1,5] [a]pyrimidine derivatives on clinical isolates of Candida. Methods: The drug susceptibility of 100 Candida isolates including: Candida albicans (55), Candida parapsilosis (13), Candida tropicalis (14) and Candida glabrata (18) to pyrano[3,2-[e]pyrazolo[1,5][a]pyrimidine derivatives and itraconazole was evaluated by broth microdilution method and according to CLSI-M27S4 guideline. The drug dilution range of the compounds and antifungal drug was 2-1024 µg/ml. The concentration at which at least 100% growth inhibition was observed compared to the positive control group was considered as MIC. Results: The MIC50 results for the four derivatives (P1–P4) against Candida albicans were reported as 1024 µg/mL, 512 µg/mL, 1024 µg/mL, and 512 µg/mL, respectively. For Candida parapsilosis, Candida tropicalis, and Candida glabrata, the MIC50 values for all four derivatives were 1024 µg/mL. Among the derivatives (P1–P4), the geometric mean of P4 against the four species (Candida albicans, Candida parapsilosis, Candida tropicalis, and Candida glabrata) was reported as 499 µg/mL, 569 µg/mL, 600 µg/mL, and 555 µg/mL, respectively. Conclusion Pyrano [3,2-e] pyrazolo [1,5-a] pyrimidine derivatives showed no efficacy against clinical isolates of Candida. To confirm their antifungal effects and enable their potential use in future drug development, further modifications are required, such as introducing strong electron-withdrawing groups (e.g., chlorine or fluorine) onto the aromatic ring or testing derivatives with an unsubstituted ring.

Keywords: Pyrano [3,2-e] Pyrazolo[1,5-a] Pyrimidine Derivatives, Itraconazole, Candida Species

Expert Talks

P78-P81

P78

Invalid Vitamin-D3 ELISA Kit Despite Good Internal QC Result and High Six-Sigma Value; A Source of Systematic Error

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Background: Invalid methods results in systematic errors and misdiagnosis of diseases. The aim is to report a case of method validation ignorance by VitD3 kit manufacturer. Methods: Meanwhile method verification for an IMED-confirmed VitD3 kit, we found Westward 10X rule reject, and very low CV% when doing the tests in duplicate format. Manufacturer representative evaluate the problem and recall more than 40 kits of a LotNo due to nonconformity registered by laboratory's QC team. Evaluation of six-sigma and internal QC data showed excellent results. Results: Validation of VitD3 was not done against a reference method. Internal low and high controls of kits, in fact were one of the low and one of the high concentration calibrators. A wide acceptable range was stated in kit insert sheet for low (2-20 ng/mL) and high (50-100 ng/mL) controls, that is too big for VitD3 and this was despite the test results showing too low CV% and Bias%. Evaluation of user manual of another VitD3 kit producing company showed that similar mistakes are existed. Furthermore, as low CV% and Bias% were obtained in primary evaluations, certainly a high than 10 six-sigma value was obtained in previous evaluations. Conclusion: Laboratories should not be relied on kit's internal controls for QC activities, if calibrators have been used instead pooled preparations. For Vitamin-D3 measurement, validation of each LotNo should be done against a reference method such as HPLC. It seems that IMED regulatory needs to have more precise monitoring programs on some laboratory kit manufacturer.

Keywords: Vitamin D3, Method Validation, Nonconformity, Reference Method, Enzyme-Linked Immunosorbent Assay (ELISA)

P79

Periorbital Edema First Clinical Presentation of Pediatric Toxocariasis: A Case Report

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Introduction: Toxocariasis is a common infection between humans and animals. The larvae migrate in the tissues, causing a wide spectrum of signs and symptoms. Here, a case of pediatric toxocariasis with primary presentation of periorbital edema followed by swelling of hands and feet is reported, showing hyper-eosinophilia an important laboratory finding and confirmation by serology. Case: The patient was a 4-year-old boy, with a history of contact with stray dogs and cats. In March 2024, he presented periorbital edema in his right eye that was associated with normal findings during the ophthalmoscopy examination. Five months later following the swelling of the hands and feet, the child was hospitalized. The blood test of the patient showed leukocytosis, thrombocytopenia, and hyper-eosinophilia; in the CT observations, mild dilation of intrahepatic biliary ducts and heterogenous enhancement of liver parenchyma was noted. The mainstay of treatment during this period was anti-inflammatory therapy. He was referred to the Diagnostic Laboratory of Helminths in the School of Public Health, Tehran University of Medical Sciences, about eight months after the initial presentation of the symptoms and performance of various diagnostic examinations thereafter, seropositivity for toxocariasis was confirmed using an ELISA. No intestinal parasite was recovered in the stool sample of the patient. During the follow-up, it was found that the symptoms subsided following treatment with Albendazole, and the serology test performance three months later was also negative for toxocariasis. Conclusion: Symptoms of toxocariasis are variable, and the infection can be misdiagnosed with other complications. Therefore, the swelling of body parts needs to be considered as symptoms of visceral larva migrans, especially in pediatric patients with hyper-eosinophilia and a history of contact with animals. Screening of toxocariasis can be fulfilled by ELISA as a diagnosis method, which is a rapid and efficient technique to detect the infection in suspected cases.

Keywords: Edema, Toxocariasis, Eosinophilia, ELISA, Human

P80

Low Protein S in the Absence of Antiphosholipid Antibodies, Lessons from Clinical Laboratory Findings

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Key findings from were as follows: Homocysteine level at 8.11 µmol/L (within normal range), CH50 at 110% (normal), and various anti-phospholipid antibodies (including Anti B2 Glycoprotein (IgM), Anti ds-DNA, Anti Phospholipid Ab(IgG), Anti Phospholipid Ab (IgM), Anti Cardiolipin Ab (IgG), Anti Cardiolipin Ab (IgM), PANCA(MPO), C-ANCA(PR3)) showing negative results (all below the positive threshold). Coagulation tests showed a PTT-LA of 58.1 seconds (above normal), and the lupus anticoagulant result was significant at 48.9 seconds, indicating potential blood clotting issues. Protein C was normal while protein S showed a decrease at 32. Lupus anticoagulant is associated with antiphospholipid syndrome, an autoimmune disorder that can cause abnormal blood clotting. APS can lead to a decrease in anticoagulant proteins, including Protein S, due to the formation of antibodies that interfere with its activity or reduce its levels. Suppose antiphospholipid antibodies are within normal ranges, yet Protein S levels are reduced in a lupus anticoagulant-positive patient. In that case, it may suggest alternative mechanisms causing the decrease in Protein S. Some possible explanations include, Immune Complex Formation, even without elevated antiphospholipid antibodies, immune dysregulation in autoimmune conditions like systemic lupus erythematosus (SLE) may lead to protein consumption or interference. Another possible reason is acquired protein S deficiency. Protein S levels can be reduced due to inflammation, liver disease, or active autoimmune flares, independent of antiphospholipid antibodies. Some medications such as Immunosuppressants, certain anticoagulants, or treatments used in managing lupus or related conditions might influence Protein S levels. Laboratitions should be keept these variabilities to avoid misinterpretation of the test results.

Keywords: Protein S, Antiphosholipid Antibodies, Lupus Anticoagulant

P81

Decreased Expression of the VCAM1 Gene in NASH Cirrhosis

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Background: Vascular Cell Adhesion Molecule 1 (VCAM-1), also known as CD106, is a glycoprotein found on the endothelial surface. The expression of the VCAM-1 gene is elevated by proinflammatory cytokines. VCAM-1 may play an anti-inflammatory role that could offer protection against liver diseases, such as cirrhosis. Cirrhosis is frequently linked to immune dysregulation and chronic inflammation. This study aimed to examine VCAM-1 gene expression in cirrhotic tissues. Methods: In this case-control study, 27 cirrhotic tissues, including 6 with hepatitis B and C virus infections (HBV/HCV), 6 with autoimmune hepatitis (AIH), 5 with primary sclerosing cholangitis (PSC), 7 with nonalcoholic steatohepatitis (NASH), and 3 with alcoholic, 6 liver with simple steatosis and 9 controls were gathered. Gene expression of VCAM1 was quantified using qRT-PCR. Results: The gene expression of VCAM1 in cirrhotic tissues significantly decreased compared to the control group. Interestingly, among cirrhotic tissues with different etiologies, VCAM1 gene expression significantly decreased only in NASH cirrhosis when compared to the control group. Additionally, VCAM1 gene expression in tissues with simple steatosis was higher than that of the controls. Conclusion: VCAM1 implicated in cirrhosis arises from inflammation of hepatocytes rather than cholangiocytes. The role of VCAM1 in NASH cirrhosis is more significant than in other cirrhotic groups.

Keywords: CSF2RB, Cirrhosis, Primary Sclerosing Cholangitis

Genomics and Transcriptomics: The Powerful Technologies in Precision Medicine

P82-P95

P82

Decreased of LncRNA-XIST in Peripheral Blood Mononuclear Cells of Non-Alcoholic Fatty Liver Patients

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Background and purpose: Understanding the molecular mechanisms underlying non-alcoholic fatty liver disease (NAFLD) is essential, as this knowledge could inform future diagnostic and therapeutic strategies. This study aimed to investigate the potential role of LncRNA-XIST in the detection of NAFLD to examine the potential mechanisms driving the disease. Materials and methods: A total of 30 participants, aged between 22 and 60 years, with NAFLD, along with 15 healthy controls, were recruited for the study. Biochemical parameters were assessed using an autoanalyzer. The levels of LncRNA-XIST gene in peripheral blood mononuclear cells (PBMCs) was assessed using the real-time PCR technique. The expression of LncRNA-XIST was evaluated following the extraction of RNA from the PBMC samples. After extracting the RNAs, cDNA synthesis was conducted. Real-time PCR was carried out using SYBR Green, and the delta Ct was calculated using the formula: Ct (reference gene) - Ct (target gene). GAPDH was employed as the reference gene. Findings: In this study, the average age of the patient group was 42.42±9.7 and the average age of the healthy group was 35.4±11.87. The average weight, BMI, waist circumference, hip circumference, systolic blood pressure and diastolic blood pressure of the patient group were higher than the healthy group. The results of this study showed that the expression level of LncRNA-XIST is significantly higher in healthy people than in patients with grade 1 and 2 fatty liver disease ($P<0.001$). Also, the findings indicated that the expression level of LncRNA-XIST was not significantly different between grade 1 and 2 patients ($P=0.68$). Conclusion: Our study shows that LncRNA-XIST expression levels in PBMCs are significantly associated with NAFLD. Down-regulation of LncRNA-XIST may serve as potential biomarkers for NAFLD diagnosis and progression.

Keywords: lncRNA-XIST, PBMC, Non-Alcoholic Fatty Acid, NAFLD

P83

Molecular Mimicry: HTLV and EBV Parthenogenesis by High Throughput Data Analysis - A Tale of Two Viruses

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Introduction: Epstein-Barr Virus (EBV) and Human T-cell Lymphotropic Virus Type 1 (HTLV-1) are distinct viruses associated with different cancers, Burkitt lymphoma and Adult T-cell Leukemia/Lymphoma (ATLL), respectively. However, they can share the exact pathogenesis. By identifying the intricate relationships between genes and uncovering their underlying patterns, we can pinpoint potential biomarkers and therapeutic targets, ultimately paving the way for more effective treatments. Method: To uncover shared mechanisms of oncogenesis, we conducted a systems biology study integrating gene expression profiles, protein interaction networks, and pathway analysis. Results: Our analysis revealed that EBV and HTLV-1 significantly impact pathways involved in the extracellular matrix and innate immune response in these diseases. Notably, the proteins FN1 (Fibronectin 1) and COL3A1 (Collagen, Type III, Alpha 1) exhibit significant upregulation in ATLL compared to normal T cells and Burkitt lymphoma compared to normal B cells. Also, the MYC family members have different expression patterns in BL and ATLL. Conclusion: FN1 and COL3A1 are critical for cell adhesion and extracellular matrix formation and may play a crucial role in modifying the tumour microenvironment, potentially contributing to tumour growth and metastasis. This study comprehensively explains the shared mechanisms underlying EBV and HTLV-1-induced oncogenesis, highlighting FN1 and COL3A1 as potential therapeutic targets for both viral cancers. In addition, the upregulation of C-MYC and the downregulation of N-MYC family members can be involved in BL and ATLL oncogenesis receptivity.

Keywords: Burkitt Lymphoma, ATLL, FN1, COL3A1, High Throughput Data Analysis

P84

Unraveling the Impact of miR-125b on B-Cell Acute Lymphoblastic Leukemia Relapse: A Bioinformatics Approach

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Background and aim: MiR-125b has been identified as an oncomiR, meaning it can promote cancer development. Its ectopic expression has been shown to induce B cell acute lymphoblastic leukemia (B-ALL) in experimental models. Thereafter, the aimed of this study was to identify the role of miR-125b family in B-ALL relapse. Methods: We started by loading necessary libraries such as `GEOquery (version 2.66.0) `the dataset of interest (GSE30647). Data processing was conducted using R software (version 4.2.2) with several packages, including limma, and AgiMicroRna. The analysis involved differential expression analysis and normalization of the data. Also, bioinformatics platform was served to enrich the target genes of miR-125b. Also, GraphPad prism was served to identify the P value. Results: The differential expression analysis of GSE30647 revealed that miR-125b-5p and miR-125b-1-3 were significantly upregulated in relapsed groups compared to controls. The p-value for was less than 0.0001 for both groups. the pathway was found to be significantly enriched was TGF-β pathway, suggesting that miR-125b may exert its effects on pathogenesis of relapse by modulating the CDKN2B, PPP2CA, IFNG, TGFBR1, ACVR2B, SMAD2, SMURF1, and NEO1 genes. Conclusion: In conclusion, the significant upregulation of miR-125b-5p and miR-125b-1-3p in relapsed B-ALL groups, along with the enrichment of the TGF-β signaling pathway, highlights the potential role of miR-125b in B-ALL relapse groups.

Keywords: B-ALL, Microarray Analysis, MiR-125b, Relapse

P85

First Case Report of Neutral Hb Earnz and Pathogenic Hb S Compound Heterozygosity in Southern Iran

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Background and Aim: Sickle cell disease (SCD) and thalassemia are common hemoglobinopathies with significant clinical implications. This report documents the first identified case of compound heterozygosity for Hb S and Hb Earnz in Southern Iran, detailing hematological indices, molecular characterization, and the absence of anemia symptoms in the patient. The objective is to elucidate the potential mitigating effect of Hb Earnz on the clinical severity of Hb S. Methods: A 34-year-old patient with no clinical signs of anemia was referred for genetic analysis. Hb S was detected using Amplification Refractory Mutation System-Polymerase Chain Reaction (ARMS-PCR). Hb Earnz was identified via Sanger sequencing method for beta gene. Results: Despite the presence of Hb S and Hb Earnz, the patient exhibited no specific clinical manifestations of anemia. The hematologic indices suggested that Hb Earnz may mitigate the clinical severity typically associated with Hb S. Hence, hematological indices were determined, RBC (5.81 x 10^6/µL), Hb (15.2 g/dL), MCV (77.8 fL), MCH (26.2 pg), Hb A1(61.5%), Hb F(2.6%), and Hb S(33.5 %) , Hb Earnz also has been identified in exon 3 with a specific mutation noted as HBB:c.-92C>G. Conclusion: The discovery of Hb S and Hb Earnz compound heterozygosity in a patient from Southern Iran, who exhibited no clinical manifestations of anemia, Evidence to support a non-pathogenic variant accompany.

Keywords: Hb Earnz, Thalassemia, Hb S, Compound Variant

P86

First Report of Co-Inheritance of -42 C>G and Hb Monroe (C.92G>C) Mutations in a Fetal Sample: A Minor Genotype

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Background and Aim: Genetic analysis of hemoglobinopathies often reveals significant insights into the interplay between different mutations. This report documents the first known case of co-inheritance of two mutations, -42 C>G and Hb Monroe (C.92G>C), in a fetal sample from Southern Iran. The aim is to investigate the genetic profile and clinical implications of these findings. Methods: A prenatal genetic analysis was conducted on a fetal sample using Sanger sequencing methods. The analysis identified the presence of two mutations in the beta-globin gene: -42 C>G and Hb Monroe (C.92G>C). Results: The fetal sample exhibited a minor genotype. The identified mutations, -42 C>G and Hb Monroe (C.92G>C), were found to be neutral with respect to anemia symptoms and has a minor genotype. Conclusion: This case report provides the first documentation of co-inheritance of the mutations -42 C>G and Hb Monroe (C.92G>C) in a fetal sample.

Keywords: Hb Monroe, Co-Inheritance, -42 C;gt,G

P87

Presentation of a Severe Deficiency Factor X Patient with Rare Pathogenic Genotype: Asp103His Phenotype

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Background and Aim: Factor X (FX) deficiency is a rare bleeding disorder with significant clinical implications. This case report documents the first identified instance of a novel hemozygous mutation in the FX gene in a 10-year-old female, highlighting the clinical presentation and genetic findings. The aim is to elucidate the genetic basis of the patient's severe FX deficiency and its clinical manifestations. Methods: A 10-year-old female presented with severe FX deficiency, with a Factor X level of 0.5%, and vaginal bleeding following hormone therapy for puberty induction. Her consanguineous parents were candidates for carrier testing. Coagulation hematology laboratory results included a PT of 64.8 seconds, INR of 6.56 (control PT: 12.8 seconds), PTT of 37.3 seconds, and Lupus Anticoagulant (DRVV-Screen) of 35.0 seconds. A mixing study was performed, and genomic DNA was extracted for Sanger sequencing and analysis with CodonCode Aligner software. Results: The patient's PT time decreased to 15.1 seconds in the mixing study, confirming FX deficiency. Genetic analysis revealed a novel hemoygous mutation in the FX gene (c.307G>C), resulting in a p.(Asp103His) alteration in the epidermal growth factor-like domains. The patient was homozygous for this variant, while her parents were heterozygous, indicating autosomal recessive inheritance. The variant was not reported in coagulation factor variant databases, confirming its novelty. Conclusion: This case report identifies a novel hemozugous mutation in the FX gene responsible for severe FX deficiency in a 10-year-old female. The patient's clinical presentation underscores the importance of genetic analysis in diagnosing rare bleeding disorders. Genetic counseling is recommended to discuss the risks and implications of the condition, and family members should be screened for the variant.

Keywords: Hemophilia, Coagulation Factor, Factor 10, Bleeding

P88

Effects of Elevated Glucose Levels on Nrf2 Gene Expression in Skeletal Muscle Cells

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Introduction and Objective Given the role of environmental factors in the development of diabetes, investigating genes associated with this disease seems necessary. Blood glucose levels affect insulin target tissues and cells. Increased glucose concentration has adverse effects on living organisms, leading to oxidative stress and inflammation. Among insulin target cells, skeletal muscle cells are the focus of this study. We aimed to investigate the effect of elevated glucose concentrations on the expression of the Nrf2 gene (NFE2L2) in C2C12 mouse muscle cell line. Methods In this experimental study, the effect of increased glucose levels on the expression of the Nrf2 (NFE2L2) gene in the C2C12 mouse cell line was investigated. For this purpose, cells were seeded and differentiated followed by 8- and 16-houtrs treatments with normal (1 g/L) (control), high (2.75 g/L), and very high (4.5 g/L) glucose concentrations. Following RNA extraction and reverse transcription, Nrf2 expression was evaluated by Real-time PCR. Results The results showed that 16-hour treatments with high and very high concentrations of glucose did not cause any significant changes in Nrf2 gene expression level, relative to the control. However, 8-hour treatments with high and very high concentrations of glucose caused 2.44 and 2.22 fold increment in Nrf2 gene expression level, respectively. Conclusion The evidence suggests that the diabetic environment causes a disruption in the Nrf2 signaling pathway. Oxidative damage and muscular complications in diabetic patients may be correlated to the observed increased expression of Nrf2 in the current investigation. The results of the current study may imply the role of Nrf2 in progression of diabetes and associated complications.

Keywords: Diabetes, Gene Expression, Hyperglycemia, Nrf2, Muscle

P89

ceRNA Network Analysis in Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (CESC)

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Background: Cervical cancer, the second most common malignancy in females, is one of the serious threats to women's health. Our study presents a comprehensive landscape of RNA networks and provides new insights into the complex interactions in cervical cancer. Methods: We performed a bioinformatics analysis based on CESC-related RNA-Seq data from the TCGA database. R software was investigated to analyze the expression, methylation, and nucleotide variation data to reach the differentially altered targets in tumor vs. normal tissue. the ceRNA network, enrichment, pathways, and survival analysis, were done by R and Cytoscape software. Results: A total of 3100 DEG, 165 DEmiRNA, 240 DElncRNA, and 619 DMGs were selected based on our criteria, and a total of 165 Hub-Gene were selected based on MCODE analysis. The "organelle organization", and "regulation of cardiac muscle contraction" ontology terms, and “cell cycle” and “renin-angiotensin system” pathways were screened in GO and KEGG analysis. Conclusion: The integrated bioinformatic analysis from this study reveals that, 1590 and 1915 Up and down-regulated RNAs (mRNA, miRNA, lncRNA), respectively, with logFC > |1.5|. There were 569 and 92 Hyper-Methylated and Hypo-Methylated genes, respectively, in CESC, with mean-diff meth > |0.4|. TTN and PIK3CA were the top mutated genes in CESC. Suppressed “organelle organization” and activated “regulation of cardiac muscle contraction” were the most significant molecular functions involved in cancer pathogenesis. The suppressed “cell cycle” and activated “renin-angiotensin system” were the most significant pathways in CESC. ASF1B, CDC25A, CDC25C, DTL, NUSAP1, PLK1, and RAD51 were screened among key genes as possible prognosis markers for CESC based on log-rank < 0.05. Bioinformatics and data mining is a useful approach to screen genes and their functions in carcinogenesis.

Keywords: HPV, Cancer, RNA-Seq, ceRNA, CESC

P90

Where Is the Intersection of the ceRNA Networks of HPV and Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (CESC)?

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Background: Cervical cancer, the second women's most common cancer in developing countries, has been linked to HPV infection. CESC has an unclear carcinogenesis process. Thus, we aimed to study CESC based on bioinformatics analysis better to understand the intersection of the CESC-HPV ceRNA network. Methods: Cytoscape software has been used to access the Human and HPV PPI networks, to map and analyze the significant genetic alterations in CESC that are directly related to HPV infection. Other required data, such as RNA expression, ncRNA-Targets, transcription factors, and related analysis were described elsewhere. The criteria in our analysis were adj.P.val < 0.05, log2FC >= |1.5|, degree cut-off =2, node Score Cut-off = 0.2, k-Core = 2. Results: In the Human-HPV-Mapped Interaction Network; The expression of 653 RNA (mRNA & miRNA & lncRNA) was upregulated and 971 RNA had a downregulated status in CESC cases. According to enrichment analysis, the DERNAs were related to Cell Cycle and System Development ontology terms; Focal adhesion, and Cell cycle pathways. 14 Human genes and HPV-E6 work as the Hub-Genes in the PPI network. The only gene that had a significant log-rank in survival analysis was PSMB5. Conclusion: Based on our analysis, most of the hub genes in the ceRNA network, belong to the proteasome family. Here we, consider the prognosis potential of the PSMB5 gene in CESC. System Development and Cell Cycle processes, activated and suppressed respectively, in GO analysis. On the other hand, based on GSEA analysis, HPV is strongly connected to the suppressed Cell Cycle pathway and activated Focal adhesion pathway which seems results to facilitate cancer progression. We can indicate that in-silico analysis and integration is a useful approach to screening for genetic alterations and understanding disease mechanisms, especially carcinogenesis.

Keywords: HPV, Cancer, RNA-Seq, ceRNA, CESC

P91

The CRISPR Revolution in Rheumatic Autoimmune Diseases: From Bench to Bedside

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Background: Rheumatic autoimmune disorders (RADs), including rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE), stem from immune dysregulation, driving chronic inflammation and tissue damage. Current immunosuppressive therapies lack curative potential, often inducing severe side effects and systemic toxicity. CRISPR-Cas9, a precision gene-editing tool, offers groundbreaking potential to correct immune dysfunction at its source, enabling curative therapies to address the root cause of RADs. Methods: This narrative review synthesizes findings from 45 high-impact studies (2019–2024) from PubMed, Web of Science, and Scopus, focusing on preclinical CRISPR technology applications in RADs. Selected studies utilized in vitro or animal models to evaluate methodologies include: (1) gRNA design for cytokine targets (TNF-α, IL-6), (2) viral (AAV/lentivirus) and non-viral (lipid nanoparticles) delivery systems, and (3) validation via qPCR/next-generation sequencing (NGS) and functional assays. Results: CRISPR-mediated cytokine silencing, targeting TNF-α and IL-6, reduced synovial inflammation by 40% in RA murine models, while FOXP3 editing restored Treg function, lowering autoantibody titers in SLE. Ex vivo editing of patient-derived T cells and hematopoietic stem cells (HSCs) achieved over 70% efficiency in mitigating B-cell hyperactivity, while nanoparticle-based delivery systems enhanced immune cell targeting with 90% specificity 90% specificity. Despite these advancements, challenges remain. Viral vectors offer high delivery efficiency but carry immunogenicity risks, whereas lipid nanoparticles and electroporation provide safer alternatives but require further optimization. Off-target effects (~15%), Cas9 immunogenicity, and ethical considerations also pose barriers to clinical translation. Cunclusion: CRISPR-Cas9 represents a paradigm shift in RAD treatment, merging precision gene editing with curative potential. Prioritizing non-viral delivery optimization, clinical safety trials, and ethical frameworks will accelerate translation. Collaborative innovation in base/prime editing and immune cell engineering promises to redefine personalized medicine for RADs, bridging the gap between genetic engineering and clinical reality.

Keywords: CRISPR-Cas9, Rheumatic Autoimmune Disorders (RADs), Gene Editing, Off-Target Effects, Personalized Therapy

P92

Investigating of Association between Coagulation Gene Polymorphism with the Incidence of Myocardial Infarction in Patients with MI History and Comparing it with Healthy People

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Background: Myocardial infarction (MI) remains a leading cause of death worldwide, especially among older adults, with about 10% of cases in those under 45. Approximately 90% of MI cases are linked to acute thrombosis from atherosclerotic plaques. The causes of MI are complex, involving both environmental and genetic factors, including hereditary thrombophilia from mutations in hemostatic pathway genes, which significantly increase the risk of thrombosis and MI. Thrombophilic genes are common risk factors for thromboembolic disorders and MI. Methods: This study uses a case-control design with 50 individuals who have a history of MI and 50 healthy controls. MI diagnosis will be confirmed through clinical records, including cardiac enzyme tests and CT imaging, validated by a specialist. After informed consent, participants will complete a demographics and health questionnaire. A 3 mL blood sample will be collected for DNA extraction and stored at -20°C. Primers for gene synthesis will be sent to Sinaclon, and specific restriction enzymes will be obtained from Neday Fan. The RFLP-PCR assay will amplify segments from 20 target genes, followed by enzyme application to assess cutting patterns and fragment sizes. Results: RFLP-PCR analysis revealed significant differences in mutation rates between case and control groups. Variants in key hemostatic pathway genes, particularly those affecting platelet function and coagulation, were more common in MI patients, indicating a genetic susceptibility to MI, especially in younger individuals with a hereditary predisposition to thrombophilia. Conclusion: This research highlights the role of genetic factors, especially thrombophilic gene mutations, in MI. It emphasizes the need for genetic screening in individuals at higher risk, particularly those with a family history of thrombosis or early-onset MI, to improve early diagnosis. Further studies are recommended to validate these findings and explore interactions between genetic and environmental factors in MI onset.

Keywords: Myocardial Infraction, Polymorphism, Coagulation Gene

P93

Identification of Novel RASGRP2 Mutations in Patients with Platelet Dysfunction

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Background: Inherited platelet function disorders (IPFDs) are rare hereditary diseases characterized by dysregulation of genes related to platelet receptors expression or signal transduction pathways. Bleeding disorder platelet-type 18 (BDPLT18) is an infrequent autosomal recessive platelet function disorder caused by RASGRP2 mutation. The RASGRP2 gene encodes calcium- and DAG-regulated guanine exchange factor-1 (CalDAG-GEFI), which plays a role in the activation of the αIIbβ3 integrin in platelets. In present study, eleven unrelated patients were examined for mutational analysis to identify mutations in RASGRP2 gene that may lead to BDPLT18. Methods and results: The study included 11 unrelated cases (6 males and 5 females) with various bleeding disorders. The patients were selected based on normal expression of CD41, CD61, and CD42b, as well as an impaired response to ADP, collagen, and arachidonic acid. The plasma coagulation parameters of the patients were normal. Polymerase chain reaction (PCR) and sanger sequencing were used to screen for mutations in the RASGRP2 gene. a total of 7 mutations were identified in the patients. Including four novel missense mutations (RASGRP2: p.F497L, p.F501L, p.N505K, p.C515G) and 3 known mutations (RASGRP2: p.D441N, p.R494Afs*54, g.10410G>T). These mutations are predicted to cause disease and alter the characteristics of the CalDAG-GEFI protein. Conclusion: Identifying RASGRP2 gene mutations and their association with bleeding episodes is crucial for confirming the diagnosis of BDPLT18, distinguishing it from other platelet disorders, and using effective therapeutics to prevent bleeding abnormalities.

Keywords: Inherited Platelet Function Disorders, Bleeding Disorder, Mutation, Platelet-Type Bleeding Disorder-18, RASGRP2 Gene, CalDAG-GEFI

P94

Identification of Important MicroRNAs Involved in Immunological Signalling Pathway in HTLV-1 Associated Adults T Cell Leukemia Lymphoma (ATLL)

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Background HTLV-1 is the etiological agent of adult T cell leukemia-lymphoma (ATLL), a fatal malignancy of CD4+ T cells with a considerably poor prognosis, and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP). MicroRNAs (miRNAs) are a group of noncoding, functional RNAs that their functions can result in mRNA targets being degraded or suppressed during translation. It is now well understood that microRNAs are implicated in developing several disorders. Important microRNAs of associated immunological pathways in ATLL pathogenicity will be discussed in this study. Material and method The GSE31629 dataset obtained with the GPL7731 platform. The dataset contains miRNA samples from peripheral blood mononuclear cells (PBMCs) and CD4+ T cells from 40 ATLL patients and 22 healthy donors. Adjusted p-value < 0.05 was determined as the threshold for DEM detection. Initial pathway analysis was performed using the Diana-mirPath web server. P53 and PI3K signaling pathways are the most important immunological pathways that can play a role in ATLL pathogenesis. Result let-7f-5p, let-7a-5p are the most significant microRNAs related to mentioned immunological pathways involved in ATLL pathogenesis. Discussion and conclusions The examined microRNAs have gene targets that can be identified and measured as potential targets for the development of. However, further studies are recommended to better understand the possible consequences of miRNAs and their relationship with the pathogenesis of ATLL.

Keywords: HTLV-1, ATLL, MicroRNA, Adult T Cells Leukemia Lymphoma, Human T-Lymphotropic Virus Type 1, P53 Signaling Pathway, PI3K Signaling Pathway

P95

Expression of TLR-7, MyD88, NF-kB, and TRAF6 in Thymus of Rats Induced by Cyclosporine A and Nano-Selenium Supplementation

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Background: The thymus is one of the most important immune organs in the body, which reacts to diseases and drugs related to the immune system. The aim of this study was investigate the expression of toll-like receptor (TLR-7), myeloid differentiation primary response 88 (MYD88), Nuclear factor kappa B (NF-κB), and TNF receptor associated factor (TRAF) in thymus of rats induced by cyclosporine A (CsA) and Nano-selenium (Nano Se) supplementation. Methods: 24 male Wistar rats (200-220 grams), were randomly divided into 3 groups of (n=8 in each group) control, CsA, and Nano Se + CsA. Rats in CsA group's received cyclosporine A and olive oil solution by subcutaneous injection for 10 days at a dose of 5 mg/kg/day. NanoSe at a dose (of 2.5 mg/kg b.w) were given to the supplement group by stomach gavage once a day 3 times a week. Real time pcr were used for gene expression of TLR-7, MyD88, NF-kB, and TRAF6 at thymus. Results: The result of this study show that CsA significantly decrease expressions of TLR-7, MyD88, NF-kB, and TRAF6 at thymus compare to control group ($p<0.05$). However, in Nano Se with CsA significantly increased expressions of TLR-7, MyD88, NF-kB, and TRAF6 at thymus compare to CsA group ($p<0.05$). Conclusion: As the results of the present study showed, the consumption of Nano Se significantly regulated the expression of TLR-7, MyD88, NF-kB, and TRAF6 genes in thymus of rats treat with cyclosporine A. Therefore, Nano supplements, especially Nano Selenium, can be used to strengthen the immune system.

Keywords: Cyclosporine A, Nanoselenium, Thymus, TLR7, NF-κβ, MyoD88, TRAF6

Harmonization of Clinical Laboratory Test Results

P96-P98

P96

Prevalence of Norovirus, Sapovirus, and Astrovirus in Pediatric Patients with Gastroenteritis Referred to a Hospital in Northwest Iran

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Background: Acute gastroenteritis (AGE) is a major cause of morbidity in children under five, with norovirus, sapovirus, and astrovirus being significant viral contributors. Despite their global impact, data on the prevalence, seasonal distribution, and demographic characteristics of these viruses remain limited in many regions. This study aimed to investigate the prevalence, seasonal patterns, and demographic associations of norovirus, sapovirus, and astrovirus in pediatric patients with AGE in northwest Iran, highlighting the need for standardized laboratory methods to ensure accurate detection and reliable epidemiological comparisons. Methods: A cross-sectional study was conducted in 2023 on 180 children under five years old presenting with AGE at a referral hospital. Stool samples were analyzed using Real-Time PCR (RT-PCR) to detect norovirus, sapovirus, and astrovirus. Data were evaluated for seasonal distribution and demographic correlations. Additionally, the study emphasizes the importance of standardized molecular diagnostic methods to enhance the comparability and reliability of results. Results: Among the detected viral pathogens, sapovirus was identified in 4.4% of cases, followed by norovirus (3.3%) and astrovirus (2.2%). No significant seasonal peak was observed for these viruses. The mean age of infected participants did not differ significantly from non-infected ones. Additionally, no significant association was found between gender and infection rates for any of the three viruses. These findings highlight the necessity of standardized molecular detection methods to improve the accuracy of prevalence estimates and facilitate epidemiological comparisons. Conclusion: Norovirus, sapovirus, and astrovirus were identified as notable causes of pediatric AGE in northwest Iran, emphasizing the need for improved surveillance and molecular diagnostics. To ensure result accuracy, fluorometry was used for nucleic acid quality control, and positive/negative controls were applied to reduce errors. Standardized diagnostic protocols and inter-laboratory harmonization are essential for enhancing data accuracy and reliability in epidemiological studies.

Keywords: Acute Gastroenteritis, Pediatrics, RT-PCR, Laboratory Standardization, Quality Control

P97

Evaluation of RNA Extraction Kits Efficacy for Diagnosing Hepatitis C Virus Infection

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Background: Various viral nucleic acid extraction kits are presently accessible in Iran for hepatitis C virus (HCV) genome extraction during RT-qPCR testing. An effective extraction kit is essential and influences RT-qPCR outcomes. The objective of this study was to assess the efficacy of these kits. Materials and Methods: HCV RNA of 7 hepatitis C patients was extracted using 4 commercial viral nucleic acid (Kit 1, Kit 2, Kit 3, Kit 4) by the same professional personnel. The isolated RNAs were assessed using an RT-qPCR kit and the Applied Biosystems Step One real-time PCR apparatus, based on the manufacturer's instructions. The Ct levels of HCV and the internal control were assessed. Results: RNA extraction kit 1 gained the best results for showing HCV among samples with lowest CT. In addition, Internal controls indicated kit 1 had more reliable CT for HCV than other tested kits. Conclusion: Viral nucleic acid extraction kits have different sensitivities to extract HCV genome. Quality control is important to verify the clinical reliability of these kits and to select best kit with high performance.

Keywords: HCV, RNA Extraction, RT-qPCR

P98

Dihydrorhodamine-123 Flow Cytometry Method: Time for Substantial Revision in Technical Procedure

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The dihydrorhodamine 123 assay is generally applied to measure the production of intracellular reactive oxygen species in neutrophils using flow cytometry and is considered a diagnostic evaluation for chronic granulomatous disease. In fact, there is a broad range of variables that can directly or indirectly affect test results, either individually or collectively. It is therefore crucial to identify the ideal requirements to achieve reliable results as well as using these requirements to provide standard operating procedures that should be taken into account. Therefore, we focus on aligning optimum results by comparing preanalytical and analytical phases that influence test results, such as the effect of various anticoagulants, transport and maintaining temperature (24°C or 4°C) of samples, test prime run time, appropriate solution concentrations, and effect of incubation temperature (24°C or 37°C) during the test run.

Keywords: Dihydrorhodamine-123, DHR-123 Assay, Neutrophil Oxidative Burst, Neutrophils, Optimum Conditions, NOI, CGD

Immunological Testing in Organ and Tissue Transplantation

P99-P106

P99

Comparative Analysis of DNA Extraction Methods: Optimizing Yield and Purity for Molecular Testing

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Background: The purity of extracted DNA plays a crucial role in the accuracy and reliability of molecular testing such as HLA-Typing. This study aimed to assess the impact of different DNA extraction methods on both the purity and concentration of the extracted DNA. Methods: Genomic DNA was extracted from whole blood using four distinct methods: chloroform-based extraction, sodium perchlorate-based extraction, heat-assisted salting-out, and solid-phase extraction. The yield and purity of the extracted DNA were evaluated using Nanodrop spectrophotometry. Results: Among the four extraction methods, the heat-assisted approach yielded the highest DNA concentration, whereas the column-based method produced the lowest. Protein contamination, assessed via the A260/A280 ratio, was most pronounced in the heat-assisted method, as indicated by the lowest mean A260/A280 ratio compared to other methods. Additionally, the A260/A230 ratio, a marker of chemical contamination, varied significantly across methods. The sodium perchlorate-based method exhibited the highest A260/A230 ratio (>1.9), suggesting superior removal of chemical contaminants relative to other extraction approaches. Conclusion: Our findings highlight DNA extraction methods' significant impact on the yield and purity of extracted DNA. The heat-assisted method provided the highest DNA concentration but exhibited the greatest protein contamination. In contrast, the sodium perchlorate-based method demonstrated superior chemical purity, as reflected by the highest A260/A230 ratio. These results emphasize the importance of selecting an appropriate extraction method for downstream molecular applications.

Keywords: DNA Extraction, Purity Assessment, Nanodrop Spectrophotometry

P100

Immunologic Assessment in Hematopoietic Stem Cell Transplantation for Acute Lymphoblastic Leukemia in a 47-Year-Old Man with Fanconi Anemia: A Case Report

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A 47-year-old man was diagnosed with Acute Lymphoblastic Leukemia (ALL) amid a history of Fanconi Anemia (FA). He presented with symptomatic lymphadenopathy, and laboratory tests revealed thrombocytopenia (94,000 platelets), anemia (hemoglobin of 8.2 g/dL), and leukopenia (3,800 white blood cells). A bone marrow biopsy showed 25% immature atypical lymphoid cells, and cytogenetic analysis confirmed Philadelphia chromosome-negative pre-B cell ALL. After receiving eight cycles of Hyper-CVAD chemotherapy in Khuzestan, he was declared minimal residual disease (MRD) negative, making him eligible for hematopoietic stem cell transplantation (HSCT). To ensure optimal donor-recipient compatibility, HLA typing was performed in Tehran, identifying his sister—a 52-year-old woman—as a full match. Both were negative for cytomegalovirus (CMV) and Epstein-Barr virus (EBV) in antibody screenings. Flow cytometry characterized the donor's immune cells, revealing 8.4 million mononuclear cells, including 7.8 million CD34-positive stem cells and 190 million CD3-positive T cells. Seven days post-transplant, the patient's white blood cell count rose to 7,700, indicating successful engraftment. Due to the patient's complex condition and potential rejection risks, a non-myeloablative conditioning regimen with cyclosporine and antithymocyte globulin (ATG) was administered. Chimerism analysis was later conducted to monitor engraftment and detect relapse. Donor lymphocyte infusion (DLI) was recommended after three months to enhance immune reconstitution. Over 24 months of monitoring post-transplant, the patient achieved successful engraftment and complete remission, demonstrating the critical need for tailored immunologic strategies in HSCT for complex cases involving leukemia and genetic factors.

Keywords: Immunologic Assessment, Hematopoietic Stem Cell Transplantation, Fanconi Anemia, Donor Lymphocyte Infusion

P101

Evaluation of the Presence of Human Parvovirus B19 Before and After Bone Marrow Transplantation

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Background: Patients receiving bone marrow transplants are prone to a variety of diseases, including viral diseases, due to the use of immunosuppressive drugs. One of the viral agents threatening these patients is Parvovirus B19 (PVB19). The virus leads to anemia and pure aplasia in the bone marrow of these patients by suppressing the RBC population. Methods: In this study, blood samples were taken from 30 patients) Mean age: 35.56 ± 18.94(before and one month after bone marrow transplantation (BMT), and after extraction, they were examined by Nested PCR. Results: PCR test of two male patients was positive for the presence of human parvovirus B19. Their hematological indices before and after transplantation did not show a statistically significant difference. Conclusion: Because bone marrow transplant patients take immunosuppressive drugs, and given that parvovirus B19 infection is clinically rare but significant, screening for the virus is recommended, at least in people with unexplained anemia.

Keywords: Parvovirus B19, Bone Marrow Transplantation, Anemia, Pure Red Cell Aplasia

P102

The Impact of KIR-HLA Class I Ligands on Chronic Rejection and Graft Loss in Kidney Transplantation

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Background and Aim: The interaction between KIR (Killer Immunoglobulin-like Receptors) and HLA Class I ligands plays a crucial role in immune regulation during kidney transplantation. Chronic rejection and graft loss are often associated with NK (Natural Killer) cell activity, triggered by mismatches between recipient KIRs and donor HLA. This review examines the impact of KIR-HLA mismatches on transplant outcomes. Methods: We reviewed studies on KIR-HLA interactions in kidney transplantation, focusing on clinical trials and cohort studies. These studies examined the role of KIR-HLA mismatches in chronic rejection and graft survival. Results: Mismatches between KIRs and HLA Class I ligands have been shown to increase the risk of chronic rejection and graft failure. Specific KIR-HLA combinations, such as KIR2DL1 with HLA-C2, were associated with higher rejection rates. Retrospective analyses indicate a 25% reduction in long-term graft survival when such mismatches occur. Conclusion: KIR-HLA mismatches significantly impact kidney transplant outcomes. Incorporating KIR genotyping into pre-transplant evaluations can improve donor-recipient matching and reduce the risk of graft rejection. Further research is necessary to explore the underlying mechanisms of NK cell-mediated rejection and develop therapeutic strategies to address KIR-HLA incompatibilities.

Keywords: KIR, HLA Class I, Kidney Transplantation, Chronic Rejection, Graft Survival

P103

Donor-Specific HLA Antibodies in Renal Transplantation: A Narrative Review

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Background and Aim: Donor-specific HLA antibodies (DSAs) critically influence renal transplant outcomes by triggering antibody-mediated rejection and reducing graft survival. Sensitizing events such as blood transfusions, pregnancies, or prior transplants can lead to DSA formation. Accurate detection of DSAs is essential for effective pre-transplant screening and post-transplant monitoring. Traditional cell-based assays—including complement-dependent cytotoxicity crossmatch (CDC-XM) and flow cytometry crossmatch (FC-XM)—have been widely used, although they exhibit limitations in sensitivity and specificity. Advanced solid-phase assays, like the Luminex Single Antigen Bead (L-SAB) method, offer improved performance. Methods: This narrative review focuses on comparing the sensitivity, specificity, and clinical relevance of CDC-XM, FC-XM, and L-SAB assays. Studies published between 2000 and 2023, including key articles such as “Donor-Specific HLA Antibodies in Predicting Crossmatch Outcome” and “Physical Crossmatching vs Virtual Crossmatching: The End of an Era?”, were examined to provide a comprehensive understanding of these techniques and their impact on transplant outcomes. Results: Evidence indicates that L-SAB assays consistently demonstrate higher sensitivity and specificity, particularly for class II antibodies. CDC-XM shows limited sensitivity, while FC-XM may produce false-positive results. Virtual crossmatching is emerging as a complementary tool but does not yet replace physical crossmatching. Conclusion: L-SAB assays remain the most reliable method for DSA detection, enhancing risk stratification and improving graft survival in renal transplantation.

Keywords: Donor-Specific Antibodies, Renal Transplantation, Crossmatching, Luminex, Virtual

P104

Renal Endothelial Antibodies and Their Role in Kidney Transplant Rejection: A Narrative Review

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Background: Antibody-mediated rejection (AMR) is a major cause of kidney graft failure. Traditionally, donor-specific anti-HLA antibodies have been a primary focus in transplant rejection studies, but recent research underscores the significant role of non-HLA antibodies, especially anti-endothelial antibodies (AEAs). AEAs target endothelial antigens, contributing to microvascular injury and acute rejection. Their pathogenic mechanisms, detection methods, and clinical relevance are still actively explored. Methods: The present study synthesizes recent research on AEAs in kidney transplantation. Key studies analyzed include Renal Endothelial Cytotoxicity Assay, XM-ONE assay and endothelin A receptor studies. We also reviewed cases of hyperacute rejection without classical complement activation and the link between preformed IgG against glomerular endothelial antigens and early acute rejection. Results: AEAs such as anti-MICA and anti-AT1R increase AMR risk. The Renal Endothelial Cytotoxicity Assay aids in detecting AEAs, while the XM-ONE assay correlates positive endothelial crossmatch with poor graft outcomes. Elevated endothelin A receptor expression is linked to acute tubular necrosis and AMR. Conclusion: Non-HLA anti-endothelial antibodies play a crucial role in kidney transplant rejection. Screening for AEAs before transplant could improve risk assessment and immunosuppressive strategies. Standardizing detection and developing targeted therapies are essential for better transplant outcomes.

Keywords: Anti-Endothelial Antibodies, Kidney Transplantation, Antibody-Mediated Rejection, Endothelial Injury, Non-HLA Immunity

P105

Molecular Signatures of Kidney Transplant Rejection: Integrating RNA-Seq and Machine Learning for Non-Invasive Diagnosis

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Background: Kidney transplant rejection typically requires invasive biopsies for diagnosis. RNA sequencing (RNA-Seq) provides a detailed analysis of gene expression, while machine learning (ML) techniques facilitate the identification of molecular signatures associated with rejection, enabling non-invasive and accurate detection. The integration of RNA-Seq and ML enhances early prediction capabilities and aids the development of non-invasive diagnostic models for graft rejection. Methods: A comprehensive literature review was conducted through PubMed, Scopus, and Web of Science using keywords such as RNA-Seq, machine learning, graft rejection, and molecular signatures. Relevant studies were screened, and key data were extracted for analysis and review. Results: The combination of RNA-Seq and machine learning allows for the identification of molecular signatures indicative of kidney transplant rejection. RNA-Seq data, typically represented as gene count matrices, undergo normalization and dimensionality reduction before being analyzed by machine learning models. Supervised algorithms, including Random Forest, Support Vector Machines (SVM), and Deep Learning techniques, predict rejection based on gene expression patterns. These models identify key genes associated with inflammation, immune response, and cellular stress. Deep learning methods, in particular, excel at detecting complex, nonlinear relationships. Unsupervised techniques, such as Principal Component Analysis (PCA) and K-means clustering, help classify patients into subgroups based on gene expression profiles, contributing to personalized treatment strategies. Conclusion: The integration of RNA-Seq with machine learning significantly improves the early detection of kidney transplant rejection, aids in the discovery of novel biomarkers, and offers a promising non-invasive approach to enhancing the accuracy of rejection diagnosis and prediction.

Keywords: Graft Rejection, Molecular Signatures, RNA-Seq, Machine Learning

P106

The Novel Insights in to Non-HLA Alloimmunity in Transplantation: A Narrative Review

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Background and Aim: Antibody-mediated rejection (AMR) remains the principal cause of long-term graft failure in solid organ transplantation. Although donor-specific anti-HLA antibodies have been extensively studied, emerging evidence indicates that non-HLA antibodies also contribute significantly to graft injury. These antibodies target diverse antigens—including non-classical MHC molecules, endothelial proteins, and cryptic self-antigens—and are implicated in both acute and chronic rejection. Methods: The present study synthesizes data from recent studies employing high-throughput protein arrays, molecular genotyping, endothelial cell crossmatch assays, and histopathological analyses to elucidate common mechanisms underlying non-HLA antibody formation and their roles in transplant rejection. Results: The literature reveals that non-HLA antibodies—such as anti-MICA, anti-AT1R, and anti-endothelial cell antibodies—are associated with an increased risk of AMR. A higher pre-transplant non-HLA antibody burden correlates with histological evidence of rejection, even in the absence of detectable HLA antibodies. These antibodies can induce injury through both complement-dependent and complement-independent pathways, including activation of intracellular signaling cascades and antibody-dependent cellular cytotoxicity. Furthermore, genetic predispositions may contribute to heightened alloimmune responses. Conclusion: Understanding non-HLA alloimmunity represents a paradigm shift in transplant immunology. Incorporating non-HLA antibody screening into pre-transplant evaluations may enhance risk stratification and inform personalized immunosuppressive strategies. Future studies should standardize detection assays and clarify the precise mechanisms of non-HLA antibody-mediated graft injury to ultimately improve transplant outcomes. Overall, these findings strongly highlight the urgent need for integrating non-HLA antibody assessment in routine clinical practice.

Keywords: Non-HLA Antibodies, Alloimmunity, Transplantation, Graft Rejection, Immunogenetics

Innovative Diagnostic Methods in Clinical Microbiology (Bacteriology)

P107-P121

P107

Drug Resistance Pattern of Mycobacterium Tuberculosis in Guilan province, Iran

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Background: Mycobacterium tuberculosis (MTB) is causative agent of tuberculosis (TB), which still remains one of the most common infectious diseases in developing countries. In the recent years, emergence and spread of multidrug-resistant (MDR) TB pointed as public health problem worldwide. This study aimed to determine the rate of drug resistance to first-line anti-TB drugs in Guilan province. Methods: MTB isolates were collected from March 2016 to July 2018. Drug susceptibility testing to rifampicin, isoniazid, ethambutol, and streptomycin was performed on Löwenstein-Jensen medium using proportion method. Results: A total of 138 MTB isolates were included to this study. The mean age of patients was 47.41, ranged from 17-84 years and 104 (84.1%) patients were male. A set of 128 (92.8%, 95% CI = 87.2%-96%) isolates were pan-susceptible and 10 (7.2%, 95% CI = 4%-12.8%) were resistant to at least one drug. Five isolates (3.6%, 95% CI = 1.6%-8.2%) were resistant to streptomycin, 6 isolates (4.3%, 95% CI = 2%-9.2%) were resistant to isoniazid, 3 isolates (2.2%, 95% CI = 0.7%-6.2%) were resistant to rifampicin, one isolate (0.7%, 95% CI = 0.1%-4%) was resistant to ethambutol. In this study three isolates (2.2%, 95% CI = 0.7%-6.2%) showed resistance to rifampicin and isoniazid then identified as MDR. Conclusions: The prevalence of drug resistant isolates in this study area point to the necessity for further enforcement of TB treatment and disease control management. Drug susceptibility testing for all TB cases and continuous monitoring of drug resistance are recommended to prevention and control of drug-resistant TB.

Keywords: Mycobacterium Tuberculosis, Tuberculosis, Multidrug-Resistant

P108

Investigating the Diagnostic Value of Real-Time PCR in HACEK Group Bacteria Involved in Infective Endocarditis

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There are various diseases that traditional methods are not used to diagnose and treat. One of the most important diseases is infectious endocarditis, which is caused by various, bacteria and fungy, Bacteria is important in this disease. The HACEK organisms are a group of bacteria that are an unusual cause of infective endocarditis, All of these organisms are part of the normal oropharyngeal flora, which grow slowly, So the importance of diagnosis and therapeutic , the use of normal culture methods for diagnosis and treatment is not useful in this study We used Real Time-PCR. Method: In this study, primitive examination of patients was performed by cardiologists. Before prescribing antibiotics to patients, blood culture samples were taken and after incubation at 37 degrees, Blood culture were negative but patients had symptoms of endocarditis. After DNA extraction, Real Time-PCR was performed. In this study, 50 samples of patients with endocarditis in Shahid Madani Hospital of Tabriz, who were diagnosed by a cardiologist but their blood culture was negative, were studied. With Special primers designed by the researcher were tested for Real Time-PCR for HACEK group bacteria. Results: After Real Time-PCR, all blood culture samples were positive for HACEK bacteria, with Haemophilus influenzae being the most common with 62% and Kingella being the lowest (1.5%). Discussion and conclusion: The results of this study showed that use of Real Time-PCR method in negative blood culture samples has a very high diagnostic value so that all negative blood culture samples with reasoned signs of infection showed the presence of one of the HACEK organisms.

Keywords: PCR, HACEK, Real Time

P109

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

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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. 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. The DST for second-line anti-TB drugs drugs; ciprofloxacin (CIP; 2 µg/mL), ofloxacin (OFX; 4 µg/mL), ethionamide (ETD; 40 µg/mL), kanamycin (KAN; 30 µg/mL), capreomycin (CAP; 40 µg/mL), cycloserin (CYN; 30 µg/mL), para-aminosalicylic acid (PAS; 1 µg/mL) (all from Sigma, USA) and amikacin (AMK; 30 µg/mL) (Exir, Iran) on the LJ medium via the proportional method and susceptibility testing for levofloxacin (LVX; 1 µg/mL) (Sigma, USA) performed on Middlebrook 7H10 agar media (BBL Microbiology Systems, Cockeysville, MD, USA), was performed for multidrug-resistant (MDR) isolates. 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. 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

P110

Biofilm Formation, Antibiotic-Resistance and Clonal Relatedness among Clinical Isolates of Acinetobacter Baumannii

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In this work, the antibiotic resistance, biofilm formation capability, and clonal relatedness of 50 A. baumannii isolates collected from three hospitals in Ardabil city, Iran, were evaluated. Antibiotic sensitivity and biofilm formation of isolates were determined by disk diffusion and microtiter-plate methods, respectively. Molecular typing of isolates was also performed using repetitive sequence-based PCR (REP-PCR). The majority of isolates were resistant to cephems, aminoglycosides, and carbapenems, with 80 % classified as multi-drug resistant (MDR). While, only isolates collected from blood and tracheal were resistant to colistin. Additionally, 42 isolates (84 %) had biofilm formation capability. According to rep-PCR results, 34 isolates showed similar banding patterns, while 16 isolates had unique banding patterns. Finally, based on the molecular analysis, there was a direct relationship between biofilm formation and the antibiotic resistance of isolates. In other words, MDR isolates had a higher ability to form biofilm.

Keywords: Acinetobacter Baumannii, Biofilm Formation, Antibiotic-Resistance, REP-PCR

P111

Trends in Vancomycin-Resistant Staphylococcus Aureus (VRSA) in Iran (2013–2024): A Systematic Review and Meta-Analysis

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Background and Aim: Staphylococcus aureus is a major pathogen causing severe infections globally. Vancomycin-resistant S. aureus (VRSA) poses significant treatment challenges, yet data on its prevalence and trends in Iran are limited. This study aims to address these gaps through a systematic review and meta-analysis of VRSA in Iran (2013–2024), mapping its epidemiology, identifying high-risk areas, and tracking resistance patterns to inform public health strategies. Methods: A systematic review identified studies on VRSA prevalence in Iran from 2013 to 2024 using PubMed, Scopus, Embase, SID, and Web of Science. A meta-analysis was performed using R Studio (version 4.3.3). Results: Among 28 included studies, VRSA prevalence was 15% ([95% CI: 0.12–0.18]) in outpatients (584 cases) and 89% ([95% CI: 0.85–0.92]) in inpatients (5,129 cases). Geographic analysis showed the highest prevalence in the East (13% [95% CI: 0.04–0.26]) and North (12% [95% CI: 0.01–0.33]), and the lowest in the West (1% [95% CI: 0.00–0.03]). Southern and central regions had moderate rates (4% each [95% CI: 0.02–0.06]). Temporal analysis revealed stable VRSA prevalence at 5% ([95% CI: 0.02–0.09]) from 2013 to 2024. Conclusion: This study highlights significant geographic variation in VRSA prevalence across Iran, with the highest rates in the East and North. Despite stable trends, VRSA's persistent burden underscores the need for targeted interventions, enhanced surveillance, and robust antimicrobial stewardship to address this public health challenge.

Keywords: Staphylococcus Aureus, Vancomycin-Resistant Staphylococcus Aureus, Drug Resistance, Bacterial, Iran

P112

The Influence of Innovative Technologies in Clinical Microbiology: Advancements in the Rapid Diagnosis of Infectious Diseases

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Clinical Microbiology Laboratories (CMLs) play a pivotal role in the rapid and accurate diagnosis of infectious agents, antimicrobial sensitivity testing (AST), and the assessment of antimicrobial resistance (AMR). They provide crucial information regarding community-acquired infections (CAI) and healthcare-associated infections (HAI), as well as insights into antibiotic stewardship and epidemiological trends in health and disease. In the current era of advanced medical technologies, CMLs have significantly enhanced their diagnostic capabilities. For example, traditional methods for detecting Mycobacterium tuberculosis require six weeks for colony formation, while modern systems such as Bac Tec can identify Brucella species within 3-5 days. Additionally, the MGITBD system allows for the detection of TB drug resistance in just 24 hours. Rapid identification techniques, including matrix-assisted laser desorption ionization/time-of-flight (MALDI-TOF) mass spectrometry, enable the diagnosis of pathogens from small colonies in under two hours. Moreover, molecular diagnostic methods like polymerase chain reaction (PCR) provide timely detection of slow-growing organisms and viral loads. With the advent of point-of-care testing (POCT) technologies, the capacity for diagnosing infectious diseases has expanded to bedside and home settings. However, traditional CML practices continue to face delays due to the uneven availability of these advanced technologies across clinical centers.

Keywords: Clinical Microbiology, Antimicrobial Resistance, Infectious Disease Diagnosis, Blood Culture Processing

P113

Prognostic Value of SARS-CoV-2 Cycle Threshold (Ct) in Hospitalized COVID-19 Patients: A Laboratory Perspective on Clinical Outcomes

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Background: Accurate laboratory diagnostics, such as the cycle threshold (Ct) value in SARS-CoV-2 qRT-PCR tests, can serve as a predictor of infection risk and disease severity in COVID-19 patients. This study investigates the hypothesis that Ct values can act as biomarkers for disease severity, clinical outcomes, and mortality in patients with COVID-19. Methods A cross-sectional analysis was conducted on SARS-CoV-2 qRT-PCR results from 443 hospitalized patients between 2019 and 2020. The association between Ct values and viral load categories (high viral load: Ct≤25; low viral load: Ct>25) was examined to determine their impact on clinical outcomes. Results The mean age of the patients was 56.7 ± 15.8 years, 243 patients (54.9%) were male. Ct values were significantly lower in deceased patients compared to those who were discharged (P=0.005). Additionally, patients hospitalized in intensive care units (ICUs) had significantly lower Ct values than those in infection control units (P=0.002). Adjusted analyses revealed that high viral load (Ct≤25) was associated with a higher risk of in-hospital death (OR=5.16, 95% CI: 2.36-11.28, P<0.001) and ICU admission (OR=6.87, 95% CI: 2.36-11.28, P<0.001). Conclusion In hospitalized COVID-19 patients, SARS-CoV-2 viral load, as indicated by Ct values, is significantly associated with mortality and ICU admission. These findings suggest that Ct values can be utilized as a diagnostic tool to identify patients at higher risk for severe outcomes, thereby aiding in clinical decision-making and resource allocation.

Keywords: COVID-19, Cycle Threshold (Ct), qRT-PCR, Prognostic Biomarkers, SARS-CoV-2

P114

The Expanding Role of Flow Cytometry in Improving Clinical Microbiology Diagnostics

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Flow cytometry is a powerful technique with growing applications in clinical microbiology laboratories. Using lasers and fluorescent markers, it enables the identification, counting, and analysis of cells and particles. In microbiology, flow cytometry is used for: Rapid and accurate identification and counting of microorganisms: including bacteria, fungi, and viruses, which is crucial in diagnosing bloodstream infections, urinary tract infections, and other critical infections. Antibiotic susceptibility testing: by examining the physiological changes of microbial cells exposed to antibiotics, it helps select the most appropriate antibiotic for treatment. Diagnosis of viral infections: such as HIV, hepatitis, and influenza, by identifying and counting infected cells. Assessment of immune system function: by identifying and counting immune cells, it aids in diagnosing immunodeficiency disorders, autoimmune diseases, and cancers. Diagnosis of specific infectious diseases: such as tuberculosis, leishmaniosis, and malaria, by identifying and counting the causative parasites or bacteria. Microbiology research: investigating the structure, function, and reproduction of microorganisms and the effects of drugs and chemicals on them. Clinical and diagnostic importance: Flow cytometry plays a crucial role in early diagnosis, disease monitoring, treatment optimization, and infection prevention by providing accurate and timely information. It is especially valuable in cases requiring rapid and precise diagnosis, such as life-threatening infections. Conclusion: With its diverse applications and increasing clinical significance, flow cytometry has become an indispensable tool in clinical microbiology laboratories, and its role is expected to grow in the future.

Keywords: Flow Cytometry, Antibiotic Susceptibility, Life-Threatening Infections, Rapid and Accurate Identification, Specific Infectious Diseases

P115

Evaluation of Antibacterial and Antibiofilm Efficacy of Gentamicin-Loaded Solid Lipid Nanoparticles (GM-SLNs) Against Acinetobacter Baumannii Infections

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Background: Acinetobacter baumannii has become a notable "superbug" due to its rapid development of resistance to multiple classes of antibiotics. This study aimed to evaluate the antibacterial and antibiofilm effectiveness of gentamicin-loaded solid lipid nanoparticles (GM-SLNs) in treating infections caused by A. baumannii. Methods: Nanoparticles were synthesized using the double melt emulsion dispersion method. A. baumannii was isolated from wounds, blood, urine, and sputum through standard microbiological techniques. Antimicrobial susceptibility was tested using the Kirby-Bauer disk diffusion method. The biofilm-forming ability of A. baumannii isolates, the antibacterial activity of GM-SLNs, and the time killing assay were conducted following standard protocols with slight modifications. The impact of GM-SLNs on the expression of biofilm-related genes was analyzed using real-time PCR. Results: A total of 37 A. baumannii strains were isolated from 41 clinical specimens. The most common antibiotic resistances were against gentamicin (GM), ciprofloxacin (CIP), ceftazidime (CAZ), and imipenem (IMP). Eighty percent of the A. baumannii isolates were classified as multidrug-resistant (MDR). GM-SLNs reduced the minimum inhibitory concentrations (MICs) for all A. baumannii strains by two, four, and even eight times compared to free gentamicin. GM-SLNs were also significantly more effective than free gentamicin in inhibiting biofilm formation in all A. baumannii isolates. Furthermore, the expression of the bap gene was significantly lower in all isolates treated with GM-SLNs compared to those treated with free gentamicin. Conclusion: Overall, GM-SLNs represent a major breakthrough in the fight against A. baumannii and other biofilm-related infections, providing hope for more effective treatment options amid the growing challenge of antimicrobial resistance.

Keywords: Acinetobacter Baumannii, Solid Lipid Nanoparticles, Gentamicin, Antibacterial, Biofilm

P116

Study of in vitro Adherence of Vaginal Lactobacilli with Potential Probiotic Properties Isolated from Healthy Women in Northern Iran

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The lactobacilli are a part of the bacterial flora of the human vagina. They may have probiotic properties and help maintain the balance and health of the vaginal ecosystem while the loss of these bacteria predisposes females to urinary and genital infections. The aim of this study was to investigate the invitro adherence of probiotic potential of vaginal Lactobacillus among healthy females in northern Iran. The Lactobacillus strains were isolated from vaginal samples and were identified by sequencing of the 16S rRNA fragment. Functional properties such as tolerance to low pH, H2O2 production & adherence ability to HeLa cells were detected. A total of 38 vaginal lactobacilli strains from five species, including Lactobacillus crispatus (n=13), Lactobacillus gasseri (n=10), Lactobacillus acidophilus (n=6), Lactobacillus jensenii (n=5) and Lactobacillus johnsonii (n=4), were identified. All of the species showed significant tolerance to low pH over 24 hours ($p < 0.001$). Nearly 21 of the strains showed the good adherence ability to HeLa cells over. According to the findings, Lactobacillus gasseri strains attached more readily to HeLa cells than did the other species therefor, this isolates are a good candidate for further studies on the potential health benefits and application of lactobacilli as probiotics.

Keywords: Lactobacillus, Probiotic, Vaginal, HeLa cells

P117

The Survey of Prevalence of Helicobacter pylori and Relationship with Calprotectin Antigen in Patients with Gastrointestinal Inflammation by ELISA Method in Tabriz City in 2023-2024

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Helicobacter pylori is a bacterial pathogen responsible for significant gastrointestinal complications. They can also lead to stomach ulcers and gastritis. H. pylori gastritis produces a combined acute and chronic inflammatory reaction that activates neutrophils and eosinophils, mast and dendritic cells. Calprotectin is a protein that is produced by endothelial cells following neutrophil and active inflammation or monocytes binding to endothelial cells. Calprotectin is an essential antimicrobial inflammatory factor and a component of the host's innate immune system. Calprotectin serum level is an important marker of inflammation. This protein responds to bacterial enzymes and intestinal protease and can be used as a marker of gastrointestinal inflammation. Method: Performing clinical routine tests of H.pylori M, H.pylori G, H.pylori A, H.pylori in Stool and Calprotectin according to the protocols of the kits used in clinical laboratories. Result: Out of the 300 people who entered our statistical population after reviewing their test results, 127 were women and 173 were men. The average age of the patients was 38.8 years. Among the 162 people who requested H. pylori G test, 111 were positive and the rest were negative. Regarding H. pylori M test, out of 121 people, 73 people were positive and 48 people were negative. Finally, about H. pylori A test, 7 people out of 17 people were positive and 10 people were negative. Regarding H. pylori in Stool test, it was requested for 111 people, of which 51 people were infected with H.pylori and 60 of them were negative. Also, about Calprotectin test, 24 people out of 51 people were positive and 27 people were negative. No significant relationship was observed between age and gender of H.pylori infection, while there was a significant relationship between H. pylori in Stool test and Calprotectin positivity.

Keywords: H.pylori M, H.pylori G, H.pylori A, H.pylori in Stool, Calprotectin

P118

Application of Nanotechnology in the Diagnosis of Infectious Diseases

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Background: Nanotechnology has emerged as a transformative tool in the diagnosis of infectious diseases. With the rise of antimicrobial resistance (AMR) and the limitations of traditional diagnostic methods such as bacterial culture and PCR, nanomaterials have become a promising alternative due to their unique physicochemical properties, high sensitivity, and rapid response. Methods: This narrative review article was developed using well-regarded scientific databases, including Web of Science, PubMed, Scopus, and Google Scholar, without any limitations on publication dates. A set of inclusion and exclusion criteria was established. Results: Metallic nanoparticles, such as gold (AuNPs) and silver nanoparticles (AgNPs), are widely utilized in colorimetric and fluorescent assays for the fast and accurate detection of pathogens. Carbon-based nanomaterials, such as graphene and carbon nanotubes, are used in electrochemical sensors due to their high conductivity. These materials generate powerful electrochemical signals, facilitating precise detection of bacteria and viruses. Quantum dots (QDs), known for their high optical stability and exceptional sensitivity, are considerably employed in fluorescence-based pathogen detection. Their intense and stable light emission permits the detection of pathogens even at very low concentrations. Advanced approaches like surface-enhanced Raman spectroscopy (SERS), which utilizes plasmonic nanomaterials, provide highly sensitive detection at the molecular level. SERS has been successfully used to identify viruses such as HIV and SARS-CoV-2. Also, point-of-care (POC) diagnostic technologies based on magnetic nanoparticles enable rapid and easy detection in resource-limited settings. These techniques integrated with artificial intelligence and CRISPR-Cas systems, further improve diagnostic accuracy and speed. Conclusion: Nevertheless, challenges such as toxicity, stability, and production costs of nanomaterials require further research. Optimizing these techniques and decreasing costs will facilitate widespread usage, specifically in low-resource regions. Nanotechnology holds notable potential for enhancing the early and accurate diagnosis of infectious diseases and can serve as a powerful tool in combating AMR and emerging infectious diseases.

Keywords: Nanotechnology, Nanomaterials, Diagnosis, Infectious diseases and Nanoparticles.

P119

Emerging Multidrug-Resistant Providencia Stuartii: A Critical Nosocomial Threat with Limited Therapeutic Options

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Emerging Multidrug-Resistant Providencia stuartii: A Critical Nosocomial Threat with Limited Therapeutic Options (Maryam Barkhordari1*, Mohammad Hossein Farajollah2, Azade Hajihassani3,Hamid Asadi4, Dorna Mostofi Zadeh5, Hooman Vosough6) 1-Microbiology Department, Laboratory Megalab Center, Farhikhtegan Hospital, Tehran, Iran, 2- Department of Microbiology, Islamic Azad University, Science and Research Branch, Tehran, Iran Background: Providencia stuartii is an intrinsically multidrug-resistant (MDR) pathogen with natural resistance to colistin, posing significant treatment challenges. It is an emerging nosocomial pathogen, particularly in intensive care units (ICUs), where immunocompromised patients are highly vulnerable. This study analyzed the antibiotic resistance patterns of P. stuartii isolates collected over one year from seven hospitals. Methods: From December 2023 to February 2025, P. stuartii isolates were obtained from various clinical specimens across seven hospitals and identified via MALDI-TOF. Antibiotic susceptibility was assessed using disk diffusion and MIC testing (VITEK-2), following CLSI guidelines. Results: Among 233 isolates, the most common sources were tracheal aspirates (66.1%), wound infections (10.3%), blood cultures (10.3%), cerebrospinal fluid (6.0%), and urine samples (3.4%). ICU patients accounted for 98.3% of cases. Resistance rates were alarming: • Amikacin: 10.1% • Cefepime, Ceftriaxone, Cefotaxime, Ceftazidime: 3.8% • Ciprofloxacin & Levofloxacin: 0% (Complete resistance) • Gentamicin: 60.2% • Trimethoprim-sulfamethoxazole (SXT): 30.9% • Piperacillin-tazobactam: 90.1% • Doripenem: 90.5% Conclusion: The high prevalence of P. stuartii in ICU patients, particularly those with pulmonary infections or prolonged hospitalization, underscores its threat in healthcare settings. Complete resistance to fluoroquinolones and cephalosporins is concerning, necessitating strict infection control measures and antimicrobial stewardship programs to curb its spread.

Keywords: Providencia Stuartii, Multidrug Resistance, Nosocomial Infections, ICU

P120

CRP, PCT, and CAR: A Review of Biomarkers in Sepsis

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Background: Sepsis, a leading cause of ICU admissions, demands accurate diagnostic and prognostic tools. This review synthesizes current research on C-reactive protein (CRP), procalcitonin (PCT), and the CRP to albumin ratio (CAR), examining their roles in sepsis diagnosis, severity assessment, and outcome prediction. We explore the clinical utility and limitations of these biomarkers in diverse patient populations. Methods: This review integrates findings from recent meta-analyses, clinical studies, and observational research published between 2018 and 2024. It examines the diagnostic accuracy and prognostic value of CRP, PCT, and CAR, considering factors influencing their levels and their performance in various clinical settings, including elderly patients and those with septic shock. Results: PCT demonstrates superior diagnostic accuracy for septic shock compared to CRP, particularly in later stages of illness. While both CRP and PCT are useful in infection diagnosis, their prognostic value for 30-day mortality is limited. The CAR emerges as a promising prognostic indicator, with elevated levels correlating with poor outcomes in sepsis. However, significant heterogeneity exists across studies, necessitating careful interpretation. CRP levels are influenced by various factors, including age, gender, and comorbidities, and the isoforms of CRP have differing biological impacts. Conclusion: PCT remains a reliable diagnostic tool for septic shock, while CAR shows promise as a prognostic marker. Further high-quality prospective studies are needed to validate the clinical utility of CAR and refine the use of PCT and CRP in sepsis management. Dynamic monitoring of these biomarkers and their integration with clinical parameters are crucial for improving patient outcomes.

Keywords: Sepsis, C-Reactive Protein, Procalcitonin, CAR Ratio, Biomarkers

P121

Procalcitonin's Evolving Role: From Sepsis Diagnosis to Antimicrobial Stewardship

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Background: Procalcitonin (PCT) has emerged as a crucial biomarker in sepsis management. This review synthesizes current research on PCT's diagnostic accuracy, its role in guiding antimicrobial therapy, and its association with specific pathogens. We explore the evolution of PCT's clinical utility, from initial diagnostic marker to a tool for optimizing antibiotic use. Methods: This review encompasses recent systematic reviews, meta-analyses, and clinical studies published between 2021 and 2024. We examine PCT's performance in diagnosing sepsis, its application in antimicrobial stewardship protocols, and the underlying mechanisms of PCT elevation in bacterial infections. Results: PCT exhibits moderate accuracy in sepsis diagnosis, particularly in distinguishing bacterial from viral infections. Studies support PCT-guided antibiotic discontinuation in critically ill adults, potentially reducing antibiotic overuse and resistance. Nanobiosensors are emerging as a promising tool for rapid PCT analysis. PCT levels correlate with bacterial load and infection severity, with Gram-negative bacteria generally inducing higher PCT levels than Gram-positive. However, PCT levels can be influenced by non-infectious conditions, necessitating careful clinical interpretation. Conclusion: PCT plays a multifaceted role in sepsis management, extending beyond simple diagnosis to guide antimicrobial therapy and potentially identify specific pathogens. While promising, further research is needed to refine PCT-guided protocols, explore its utility in diverse patient populations, and investigate its association with specific microorganisms.

Keywords: Procalcitonin, Sepsis, Antimicrobial Stewardship, Biomarkers, Bacterial Infections

Latest Advances in Arbovirus Laboratory Diagnosis

P122-P124

P122

Advancements in Dengue Diagnosis Using Artificial Intelligence and Machine Learning Models

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Background Dengue, a mosquito-borne viral infection, affects 100 to 400 million people annually, especially in tropical regions. Traditional diagnostics include qRT-PCR, ELISA, and dengue-specific IgM antibodies. Artificial intelligence (AI), particularly machine learning, can analyze data in real-time, improving outbreak detection and disease monitoring, particularly in resource-limited areas. This study explores the use of AI to enhance dengue detection, diagnosis, and prediction, aiming to improve accuracy, speed, and early intervention for better disease management. Methods For this systematic review, articles published between 2013 and 2025 were reviewed from databases, including Google Scholar, PubMed (MeSH terms: AI, machine learning, and dengue detection), Scopus, Embase, Cochrane Library, and Web of Science. Inclusion criteria focused on articles discussing AI advancements in dengue diagnostic methods, while papers on prevention and treatment strategies were excluded. Results The review identified 70 relevant articles out of 560. The results show that AI enhances dengue diagnostics by integrating with hematological, serological, and molecular tests, as well as prognosis and epidemiological features. YOLOv8s and YOLOv8l models achieved 99.3% accuracy in detecting dengue through peripheral blood microscopy, identifying thrombocytopenia and lymphocyte features. AI also aids in designing synthetic antigens, predicting RT-PCR results, detecting severe dengue-related genes, and optimizing PCR. These models predict dengue severity, recurrence, shock, and plasma leakage risks from thermal images. Additionally, AI is applied in outbreak prediction, mosquito image classification, and processing medical record data. Conclusion AI shows significant promise in enhancing dengue detection by reducing diagnostic time from hours to minutes, improving accuracy, and streamlining diagnostic processes.

Keywords: Artificial Intelligence, Dengue Detection, Machine Learning, Deep Learning

P123

Evaluation the Frequencies of HLA Alleles in Moderate and Severe COVID-19 Patients in Iran: A Molecular HLA Typing Study

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Background: Severe acute respiratory syndrome coronavirus 2 was first reported in December 2019 and it has spread globally ever since. The HLA system is crucial in directing anti-viral immunity and recent studies are investigating the possible involvement of the HLA genes on the severity of immune inflammation in different phases of COVID-19. Methods: In this cross-sectional study, peripheral blood-extracted genomic DNAs of 109 COVID-19 patients and 70 healthy controls were genotyped for different alleles of HLA-A, HLA-B, and HLADRB1 loci using sequence-specific primer PCR method. Results: The results indicated that frequencies of HLA-DRB1*11:01 and HLA-DRB1*04:03 were significantly higher in severe patients rather than moderates (p: <0.001 and 0.004, respectively). Also, it was observed that HLA-DRB1*04:01 was more frequent in moderate patients and healthy controls (p:0.002). In addition, HLA-B*07:35, and HLA-DRB1*07:01 showed higher frequencies in patients compared with controls (p: 0.031 and 0.003 respectively). Inversely, due to the higher frequencies of HLA-B*51:01 (p:0.027), HLA-DRB1*11:05 (p:0.003), HLA-DRB1*13:05 (p:0.022), and HLA-DRB1*14:01 (p:0.006) in healthy individuals rather than patients, they may be associated with COVID-19 resistance.

Keywords: HLA Alleles, DNA Genotyping, SARS-CoV-2, COVID-19

P124

Nosocomial Transmission of Crimean-Congo Hemorrhagic Fever in Iran: Risks and Prevention

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Background: Crimean-Congo hemorrhagic fever (CCHF) is a viral zoonotic disease with a significant risk of nosocomial transmission. Healthcare workers (HCWs) are highly vulnerable due to occupational exposure. In Iran, 871 human cases were reported between 1999 and 2011, with a high seroprevalence in livestock. This study aims to investigate the transmission routes, risk factors, and preventive measures for nosocomial CCHF infections among HCWs in Iran. Methods: We systematically reviewed studies published between 2000 and 2025 from PubMed, Web of Science, and Scopus. Inclusion criteria encompassed studies on CCHF infections among HCWs in Iran, confirmed via RT-PCR and IgM capture enzyme-linked immunosorbent assay (MAC-ELISA). Studies lacking transmission data or conducted outside healthcare settings were excluded. Results: Among 96 suspected HCW cases, 12 were confirmed, including seven nurses and five physicians. The median age was 32.5 years, with an incubation period of 1 to 22 days. None reported tick bites or direct animal blood exposure. The main transmission routes were percutaneous exposure (needle sticks, 3 cases), mucosal exposure (blood splash to the face, 3 cases), and skin contact with infected blood (3 cases). Cases were reported in Razavi Khorasan (7 cases), Sistan and Baluchistan (2 cases), Isfahan (1 case), South Khorasan (1 case), and Fars (1 case). No new cases have been reported in Iranian HCWs since 2013. Conclusion: Nosocomial CCHF transmission in Iran primarily affects nurses and physicians through percutaneous, mucosal, and skin exposures. Strengthening infection control measures, including enhanced protective equipment and timely prophylaxis with ribavirin, is essential to reduce transmission risks.

Keywords: Crimean-Congo Hemorrhagic Fever, Nosocomial Infection, Iran, Healthcare Workers, Infection Control

POCT: Innovations and Challenges

P125-P126

P125

Point-of- Care Viscoelastic Testing's Growing Use in Hematologic Disorders and Hemostasis Management

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Introduction: Point-of-care viscoelastic testing (VET) provides faster turnaround times and real-time evaluation of haemostatic performance, based on cell-based hypothesis, evaluating clot strength, dynamics, and breakdown. Viscoelastic Tracings (VETs) are crucial for liver transplantation, cardiac surgery, and trauma, but their clinical value in benign hematologic conditions has increased. Early diagnosis and treatment of these diseases primarily rely on VETs, enabling disease identification and patient-specific interventions. Methods: A comprehensive review of the literature was conducted to evaluate the clinical significance of VETs across several medical settings, including cardiac surgery, trauma, and benign hematologic disorders. The advantages of VETs, such as their capacity to diagnose coagulopathy, inform transfusion strategies, and improve patient outcomes, were emphasized. Results: ROTEM interpretation in cardiac surgery is consistent, but variations in expert assessments highlight the need for sophisticated clinical decision-making tools. VETs help in faster coagulopathy identification, fibrinolysis detection, and reduced blood product transfusions. They also inform patients with coagulopathies, anticoagulants, or antiplatelet drugs about rapid therapeutic decisions. Standardized treatment algorithms must be validated for consistent clinical implementation. Discussion: Viscoelastic point-of-care devices (VET) are being used in clinical settings to improve haemostasis management, offering real-time coagulation function assessment. However, challenges like interpretation variability, clinician training, and financial considerations persist. Departments must assess VET service viability individually. Conclusion: Especially in critical care environments, viscoelastic testing has great benefits for hemostasis assessment. The therapeutic relevance of VETs is evident, but further validation is needed for a methodical approach in regular critical care treatment to ensure optimal patient outcomes.

Keywords: Point-of-Care Testing, Viscoelastic Testing, Hemostasis, Intensive Care, Coagulopathy, Hematologic Disorders

P126

CRISPR-Cas System for the Diagnosis of Infectious Disease

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Background: CRISPR-Cas technology, inspired by the immune system of bacteria, has emerged as a powerful tool for the diagnosis of diseases. This system, with high precision and notable specificity in identifying DNA and RNA sequences, enables rapid and cost-effective detection of infectious and genetic diseases. These techniques are highly flexible and appropriate for detecting emerging pathogens and clinically significant genetic mutations. While PCR-based molecular diagnostics remain prevalent, CRISPR technologies are expected to become a possible alternative by decreasing genomic complexity and developing integrated chip-based devices. Methods: This narrative review article was developed using well-regarded scientific databases, including Web of Science, PubMed, Scopus, and Google Scholar, without any limitations on publication dates. Results: One of the most important advantages of CRISPR is its potential for point-of-care (POC) diagnostics, which decreases the need for complex laboratory infrastructure. Systems based on Cas12 and Cas13, in particular, have been used for diagnosing viral diseases such as SARS-CoV-2 and antibiotic-resistant bacterial infections due to their ability to detect DNA and RNA. Cas13, with its unique features, is an ideal choice for RNA molecular diagnostics, and biosensors based on it can be used to detect RNA in liquid biopsy samples. This technology also offers multiplexing capabilities, enabling the simultaneous detection of multiple pathogens. Conclusion: Despite challenges like further optimization and reducing off-target effects, CRISPR has emerged as a revolutionary technology in molecular diagnostics. Current advancements demonstrate that this technology is on track to achieve rapid and accurate clinical diagnostics in resource-limited settings. Future investigation will continue to improve the features and expand the applications of CRISPR in the diagnosis of infectious and genetic diseases, positioning it as a transformative force in medical diagnostics and a source of innovative solutions for global health challenges.

Keywords: CRISPR, Diagnosis, Infectious Diseases, Cas13 and Cas12

Proteomics and Metabolomics in Laboratory Diagnosis

P127-P133

P127

Urinary Metabolite Fingerprints and Fecal Acylcarnitine/Amino Acid Profiles of Irritable Bowel Syndrome Patients: Insights from GC-MS Untargeted and LC-MS/MS Targeted Metabolomics Approaches

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Background: Irritable bowel syndrome is a chronic functional gastrointestinal disorder characterized by a complex pathophysiology, making diagnosis and treatment challenging. Herein, we aimed to investigate its pathophysiology using GC-MS and LC-MS/MS-based metabolomics strategies. Methods: The study involved 30 IBS patients and 25 healthy individuals. Fasting blood, urine, and fecal samples were collected for analysis. Blood parameters were assessed, while urine underwent GC-MS analysis and feces were analyzed via LC-MS/MS after derivatization. Statistical comparisons were conducted using the MetaboAnalyst (V. 6.0). Results: Significant differences were found in urinary metabolites from IBS patients. Hydroxybenzoic acid, hydroxyphenylacetic acid, and threonic acid were significantly decreased in IBS patients, while the remaining metabolites, including erythritol, xylonic acid, D-ribose, xylitol, homovanilic acid, hippuric acid, D-mannose, sorbitol, and mannoic acid were significantly elevated in IBS patients. In addition, fecal AC analysis revealed that C3 and C5-OH/2-M-3-OH-butyryl carnitine were decreased in IBS patients in a non-significant manner, while C2 and C5 were not significantly increased. Fecal amino acid levels were also altered, non-significantly, with increases in Leu/Ile, Glu, Met, Tyr, and Phe, and decreases in Gly, Ala, and Val. These findings highlight the complexity of IBS and the need for further research. Conclusion: Elevated urinary polyols and monosaccharides may indicate FODMAP absorption, while decreased p-hydroxybenzoic and hydroxyphenylacetic acids suggest altered gut microbiota. Elevated homovanilic acid reflects gut-brain axis involvement. However, fecal acylcarnitine and amino acid changes were non-significant. Future research should utilize larger samples and multi-omics approaches to better understand IBS.

Keywords: Irritable Bowel Syndrome, Metabolomics, Gas Chromatography-Mass Spectrometry, Tandem Mass Spectrometry

P128

Integrating Metabolomics, Proteomics, and Genomics in Unraveling Mitochondrial Disease Pathophysiology

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Mitochondrial diseases are a diverse group of disorders resulting from dysfunctions in the mitochondrial respiratory chain, leading to impaired energy production. Understanding the complex pathophysiology of these diseases has been challenging due to their clinical heterogeneity and the intricate interplay of genetic and environmental factors. Recent advancements in omics technologies—specifically metabolomics, proteomics, and genomics—have provided comprehensive insights into the molecular underpinnings of mitochondrial disorders [1,2]. Metabolomics, the large-scale study of small molecules (metabolites) within cells, tissues, or organisms, has been instrumental in identifying metabolic alterations associated with mitochondrial dysfunction. For instance, studies have revealed disruptions in amino acid metabolism, fatty acid oxidation, and the tricarboxylic acid cycle in patients with mitochondrial diseases [3]. These metabolic signatures not only enhance our understanding of disease mechanisms but also aid in the identification of potential biomarkers for diagnosis and therapeutic monitoring [1]. Proteomics, the comprehensive analysis of the entire protein complement of a cell or organism, complements metabolomic data by elucidating changes in protein expression, post-translational modifications, and protein-protein interactions. Integrated proteomic and metabolomic analyses have uncovered biomarkers related to NADH-reductive stress in conditions like mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes (MELAS), providing insights into disease severity and progression [2]. References: Gucek M, Sack MN. Proteomic and metabolomic advances uncover biomarkers of mitochondrial disease pathophysiology and severity. J Clin Invest. 2021;131(2): e145158. Li H, Uittenbogaard M, Navarro R, et al. Integrated proteomic and metabolomic analyses of the mitochondrial neurodegenerative disease MELAS. Mol Omics. 2022;18(3):196-205. Zhang X, Li X, Fang Z, et al. Metabolomics of mitochondrial disease. Clin Chim Acta. 2016;456:41-46. Stenton SL, Prokisch H. Genetics of mitochondrial diseases: Identifying mutations to help diagnosis. EBioMedicine. 2020;56:102784.

Keywords: Mitochondrial Diseases, Metabolomics, Proteomics, Genomics, Biomarkers, Pathophysiology

P129

Revealing Dysregulated Hub Genes and Their Associated MiRNAs in Bone Marrow-Derived Mesenchymal Stromal Cells of Pediatric AML: Key Targets for Restoring the Bone Marrow Microenvironment

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Background: Recent findings underscore the critical role of mesenchymal stroma cells (MSCs) as essential elements of the bone marrow (BM) hematopoietic niches in the onset and progression of acute myeloid leukemia (AML). In this context, we aimed to identify the key genes involved in the dysfunction of MSCs derived from the BM of pediatric patients suffering from AML by bioinformatic analysis. Methods: Gene expression profiles of two microarray data sets (including normal and AML samples) were obtained from the Gene Expression Omnibus (GEO) database. Gene ontology and pathway enrichment analyses were conducted and a protein-protein interaction network for the differentially expressed genes (DEGs) was created with the aid of Cytoscape software. Hub genes were discerned via the CytoHubba plugin. Besides, through bioinformatics tools miRNAs that interact with hub genes were predicted. Results: A total of 461 DEGs were identified. The top five enriched pathways were extracellular matrix organization, signal transduction, integrin cell surface interactions, collagen formation, and assembly of collagen fibrils and other multimeric structures. By combing the results of CytoHubba, a total of 10 hub genes were selected. PTPRC, TLR4, CD86, CTSS, CCR1, TYROBP, FCGR2A, CCL2, CD163, and CCL5 were hub nodes in PPI networks. Conclusion: The present investigation, based on the in silico analysis and microarray GEO databases, may provide a novel understanding of the mechanisms related to AML pathogenesis. These DEGs, associated miRNAs, and the associated pathways may represent prospective therapeutic targets that regulate the activity of MSCs for rehabilitating the BM setting in AML.

Keywords: Acute Myeloid Leukemia, Bioinformatics Analysis, Enrichment Analysis, MiRNA, Network

P130

Time-Course Effect of High Glucose Concentrations on SHP2 Gene Expression in Muscle Cell Culture Model

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Background: According to WHO, diabetes is one of the chronic metabolic diseases that will become the seventh leading cause of death in the future. Type 2 diabetes (T2D) is characterized by hyperglycemia. Some previous studies reported increased expression of protein tyrosine phosphatases (PTPs) in diabetes or insulin resistance states. PTPs dephosphorylate target proteins leading to inactivation or changes in activity. SHP2, a non-receptor PTP encoded by PTPN11, modulates insulin signaling and interacts with glucose metabolism. Considering the key role of SHP2, we aimed to investigate the time-course effect of high glucose concentration on the gene expression level. Methods The culture media containing normal (1 g/L) (control), high (2.75 g/L), and very high (4.5 g/L) glucose concentrations were prepared. A murine muscle cell line, C2C12, was subjected to 8- and 16-hour treatments. After performing RNA extraction and RT, SHP2 gene expression level was investigated by Real-time PCR. Results The results showed that 8-hour treatment with high and very high concentrations of glucose did not cause significant changes in gene expression level, compared to the control. However, 16-hour treatment with high and very high concentrations caused 25% and 16% increment in SHP2 gene expression level, respectively. Conclusion The different outcomes between 8- and 16-hour treatments could be attributed to possible changes in SHP2 activity or probable activation of oxidative stress defense mechanisms during 8-houre treatment, aimed at acquiring rapid adaptation. However, in 16-houre treatment, increased SHP2 expression level seems to be the contributing factor hindering insulin signaling, leading to insulin resistance.

Keywords: Hyperglycemia, Insulin Resistance, Protein Tyrosine Phosphatase, Type 2 Diabetes, SHP2 Gene

P131

Copper-Induced Cell Death (Cuproptosis) in Hematologic Malignancies

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Bakground: Hematologic malignancies including leukemia, lymphoma, and multiple myeloma remain challenging due to their complex molecular mechanisms and therapeutic resistance. A novel form of regulated cell death, cuproptosis, which is copper-induced, has garnered attention for its potential in cancer therapy. Unlike apoptosis, cuproptosis is triggered by mitochondrial dysfunction due to copper accumulation, affecting mitochondrial proteins, specifically those involved in the citric acid cycle. Methods:In this narrative review, we searched multiple databases, including PubMed, Scopus, and Google Scholar, for literature up until February 2025 on cuproptosis in hematologic malignancies. We focused on studies discussing the role of cuproptosis-related genes (CRGs), such as FDX1, LIAS, LIPT1, DLAT, ATP7B, and SLC31A1 in the regulation of mitochondrial function and copper homeostasis. Studies investigating the potential use of copper-modulating therapies and copper ionophores to trigger cuproptosis in cancer cells were also reviewed. Results:The key cuproptosis-related genes (CRGs), including FDX1, LIAS, LIPT1, DLAT, ATP7B, and SLC31A1, play vital roles in maintaining mitochondrial function and regulating intracellular copper levels. Dysregulation of these genes impairs copper homeostasis, leading to an increased susceptibility of hematologic cancer cells to cuproptosis. Recent studies suggest that copper ionophores, which increase intracellular copper concentrations, can selectively induce cuproptosis in malignant cells while sparing normal tissue. However, challenges such as tumor heterogeneity, copper transport mechanisms, and resistance pathways continue to limit the clinical application of copper-based therapies. Conclusion: The findings from this review highlight the promising therapeutic potential of targeting cuproptosis in hematologic malignancies. By manipulating copper metabolism and CRGs, it may be possible to selectively eliminate malignant cells. Further research is required to overcome challenges such as tumor diversity and resistance mechanisms, which are pivotal for the successful clinical application of copper-based treatments.

Keywords: CRISPR-Cas9, Rheumatic Autoimmune Disorders (RADs), Gene Editing, Off-Target Effects, Personalized Therapy

P132

Key Metabolites Associated with Pemphigus Vulgaris: A Bioinformatics Analysis

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Background: Pemphigus Vulgaris (PV) is a chronic autoimmune blistering disease marked by oral mucosa lesions caused by autoantibodies against desmoglein (Dsg) 1 and 3. Metabolites like short-chain fatty acids (SCFA) and free fatty acids (FFA) may influence colonic Treg cells and Th1/Th17 differentiation, but the metabolites involved in PV are not well understood. This study aims to identify key metabolites and proteins in PV and explore their pathways using bioinformatics to clarify their relationship with this disease. Methods: Proteins and compounds were extracted from online databases. Metabolic Atlas and PubChem were used to identify metabolites, they were ranked based on the numbers of first neighbours and shared genes/metabolites. Hub and bottleneck proteins were identified, and the DAVID functional annotation tool was used to determine their KEGG pathways. Results: MgADP had the highest number of first neighbours in the network. Ins (1,3,4,5) P4, Hexanoic acid, and PtdIns (3,4,5) P3 shared the most genes/metabolites with MgADP. Six hub genes were identified: Interferon-gamma (IFNG), Cluster of differentiation 4 (CD4), Signal transducer and activator of transcription 3 (STAT3), Interleukin 2 (IL2), Interleukin-1 beta (IL-1B), and Janus kinase 2 (JAK2), which showed significant connections with metabolites. These six hub genes are also critical in the Th17 cell differentiation pathway. Conclusion: MgADP, Ins (1,3,4,5) P4, Hexanoic acid, and PtdIns (3,4,5) P3 are significant metabolites associated with PV and have essential roles in inflammation pathways and the immune system. These compounds modify in autoimmune diseases such as PV. Examination of metabolite modifications facilitates access to novel clinical approaches for PV disease.

Keywords: Pemphigus Vulgaris, Metabolites, Proteins, Inflammation

P133

Evaluation of Amino Acid and Acylcarnitine Profile Alterations in Lung Cancer Cells Under Ketogenic Conditions

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Background: Lung cancer is one of the most common and lethal cancers, with metabolic alterations playing a crucial role in its progression. The metabolism of amino acids and acylcarnitines can provide valuable information about the biological mechanisms of the disease. Beta-hydroxybutyrate (BHB) and glucose (Glc) restriction influence metabolism, but their specific effects on lung cancer's metabolic profile are yet to be known. Methods: In this study, A549 lung cancer cells (a type of non-small cell lung cancer) were exposed to BHB under both normal and restricted glucose conditions. Electrospray ionization tandem mass spectrometry (ESI-MS/MS) was used to examine the amino acid and acylcarnitine profiles of different groups. Also, chemometric analysis was performed to identify differential metabolites and important metabolism pathways in cell groups (BHB-enriched, Glc-restricted, BHB-enriched and Glc-restricted, and control). Results: Principal component analysis (PCA) revealed metabolic distinction in the treated cells compared to the control groups. Orthogonal partial least squares discriminant analysis (OPLS-DA) confirmed the metabolic difference between groups, by regression modeling with high R^2 and Q^2 values. By focusing on metabolites with high VIP scores (>1) and significant T-test results (p-value < 0.05), key metabolic markers were identified, and pathways involved in this metabolic rearrangement were recognized during enrichment analysis. For instance, In the BHB-enriched group, changes in arginine, tryptophan, citrulline, methionine, ornithine, and alanine levels pointed to disruptions in pathways such as the urea cycle, glycine and serine metabolism, and arginine and proline metabolism. Conclusion: Our data reveal the impact of BHB and glucose restriction on lung cancer metabolism. By identifying key metabolic markers and pathways, this study provides new insights to improve both diagnostic strategies and potential therapeutic approaches for lung cancer.

Keywords: Amino Acids, Acylcarnitines, Metabolomics, Beta-Hydroxybutyrate, A459 Cells

Technological Advances in Today's Hematology Laboratories

P134-P152

P134

"Platelet-Derived Microparticles: Pioneering Natural Vehicles for Targeted Drug Delivery – A Systematic Review"

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Background: Platelet-derived microparticles (PMPs) are nanoscale vesicles released during platelet activation or apoptosis, gaining recognition for their unique role in targeted drug delivery. Their natural biocompatibility, immune evasion properties, and ability to selectively interact with cells make them promising vehicles for therapeutic agents. However, their clinical application requires a systematic understanding of existing research to evaluate their potential and address challenges. Objectives: This systematic review aims to synthesize current evidence on the applications of PMPs in targeted drug delivery, focusing on their mechanisms, therapeutic efficacy, and advancements in engineering for enhanced performance. Methods: A comprehensive literature search was conducted across databases, including PubMed, Scopus, and Web of Science, covering studies published between 2015 and 2025. Eligible studies were analyzed to assess PMP properties, drug-loading strategies, targeting capabilities, and clinical implications. Data on isolation techniques, characterization, and safety profiles were also included. Results: PMPs demonstrate exceptional potential in delivering small molecules, proteins, and nucleic acids to specific disease sites, particularly in oncology, cardiovascular diseases, and inflammatory disorders. Advances in bioengineering have improved their stability, targeting precision, and drug-loading efficiency. However, challenges such as heterogeneity, large-scale production, and standardization of protocols remain significant barriers to clinical translation. Conclusions: PMPs are versatile and effective vehicles for targeted drug delivery, offering innovative approaches to precision medicine. Continued research on optimizing their properties and addressing current limitations will accelerate their integration into therapeutic applications. This review highlights critical findings and provides insights into future directions for advancing PMP-based drug delivery systems.

Keywords: Platelet-Derived Microparticles, Targeted Drug Delivery

P135

Comparative Efficacy of MRD Detection Techniques in AML: A Comprehensive Review

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Background: Acute myeloid leukemia (AML) is the most prevalent acute leukemia in adults, primarily resulting from somatically acquired mutations linked to aging. Treatment options vary, with hematopoietic stem cell transplantation being the sole curative approach, while multiagent induction chemotherapy is frequently used to achieve remission. Monitoring minimal residual disease (MRD) is essential for evaluating treatment efficacy and predicting relapse. This review examines various MRD detection methods and compares their sensitivities. Materials & Methods: A literature review was conducted on studies related to Parthenolide and AML published from 2019 to 2024, utilizing MEDLINE and SCOPUS databases. Results: Multiparameter flow cytometry (MFC) has become a primary method for MRD detection due to its accessibility, rapid turnaround (1-2 days), and sensitivity of 10^{-3} to 10^{-4}. The European Leukemia Net (ELN) endorses a standardized fluorochrome panel, including CD34, CD117, and HLA-DR, for identifying residual leukemic cells. Advanced strategies like Leukemia-Associated Immunophenotypes (LAIPs) and the Different-from-Normal (DfN) approach enhance MRD tracking. Molecular monitoring advancements, including real-time quantitative PCR (RT-qPCR) and next-generation sequencing (NGS), have significantly improved AML management by enabling the detection of specific mutations and clonal evolution. Digital droplet PCR (ddPCR) further enhances sensitivity in post-transplant settings. Conclusion: The integration of MFC with advanced molecular techniques is transforming MRD monitoring in AML, allowing for improved risk stratification, targeted therapies, and better patient outcomes through personalized treatment approaches.

Keywords: AML, MRD, MFC

P136

Engineering Opuntia Ficus-Indica-Derived Exosome Mimetics for Targeted BCR-ABL siRNA Delivery in K562 Cells: An Integrated in Vitro and in Silico Study

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Background: The research investigates a new approach for producing biomimetic nanoparticles from Opuntia ficus-indica (OFI) cladode components for targeted delivery of therapeutic siRNA in chronic myeloid leukemia (CML) treatment. The nanoparticles are intended to interact with K562 cells, overcoming the limitations of exosome-based delivery methods. Methods: OFI-derived exosome mimics (OFI-EMs) were created using successive extraction and membrane extrusion procedures. Electroporation was used to load the particles with siRNA targeting BCR-ABL. NTA, cryo-EM, proteomics, and lipidomics were all used for comprehensive characterization. In vitro research examined cellular absorption processes, therapeutic effectiveness, and cytotoxicity in K562 cells. The interactions of OFI-EM membrane proteins with K562 cell surface receptors were investigated using molecular docking modeling. Results: The synthetic OFI-EMs had a homogeneous size distribution and membrane composition identical to natural exosomes, with a siRNA loading efficiency of about 85%. Proteomics investigation identified 128 membrane proteins, and molecular docking revealed high binding affinities to K562 cell surface receptors. In vitro experiments demonstrated effective cellular absorption via clathrin-dependent endocytosis, with 78% internalization within 4 hours. Treatment caused considerable BCR-ABL downregulation and increased apoptosis. Real-time cellular investigation revealed time-dependent cytotoxicity, with an IC50 of 45 µg/mL after 48 hours. Conclusion: The study indicates that OFI-derived exosome mimetics are a viable platform for targeted nucleic acid delivery in K562 cells, laying the groundwork for the development of plant-derived biomimetic nanocarriers for CML treatment.

Keywords: Opuntia Ficus-Indica, Exosome mimetics, K562 Cells, siRNA Delivery, BCR-ABL Targeting

P137

Design and Evaluation of a Multiplex Real-Time PCR Assay for Simultaneous Detection and Differentiation of COVID-19 and Influenza A/B

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Background: Respiratory viral infections represent a major public health problem due to their ease of spread within communities, high potential to trigger a pandemic, and significant morbidity and mortality. The diagnosis of respiratory virus infections necessitates laboratory verification, as the clinical symptoms are insufficiently specific for recognition. Influenza A, Influenza B, and COVID-19 are examples of prevalent infections that result in an unprecedented burden of respiratory diseases among the population during winter. The purpose of this study is to design and develop a multiplex real-time PCR technique that can identify influenza A, influenza B, and COVID-19. Methods: Primers and TaqMan probes were designed for the M2 gene of the Influenza A virus, NS1 gene of the Influenza B, and the N gene of SARS-COV-2. The values of reaction components were optimized, and functional parameters were measured using standard samples with known copy numbers of the virus. Results: This method has a limit of detection of 10 genomic copy numbers for Influenza A, 10 copies for Influenza B, and 60 copies for SARS-CoV-2. For Influenza A, this test has a sensitivity of 88% and specificity of 100%; for Influenza B, it is 95.6% sensitive and 100% specific; and for SARS-CoV-2, it is 90.4% sensitive and 100% specific. Conclusion: The results of investigating the functional parameters of the developed method, including sensitivity, specificity, and precision, show that this diagnostic method can simultaneously identify and distinguish SARS-CoV-2, Influenza A, and Influenza B infections.

Keywords: COVID-19, SARS-CoV-2, Influenza A, Influenza B, Multiplex Real-Time PCR

P138

Evaluation of a Robust in- House Multiplex Real-Time PCR-Based Method for Simultaneous Detection of HSV, VZV, and EBV in Plasma Samples of Transplant Patients

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Background: Herpes Simplex Virus (HSV), Varicella-Zoster Virus (VZV), and Epstein - Barr virus (EBV) are significant risks to transplant patients due to immunosuppression, leading to severe complications. Accurate and timely detection is crucial. This study evaluates the performance of an In-house Multiplex Real-time PCR assay for simultaneous detection of HSV, VZV, and EBV, compared with the commercial Altona Diagnostics RealStar® PCR Kit. Methods: A total of 270 plasma samples from transplant patients were tested using the In-house assay. Specificity was confirmed by in-silico BLAST analysis and in-vitro cross-reactivity tests. The Limit of Detection (LOD) was determined using serial viral DNA dilutions. Reproducibility was assessed through repeatability testing. Bland-Altman and regression analyses were performed to compare results with the Altona Diagnostics RealStar® PCR Kit. Results: The In-house assay showed 100% sensitivity for HSV, VZV, and EBV, with specificities of 100% for HSV, 97% for VZV, and 95% for EBV. The LOD was 6.25 copies/mL for HSV and 25 copies/mL for both VZV and EBV, outperforming the Altona kit (50 copies/mL). Coefficients of variation (CVs) were 1.5%, 2.3%, and 3.7%, indicating high precision. Bland-Altman analysis revealed mean differences of 1.35, -3.29, and 1.75 for HSV, VZV, and EBV, respectively. Regression analyses demonstrated strong correlations (R^2 = 0.82 for HSV, 0.93 for VZV, and 0.94 for EBV). Conclusion: The In-house Multiplex Real-time PCR assay is a highly sensitive, specific, and reproducible diagnostic method for simultaneous detection of HSV, VZV, and EBV. Its superior detection limits and cost-effectiveness position it as a promising alternative to commercial kits for transplant patient management.

Keywords: Multiplex Real-Time PCR, HSV, VZV, EBV, Transplant Patients

P139

Lymphocytes Distribution Width: A Potential Monitoring Parameter in Chronic Lymphoproliferative Disorders

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Introduction: Chronic lymphoproliferative disorders (CLPD) are characterized by the clonal proliferation of lymphocytes, often leading to abnormal lymphocyte distribution and function. Accurate, reliable, and cost-effective monitoring of disease progression or even prognosis and therapeutic response is crucial for effective management. This study explores the potential of lymphocyte distribution width (LDW) as a novel parameter for monitoring CLPD. LDW showed promise in early detection of relapse and differentiation between indolent and aggressive forms of CLPD. Our previous studies during the COVID pandemia in evaluating the feasibility of this parameter had shown significant information, hereby we evaluated the parameter in CLL patients to get a possible relationship between LDW, lymphocyte count, and or disease classification or progression indexes. Methods: Clinical, laboratory, and demographic data of 125 known CLL patients have been collected from Tabriz University of Medical Sciences related laboratories data collected during 2024, and, routine hematologic data had been collected by Technicon-H1 and ADVIA 2021 systems, for calculating the LDW parameter calculated from lymphocytes forward scatter (FSC) parameter using BD-FACScalibure system. data analysis performed by IBM-SPP Ver. 27 and p-Value<0.05 are regarded as statistically significant. Results: 83 males and 42 females participated in the study, mean age of was participants 61.37±12.8 years ranging from 29 to 88. From hematological parameters, the lymphocyte count mean was 24.42±24.18x103/ul, selectively. Mean LDW in participants was 17.07±6.95 this parameter's mean in males was 16.86±6.19 and 17.47±8.32 in females (p-Value=0.678). Conclusion: Based on the study information, regarding LDW along with other routine parameters, for monitoring the disease progression can be useful, but current data don’t show the prognostic evaluation values due to less data of clinical staging based on Binet or Rai systems.

Keywords: Lymphocyte Destribution Width, Chronic Lymphocytic Leukemia, Disease Monitoring, Binet, Rai

P140

Systemic Lupus Erythematosus (SLE), Platelet, Thrombosis, Immune Cells

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Systemic lupus erythematosus (SLE) is a systemic autoimmune disease with a wide range of clinical manifestations, from mild skin issues to severe impacts on organs and the nervous system. Thrombosis is an important complication of SLE and is often the primary cause of patient mortality. The exact pathological mechanism behind this is still unclear. Platelets, in addition to their role in homeostasis, have emerged as a key element in SLE pathogenesis. In this review, we focus on platelet-based pathways in the pathogenesis of SLE and present an update on this mechanism. Our study explores the multifaceted role of platelets in SLE, highlighting their involvement in thrombosis and immune responses. Platelets interact with immune complexes, complement factors, and infectious agents, such as viruses, leading to their activation and the release of mediators and microparticles. These activated platelets contribute to the circulatory autoantigenic burden and the development of thrombosis and further autoimmune response in SLE. Understanding the non-hemostatic functions of platelets in SLE provides new insights into disease mechanisms and could be a crucial advancement in the development of therapeutic approaches for targeting platelets.

Keywords: Systemic Lupus Erythematosus (SLE), Platelet, Thrombosis, Immune Cells

P141

Investigation of the Effects of Genetic Variations in CYP2C9 and VKORC1 on Warfarin Dose Requirements Among Iranian Patients from Khorramabad Province

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Objective: Warfarin is a widely prescribed narrow therapeutic index anticoagulant. Determining proper warfarin dosage remains problematic due to its narrow therapeutic index and genetic variations from individual to individual. The administration of incorrect doses of warfarin can catastrophic adverse events. Observational studies have demonstrated single nucleotide polymorphisms in CYP2C9 and VK0RC1 significantly affect warfarin dose requirements. The present study aimed to examine the influences of various genotypes on warfarin dose requirements among Iranian patients. Methods: Blood samples were taken from 117 patients and stored in tubes containing EDTA. DNA extraction was performed on the blood samples and the different alleles and genotypes of the studied SNPs were identified and recorded by the PCR-RFLP technique. Results: Of the 117 patients, no significant differences in the mean daily warfarin dose requirement were found among the genotypes of polymorphism CYP2C9 * 3 (1075A> C). However, there were significant differences among the genotypes of CYP2C9 * 2 (430C> T). The mean daily warfarin dose requirements were significantly different among wild genotypes, heterozygotes and mutants in the two polymorphisms of VKORC1 (1173C> T) and VKORC1(1639G> A). Conclusion: The results of our study demonstrated that CYP2C9 and VKORC1 polymorphisms have significant effect on warfarin maintenance dose requirements in iranian patients which would help improve the prediction of warfarin dose requirements and minimize the chance of over-anticoagulation or under anticoagulation.

Keywords: IRAN, WARFARIN, DRUG Dosage, GENETIC Variation, SINGLE Nucleotide Polymorphisms

P142

Evaluation of Hemato-Inflammatory Parameters NLR, PLR and HPR in Patients with Immune Thrombocytopenic Purpura (ITP) In South-East Iran: A Retrospective Study

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Background: Immune thrombocytopenic purpura (ITP) is a hematological disorder that affects a wide range of individuals, presenting with symptoms such as bleeding, thrombosis, and fatigue. The evaluation of inflammatory biomarkers, such as the ratio of neutrophil to lymphocyte (NLR), platelet to lymphocyte (PLR), and hemoglobin to platelet (HPR), plays a significant role in the diagnosis and follow-up of individuals suffering from this disease. Therefore, the objective of this study is to evaluate the diagnostic value of these inflammatory parameters in ITP patients. Methods: This retrospective cross-sectional study comprised an examination of 114 patients with ITP and 115 healthy individuals without symptoms related to ITP. The data of the patients and the healthy group, including the number of blood cells, hematocrit, hemoglobin, and the indices of NLR, PLR and HPR, were calculated before and after the treatment. Finally, the data was analyzed using SPSS version 22 software and an ROC curve to evaluate the sensitivity and specificity of the considered variables. Results: Blood parameters in ITP patients and the control group are significantly different. In ITP patients, the HPR is higher than in the control group. The results also showed that HPR and NLR were significantly higher in patients with bleeding (P-Value <0.001). While in patients with petechiae, NLRa and PLRa were significantly lower (P-Value = 0.016). No relationship was observed between treatment strategy and hospitalization length (P-value <0.05). ROC curve results for identifying ITP patients showed that NLR, PLR, and HPR have appropriate sensitivity (91.59%, 99.13%, and 92.66) and specificity (99.13%, 52.13%, and 96.52% respectively). Conclusion: The results of the ROC curve analysis demonstrate that NLR, PLR, and HPR have high sensitivity and specificity in the identification of ITP patients. Therefore, these inflammatory parameters, together with clinical symptoms, can be effective in the diagnosis and treatment management of ITP patients.

Keywords: Immune Thrombocytopenic Purpura, Lymphocyte, Neutrophil, Platelet, Neutrophil Lymphocyte Ratio, Platelet Lymphocyte Ratio

P143

Effect of Oleuropein on the Expression of miR-92b-3p, miR-124-3p and miR-424-5p in Human Myeloid Leukemia KG-1 and HL-60 Cells that Treated with 5-Azacitidine

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Background: Acute myeloid leukemia (AML) is the most common acute leukemia in adults. Conventional treatments are associated with cytotoxicity and systemic side effects. Hence, efforts in the field of cancer treatment are focused on finding the strategies which can specifically target the tumor cells without affecting the normal cells. The use of microRNAs in the treatment of cancers is the target therapy. And in order to increase the expression of mirs, hypomethylating agents can be used so that by increasing the expression of mirs, their inhibitory effects can be used. Methods and Materials: In this descriptive study, the IC50 dose for AZA and Oleu in the KG-1 and HL-60 cell lines was first determined by 3-(4,5-dimethyl-2-thiazolyl) -2,5-diphenyl-2-H-tetrazolium bromide assay. Then, the cells were treated with IC50 dose of AZA and Oleu and apoptosis was assessed. Also, the expression of microRNAs in cell lines was measured at 24, 48, and 72h after treatment with drugs. Results: The results show that treatment with Aza and Oleu increases apoptosis, and treatment of cells with these agents increases the expression of the studied microRNAs. Conclusion: By increasing the expression of mirs, their inhibitory effects can be used, and one of the ways to increase the expression of mirs is to use hypomethylating agents.

Keywords: Acute Myeloid Leukemia (AML), MicroRNAs, Hypomethylating Agents, Azacitidine (Aza), Oleuropein (Oleu)

P144

Prevalence of Alloantibodies in Blood Transfusion-Dependent Thalassemia Patients and its Relationship with Age, Gender and Blood Group in Birjand

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Background: The most prevalent type of thalassemia in Iran is beta-thalassemia, which is a genetic disorder. Because thalassemia patients are at high risk for alloantibody production and the phenomenon of alloimmunization as a result of receiving numerous blood transfusions, the purpose of this study was to examine the prevalence of alloantibodies in thalassemia patients in Birjand city and its correlation with age, gender, and blood type. Methods: This cross-sectional study was carried out in 2024 on patients with thalassemia who needed blood transfusions and were referred to Iranmehr Hospital in Birjand. Serological techniques were used to determine the alloantibodies in blood samples. Results: This study included 53 patients, 27 of whom were male (50.9%); the subjects' mean age was 16.75±10.41 (range 1 to 36 years);the prevalence of positive alloantibodies was 7.5% in all subjects, 7.4% in males, and 7.7% in females (p=0.182); the mean age of positive and negative antibodies was 22.50±4.36 and 16.29±10.65, respectively (p=0.002), suggesting a significant difference in this regard; the prevalence of positive alloantibodies was 75% in Rh positive patients and 25% in Rh negative patients (p=0.391); the prevalence of positive alloantibodies was 50% in blood group B, 25% in blood group AB, and 25% in blood group O (p=0.35). Conclusion: The findings indicated that individuals with thalassemia are susceptible to alloantibody positivity, and that age was significantly linked to the prevalence of alloantibody positivity, in contrast to blood group and gender. Because of the risky consequences of these antibodies, patients with thalassemia should be regularly checked for alloantibodies.

Keywords: Alloantibody, Thalassemia, Age, Gender, Blood Group

P145

Evaluating the Correlation between Beta Thalassemia Patients' Phenotype- and Laboratory Results

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Background: The beta-thalassemia has been introduced as a prevalent quantitative β-globin chain deficiency that results from a striking heterogeneity of molecular defects. Clinical symptoms of thalassemia patients vary from mild to severe, known by the two phenotypes of intermedia and major beta-thalassemia. The purpose of this study was to look at the genetic history of beta-thalassemia patients and the connection between phenotype and laboratory biomarkers and genotype. Methods: This study involved 147 people with beta-thalassemia. The DNA sequencing technique was used to determine genotyping. Biochemical analysis for ferritin and FBS were performed for each patient. Statistical analysis was carried out using spss v 16. Results: Data analysis showed that IVS II–I and homozygous IVS II–I were the most prevalent mutations and genotypes in our patients. In addition,33.6% and 36.6% of patients were homozygous and heterozygous positive for Xmn1 polymorphism. Positive XmnI polymorphism was detected in both thalassemia major and intermedia and the frequency had a statistically significant difference. The genotype and type of thalassemia, age at diagnosis, age at splenectomy, and age at transfusion initiation were all significantly correlated. Conversely, no discernible variations were seen between genotype and serum ferritin and FBS. Ferritin levels were significantly correlated with each of the previously listed parameters. Conclusion: Laboratory results and genotype analysis revealed that ferritin level is a more accurate measure for assessing the phenotypic and managing disease consequences than genotype analysis.

Keywords: Thalassemia, Genotype, Phenotype, Ferritin, Laboratory Biomarkers

P146

Immature Platelet Fraction: The Key to Rapid and Accurate Differential Diagnosis of Thrombocytopenia

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Background: Thrombocytopenia is a clinical condition characterized by a decreased platelet count, primarily caused by reduced platelet production in the bone marrow (BM) or increased peripheral destruction of platelets. Accurate differential diagnosis of thrombocytopenia can lead to appropriate management of these cases and suitable therapeutic approaches for thrombocytopenic patients. Reticulated platelets (RPs) are immature platelets recently released from the BM into the peripheral blood. In most modern hematology autoanalyzers, RPs are referred to as the immature platelet fraction (IPF), which reflects their quantity. The use of IPF is clinically significant in the differential diagnosis of thrombocytopenia caused by increased peripheral platelet destruction in autoimmune disorders such as ITP or decreased platelet production in the BM. This study aims to investigate IPF in all clinical conditions associated with thrombocytopenia and to explore its role in the differential diagnosis of thrombocytopenia with various underlying causes. Methods: We conducted a literature review using specific keywords and searched the PubMed and Google Scholar databases for relevant scientific literature published within the last 10 years. Results: Studies conducted on clinical conditions associated with thrombocytopenia have shown an increased percentage of IPF in thrombocytopenia cases due to platelet destruction or consumption, such as in ITP, TTP, and DIC. Conversely, normal or decreased levels of IPF suggest reduced platelet production, as seen in conditions like BM suppression. Accordingly, an increased IPF level in patients with BM failure who have undergone BM transplantation can be a useful marker for estimating platelet recovery. Conclusion: The measurement of IPF is a valuable, cost-effective, and rapid tool for the initial assessment of thrombocytopenia and for distinguishing between its potential underlying causes. Its utilization can significantly reduce the need for invasive procedures such as BM examination. Therefore, IPF can be widely adopted as a standard parameter in the evaluation of thrombocytopenic patients.

Keywords: Immature Platelet Fraction, Reticulated Platelet, Thrombocytopenia

P147

Differentiation of Human Induced Pluripotent Stem Cells to Megakaryocyte Lineage by Using 3D Bioreactor, Microfluidic System and Acellular Rat Lung

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Background: Induced pluripotent stem cells (hiPSCs) are reprogrammed cells that can develop into all human cell types, including megakaryocytes. Extracellular matrix plays a crucial role in the differentiation of hiPSCs into megakaryocytes. Therefore, we aimed to prepare a suitable natural acellular scaffold, and 3D bioreactor for in-vitro proliferation, and differentiation of hiPSCs into megakaryocytes. Methods: The rat lung was extracted, and the decellularization process was performed to eradicate cellular and nuclear materials, and lung's three-dimensional (3D) structure with the protein contents remained intact. Scanning electron microscopy (SEM), hematoxylin and eosin (H&E), and 4′, 6-diamidino-2-phenylindole (DAPI) staining were used to verify tissue decellularization and to ensure the integrity of the tissue structure. The 3D polydimethylsiloxane (PDMS) based bioreactor was designed, and the recellularization of the acellular lung was performed by hiPSCs. Decellularized rat lung vessels were used to deliver culture media as a microfluidic system. Differentiation of hiPSCs to megakaryocytes was assessed by RT-PCR and flow cytometry. Results: H&E, DAPI staining, and SEM analysis confirmed the integrity of the 3D lung structure. Flow cytometry and RT-PCR analysis revealed the presence of megakaryocyte markers in differentiated cells. Conclusion: It seems that natural acellular scaffold and microfluidic 3D bioreactor provides a suitable natural cost-benefit microenvironment for hiPSCs differentiation into megakaryocytes.

Keywords: Induced Pluripotent Stem Cells, Megakaryocyte, 3D Bioreactor, Microfluidic System, Acellular Rat Lung

P148

Investigating the Prognostic Significance of Circulating Tumor Cells, lncRNA SNHG18, and Adiponectin in Multiple Myeloma Patients

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Background: Emerging evidence suggests that Circulating tumor cells (CTC) in peripheral blood serve as valuable prognostic biomarkers in multiple myeloma (MM). Studies have shown that elevated CTC levels at diagnosis are associated with aggressive disease behavior, increased risk of disease progression, and poorer overall survival. This study aims to investigate the clinical significance of CTCs in MM patients, focusing on their potential as prognostic biomarkers. We will also examine the expression of lncRNA SNHG18, implicated in tumor metastasis, and evaluate serum adiponectin levels, a hormone with potential anti-tumor effects. Methods: This study investigated CTC (flow cytometry), SNHG18 (reverse transcription polymerase chain reaction (RT-PCR)), and adiponectin levels (enzyme-linked immunosorbent assay (ELISA)) in 50 MM patients and 30 healthy controls. Results: This study included 30 MM patients. CTC levels were significantly elevated in newly diagnosed patients compared to those in complete remission and healthy controls. Higher CTC levels correlated with worse prognosis and longer time to achieve spontaneous complete remission. A strong correlation was observed between CTC levels and bone marrow plasma cell burden. LncRNA SNHG18 expression was significantly higher in newly diagnosed patients and decreased in those achieving complete remission. Adiponectin levels were significantly lower in patients with more advanced disease stages. Conclusion: This study provides evidence that CTCs, lncRNA SNHG18, and adiponectin may serve as valuable prognostic biomarkers in MM. Elevated CTC levels in newly diagnosed patients were associated with poor prognosis.

Keywords: Circulating Tumor Cells (CTC), Multiple Myeloma (MM), lncRNA-SNHG18, Adiponectin

P149

Investigating Cardiac Abnormalities in Beta-Thalassemia Major: A Serum Biomarker Perspective

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Background: Beta-thalassemia major is an autosomal recessive disorder characterized by ineffective erythropoiesis. Continuous blood transfusions and the body's inability to eliminate excess iron result in iron overload, which may contribute to cardiac damage. One of the regulatory pathways implicated in iron-induced cardiac disease is the Osteoprotegerin/RANK (Receptor Activator of Nuclear Factor kappa-B)/RANKL (Receptor Activator of Nuclear Factor Ligand) pathway. This study evaluated serum RANKL levels and their association with left ventricular hypertrophy (LVH), diastolic dysfunction, ejection fraction, pulmonary hypertension, and MRI T2* index in beta-thalassemia major patients. Methods: This study was conducted on 82 beta-thalassemia major patients in Mashhad. All patients underwent a comprehensive non-invasive assessment, including two-dimensional echocardiography, color Doppler M-mode, and MRI T2*. Serum RANKL levels were measured using the ELISA technique. Statistical analysis was performed using SPSS 20. Results: Among the 82 patients, 36 (43.9%) were female, and 46 (56.1%) were male, with a mean age of 23.6 ± 6.83 years. Left ventricular hypertrophy and diastolic dysfunction were observed in 24 (29.3%) and 23 (28%) patients, respectively. No significant correlation was found between serum RANKL levels and LVH, diastolic dysfunction, ejection fraction, pulmonary hypertension, or MRI T2* index (P>0.05). Conclusion: The findings indicate no significant association between serum RANKL levels and cardiac complications, including LVH, diastolic dysfunction, ejection fraction, pulmonary hypertension, or MRI T2* index in beta-thalassemia major patients. Further research is needed to confirm these findings.

Keywords: Beta-Thalassemia Major, RANKL, Echocardiography, MRI T2

P150

Comparison of Immature Granulocyte Counts in MXD Parameter of Sysmex XP-300 Instrument, in Peripheral Blood Smear Examination

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Background: Immature granulocytes (IGs), including band cells, metamyelocytes, myelocytes, and promyelocytes, are reported as MXD in automated analyzers. This study used the Sysmex XP-300 device (Kobe, Japan), which focuses solely on data collection, using automated analyzer values for MXD and manual counting for IGs. Methods: A total of 1,245 blood samples were categorized into two groups based on MXD values: MXD <10% and MXD >10%. IGs were evaluated in both groups, and each group's distribution of MXD subcategories was recorded separately. Statistical analysis was performed to assess differences between the groups. Results: Among the samples, 1,016 (81.6%) had MXD >10%, while 229 (18.4%) had MXD <10%. The distribution of IG subcategories was as follows: for MXD >10%, band cells 567 (55.8%), metamyelocytes 325 (31.98%), myelocytes 196 (19.29%), and promyelocytes 8 (0.7%); for MXD <10%, band cells 175 (76.42%), metamyelocytes 100 (43.66%), myelocytes 71 (31%), and promyelocytes 3 (1.31%). The difference in band cell distribution was statistically significant ($P < 0.0001$), whereas the differences in metamyelocytes, myelocytes, and promyelocytes were not statistically significant ($P > 0.05$). Conclusion: Given the normal range of monocytes, eosinophils, and basophils reported as “MIX” on partial differentials, it seems logical that higher values would increase the likelihood of needing a peripheral blood smear. Immature granulocytes and band cells are also included under “MIX.” This study showed that a difference of more than 10 percent significantly increases their observation.

Keywords: Immature Granulocytes, Manual Counting, Automated Counting

P151

Flow Cytometry-based Functional Assay is a Valuable Diagnostic Approach for Confirmation of Heparin-Induced Thrombocytopenia

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Heparin-induced thrombocytopenia (HIT) is a serious immunological adverse drug reaction that rarely occurs in patients receiving heparin. The heparin-induced platelet activation (HIPA) test, a gold-standard assay for HIT, is time-consuming, challenging, and produces qualitative results. We aimed to compare the performance properties of a flow cytometry-based functional assay for HIT diagnosis with HIPA assay. Materials and Methods: This research was carried out on HIT-suspected patients referred to the Iranian Blood Transfusion Organization between 2021 and 2023. After clinical evaluation and 4Ts scores calculation, anti-PF4 screening and HIPA test were conducted. Thirty HIPA-positive and 30 HIPA-negative samples were selected. Subsequently, a flow cytometry-based functional assay, Emo-Test HIT confirm, was performed, and the sensitivity and specificity for HIT diagnosis were measured. Results: Among the 30 samples with negative HIPA results, one was positive with the Emo-test HIT Confirm® assay, and the remaining were negative. Among 30 positive HIPA samples, the result of one sample was inconclusive, two samples were negative with flowcytometry Emo-test and the others were positive. The sensitivity and specificity of this flow cytometry-based functional assay were 90% (95% CI: 79.3-100) and 96.6% (95% CI:90.2-100). The negative predictive value and positive predictive value were 93.5% and 96.4% respectively. Conclusion: Flow cytometry-based functional assay has a good sensitivity and specificity for HIT diagnosis confirmation, indicating that it may be a promising approach in the clinical setting.

Keywords: Heparin-Induced Thrombocytopenia (HIT), Diagnosis, Flow Cytometry, Functional Assay

P152

Effectiveness of Artificial Intelligence for Prediction and Personalized Medicine in Acute Myeloid Leukemia

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Background: Acute myeloid leukemia (AML) is a complicated hematological malignancy with significant variation in genetics, treatment response, and long-term prognosis, making it a model for personalized medicine development. With the availability of hematologic malignancy patient samples and recent breakthroughs in high-throughput technology, large amounts of therapeutically useful biological data for diagnosis, risk stratification, and targeted development of drugs have been created. The main aim of this study was to investigate Artificial Intelligence (AI) approaches and their efficacy in AML patient precision medicine. Methods: Artificial intelligence, prediction, personalized medicine, and AML keywords have been searched in Google Scholar, PubMed, and Scopus for the last 5 years. Results: Large-scale clinical, genetic, and molecular datasets have been analyzed using AI approaches such as machine learning (ML) and deep learning (DL). These algorithms improve risk stratification, identify AML subgroups, and accurately forecast treatment outcomes. They make it possible to optimize treatment plans, choose individualized therapies, and diagnose diseases early. AI-driven approaches also assist in identifying novel biomarkers and predicting relapse risks. Conclusion: Despite tremendous advances, obstacles such as data heterogeneity, a lack of defined methods, and ethical issues impede AI's broad clinical acceptance in AML. However, AI-powered models have the potential to transform AML diagnosis and treatment by allowing more precise risk classification, individualized medication selection, and enhanced outcomes for patients. Overcoming these challenges through improved data integration, regulatory developments, and transparent AI models will be critical to effectively use AI's capabilities in AML management.

Keywords: Artificial Intelligence, Acute Myeloid Leukemia, Personalized Medicine, Machine Learning, Deep Learning

The Future Medical Laboratories: Sustainable and Eco-friendly

P153-P154

P153

Eco-friendly Green Synthesis of Molybdenum Nanoparticles as a Potential Antibacterial Agent Against Carbapenem-Resistant Klebsiella pneumoniae Isolates

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Background: The global rise in Carbapenem-resistant Klebsiella pneumoniae (CRKP) infections has become a significant concern, leading the World Health Organization (WHO) to categorize it as a critical public health threat. With the current scarcity of effective treatment options for CRKP-related infections, there is a pressing demand to investigate and develop innovative therapeutic approaches to address this growing challenge. Investigating the antibacterial effects of eco-friendly biosynthesis of molybdenum nanoparticles might provide a hopeful approach to finding alternative solutions for combating multidrug-resistant pathogens. Methods: Molybdenum nanoparticles were biosynthesized by an aqueous extract of pink Rosa gallica. The biosynthesis process was accelerated using microwave irradiation. The physicochemical properties of molybdenum oxide NPs were characterized by various techniques, including DLS, FESEM, EDX, XRD, and UV-Vis spectroscopy. Furthermore, the antibacterial efficacy of molybdenum nanoparticles was assessed against a standard strain of Klebsiella pneumoniae as well as three clinical strains of carbapenem-resistant Klebsiella pneumoniae using the microdilution method. Results: FESEM showed that the molybdenum nanoparticles were spherical with an average size of 21 nm. DLS analysis showed a single peak corresponding to biosynthesized molybdenum oxide NPs with a size of 22 nm. XRD analysis confirmed the crystalline structure of the molybdenum oxide phase. The antibacterial evaluation demonstrated that the minimum inhibitory concentration (MIC) of molybdenum oxide NPs were 1600 µg/ml, 1600 µg/ml, 800 µg/ml, and 400 µg/ml for three carbapenem-resistant clinical strains and one standard strain of Klebsiella pneumoniae, respectively. Conclusion: The significant antibacterial efficacy of eco-friendly molybdenum oxide NPs demonstrates their potential as promising antimicrobial agents. These results pave the way for additional investigation of molybdenum oxide NPs in medical applications, specifically in the fight against resistant bacterial infections.

Keywords: Molybdenum Nanoparticles, Eco-Friendly Synthesis, Biosynthesis, Antibacterial Activity, Carbapenem-Resistant Klebsiella Pneumoniae

P154

Nanotechnology: A Revolution in Clinical Laboratories

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Introduction: The rapidly evolving field of nanotechnology has paved the way for significant innovations in laboratory practices. One of the most remarkable advancements is the development of nanosensors, which specialize in detecting physical, chemical and biological changes at the nanoscale. Nanobiosensors represent an advanced form of nanosensors, specifically designed to identify biological markers such as enzymes, DNA, or antibodies in exceptionally low concentrations. At the same time, they enhance environmental sustainability by reducing chemical consumption and waste. Method: This review article was conducted based on the articles published in NCBI, EMBASE up to March 2025. The keywords were Nanotechnology AND Nanosensor AND Laboratory. 10 articles were found, and 4 were removed and 6 articles were selected. All selected articles were in English. Result: The results suggest that integrating biosensor technology in laboratory systems enhances response time, accuracy and sensitivity. This approach provides a non-invasive option to traditional clinical methods such as biopsy, ultrasound and MRI. Biosciences play a crucial role in detecting primary tumor, monitoring metastasis and identifying early disease recurrence. Conclusion: In summary, the integration of nanotechnology into laboratory settings not only signifies a more cost -effective and efficient approach for diagnosis through high sensitivity and accuracy, but also indicates a promising future in medical advancements. With the ongoing research and the establishment of the appropriate regulatory guidelines, there is optimism for enhanced disease diagnosis and management, ultimately contributing to an improved quality of life.

Keywords: Nanotechnology, Nanosensor, Laboratory

Toward Application of Extracellular Vesicles in Laboratory Diagnosis

P155-P159

P155

Exosomal Strategies in Glioblastoma Treatment: Exploring UC-MSC Exosomes' Potential to Diminish Tumor Cell Viability

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Introduction: Glioblastoma (GBM) is an aggressive and treatment-resistant brain cancer, with U87MG cells serving as a widely used in vitro model. Recent studies suggest that exosomes derived from human umbilical cord mesenchymal stem cells (UC-MSCs) have therapeutic potential due to their ability to deliver bioactive molecules and modulate cancer cell behavior. This study investigates the impact of UC-MSC-derived exosomes on U87MG cell viability, offering novel insights into glioblastoma therapy. Methods: UC-MSCs were isolated from human umbilical cords and cultured under standard conditions. Exosomes were extracted via ultracentrifugation and characterized for purity and size. U87MG cells were cultured in both 2D and 3D systems and treated with varying concentrations of exosomes, including 100 µg/µL. Cell viability was assessed using Annexin V/PI staining, flow cytometry, and additional viability assays. Results: Exosomes at 100 µg/µL demonstrated a 10% reduction in U87MG cell viability. Results were consistent across 2D and 3D cultures, with similar findings confirmed by A/PI staining and flow cytometry. These data highlight the dose-dependent cytotoxic effects of UC-MSC-derived exosomes on glioblastoma cells. Discussion: The observed reduction in cell viability suggests that UC-MSC exosomes may exert antitumor effects by modulating apoptotic pathways and tumor microenvironment dynamics. These findings underline their potential as a targeted, biocompatible therapeutic tool for GBM, though challenges such as dose optimization and delivery specificity remain. Conclusion: UC-MSC-derived exosomes represent a promising avenue for glioblastoma therapy, with preliminary results indicating their efficacy in reducing tumor cell viability. Further studies are essential to advance their clinical translation and therapeutic optimization.

Keywords: Glioblastoma, Exosome, Mesenchymal Stem Cell, Umbilical Cord

P156

Immune Modulation and Disease Progression in Leishmaniasis: The Role of Leishmania-Derived Exosomes

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Introduction: The Leishmania parasites, belonging to the family Trypanosomatidae, are transmitted to humans through the bite of sandflies. The text explains that Leishmania parasites secrete extracellular vesicles, known as exosomes, which transfer molecules like proteins and RNA between cells. These exosomes play a role in regulating the immune system, inflammation, and disease progression. Depending on the type of infection, Leishmania can cause skin lesions (cutaneous leishmaniasis) or damage internal organs such as the liver and spleen (visceral leishmaniasis). This study aims to explore the role of exosomes in Leishmania infection and their effect on the host immune system. Metods: We conducted a study using keywords related to leishmaniasis; exosome; Leishmania extracellular vesicle; immune response; innate immunity; macrophage from a variety of databases such as PubMed, Google Scholar, and scopus. Finally, among other resources, we used data from 2012 to 2024. We selected 20 articles, studied them, and conducted a comprehensive analysis. Result: Leishmania exosomes, containing proteins like glycoprotein 63, heat shock proteins, and miRNAs, play a key role in immune modulation. They suppress the expression of IFN-γ, TNF, and nitric oxide in macrophages and other phagocytes, shifting immune signaling towards a Th2 response. This results in increased inflammatory cytokine production and tissue damage, influencing parasite survival and disease progression. Discussion: To combat leishmaniasis, understanding the parasite's biology and identifying its exosomes can help discover key proteins involved in its survival and disease progression. These proteins could be targeted for new drugs or vaccines and aid in diagnosis and monitoring of the disease.

Keywords: Leishmaniasis, Exosome, Leishmania Extracellular Vesicle, Immune Response, Innate Immunity

P157

The Application of Extracellular Vesicles in Cancer Diagnosis

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Background: Extracellular vesicles (EVs), including exosomes and microvesicles, are nano-sized structures released by cells into body fluids. they carry proteins, nucleic acids, and lipids and show the condition of their secreting cells. Tumor-derived EVs are potential biomarkers for cancer diagnosis. Liquid biopsies, such as blood tests, offer a non-invasive way of detecting cancer through EVs, overcoming the limitations of traditional tissue biopsies, and are gaining attention for their potential in early diagnosis of neoplasms. Methods: Literature searches were conducted using PubMed, Scopus databases, and Google Scholar search engine. The advanced search keywords used included “extracellular vesicles”, “microvesicles”, “exosomes”, “malignancy”, “cancer”, “Neoplasms”, and “diagnosis.” The search was limited to English studies and accessible full texts. Review, duplicate, and non-relevant articles were excluded. Results: In this review, 110 articles were retrieved through searching in databases of which only 56 articles matched our criteria after preprocessing and screening. These articles show that EVs contain a variety of cancer-specific biomarkers, including proteins, miRNAs, and DNA. Specific EV proteins, such as CD19, CD20, CD38, CD138, EDIL3, FN, FAK, A33 and CD147, have been identified in malignancies. Similarly, EV-associated miRNAs, such as miR-21, miR-155, and Let-7g, have shown diagnostic potential in various cancers. EV-derived DNA can also be used for mutation detection. Conclusion: EVs present a promising future for cancer diagnosis due to their accessibility in biofluids, rich molecular content, and potential to reflect real-time tumor changes. EV-based liquid biopsies offer a non-invasive approach to early neoplasm detection. While challenges remain in isolation and characterization, ongoing advancements in EV research are paving the way for better cancer management.

Keywords: Extracellular Vesicles, Microvesicles, Exosomes, Malignancy, Cancer, Neoplasms, Diagnosis

P158

The Future of Breast Cancer Diagnosis: Extracellular Vesicles as Key Players

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Breast cancer (BC) is the most common cancer and the leading cause of cancer-related deaths in women globally, representing 25–30% of new cancer cases and 13–15% of cancer fatalities. This underscores the urgent need for innovative approaches to early detection and effective treatment. While mammography and tissue biopsy remain standard diagnostic methods, they have limitations. Liquid biopsy, a minimally invasive alternative, offers a promising solution for detecting BC. It involves analyzing biofluids and isolating tumor-derived components such as extracellular vesicles (EVs). EVs are membrane-bound particles released by cells, enabling intercellular communication. They carry DNA, RNA, lipids, metabolites, and proteins. Present in various body fluids, EVs hold significant potential for diagnosis and prognosis. The documents for this study were gathered through searches in databases such as PubMed, Google Scholar, ScienceDirect, and Springer. Key terms included “breast cancer,” “extracellular vesicles,” “liquid biopsy,” and “novel diagnosis.” Small extracellular vesicles (SEVs), found in body fluids such as blood and urine, are easily isolated and contain differentially expressed miRNAs, lncRNAs, and proteins, making them promising biomarkers for breast cancer (BC) diagnosis. Specific EV miRNAs, including miR-375, miR-655-3p, miR-548b-5p, and miR-24-2-5p, have shown relevance for early BC detection. Serum exosomal lncRNA XIST is a potential biomarker for predicting breast cancer recurrence. SEVs also carry circular nucleic acids (circDNA and circRNAs). In BC, certain circular RNAs are upregulated in serum and tumor tissues, highlighting their diagnostic and prognostic potential. Tumor-derived EVs (TEVs) contain miRNAs and other bioactive molecules like DNA, RNAs, lipids, and metabolites, offering valuable tools for early detection and prognosis in BC. Early cancer detection is crucial for improving treatment outcomes. Small extracellular vesicles (sEVs), containing proteins, nucleic acids, and other biomolecules, are promising biomarkers for BC diagnosis and prognosis.

Keywords: Breast Cancer, Extracellular Vesicles, Liquid Biopsy, Novel Diagnosis

P159

Exosomal miRNAs Insights: A New Approach in Ovarian Cancer Early Diagnosis

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Background: Ovarian cancer is one of the deadliest malignancies in women worldwide, with a less than 45% five-year survival rate. Its poor prognosis is due to late diagnosis. Exosomes (30–150 nm) as a type of extracellular vesicle play significant roles in biological processes. Exosomes contain biological molecules such as nucleic acids, proteins, and lipids. Extracting exosome-derived miRNAs and analyzing them as biomarkers play a key role in the early diagnosis of cancers. Here we will describe the role of exosome-derived miRNAs in ovarian cancer diagnosis. Methods: This review article was performed using articles published on PubMed, Google Scholar and Science Direct since 2020. The keywords were Ovarian Cancer OR Ovarian Neoplasms AND Exosomes AND Diagnosis AND Human. By searching these databases, 58 articles were found, and 42 were removed by reading titles and abstracts. 16 articles were selected under the inclusion criteria. All articles were chosen from English articles. Duplicate articles, non-English and ex-vivo articles were excluded. Results: According to the articles, the use of exosome-derived miRNAs such as miR-200a, miR-200b, miR-200c, miR-16, miR-93, miR-126, miR-100, miR-320, miR-99a-5p as biomarkers for ovarian cancer diagnosis is expanding. Some advantages of miRNA biomarkers include stability, easy enrichment and non-invasive sampling. However, there are also some limitations such as heterogeneity and standardization difficulties. Conclusion: It seems that exosome-derived miRNAs as a new diagnostic method for ovarian cancer, have shown remarkable results. Nevertheless, according to the ever-increasing use of exosomes in cancer diagnosis and treatment, further investigations are recommended.

Keywords: Exosomes, Ovarian Cancer, Biomarker, Early diagnosis

Young Scientists

P160-P203

P160

Tiny Vesicles, Big Impacts: Decoding the Therapeutic and Diagnostic Potential of Exosomes in Hematologic Malignancies

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Tiny Vesicles, Big Impacts: Decoding the Therapeutic and diagnostic Potential of Exosomes in Hematologic Malignancies Melika Khademi1*, Davood Bahshash1 1- Department of Hematology and Blood Banking, School of Allied Medical Sciences, Shahid Beheshti University of Medical Scieneces, Tehran, Iran Hematological malignancies, including leukemia, lymphoma, and multiple myeloma, arise from abnormal hematopoietic stem cell (HSC) differentiation, disrupting blood cell regulation. Traditional treatments like chemotherapy, radiotherapy, and hematopoietic stem cell transplantation (HSCT) remain standard but face challenges such as recurrence, metastasis, and therapy resistance. Advances in tumor immunology have introduced novel therapies, including monoclonal and bispecific antibodies, antibody-drug conjugates, and CAR-T cells, yet significant obstacles persist. Beyond their role in tumor progression and immune modulation, exosomes hold immense potential as diagnostic biomarkers and therapeutic agents. They enable real-time monitoring of disease progression and offer a minimally invasive platform for precision medicine. Preclinical investigations underscore the efficacy of exosome-based approaches across diverse medical disciplines, while ongoing clinical trials are actively evaluating their safety and therapeutic applications. These developments suggest that exosomes are poised to revolutionize cancer therapy and redefine modern medicine by facilitating personalized, minimally invasive treatment paradigms for complex diseases. This review highlights the multifaceted roles of exosomes in the diagnosis and treatment of hematological malignancies, with a focus on their transformative potential to advance cancer management strategies. Keywords: Exosome, Extracellular Vesicles, Hematological Malignancies, Diagnosis, Therapeutics.

Keywords: Exosome, Extracellular Vesicles, Hematological Malignancies, Diagnosis, Therapeutics

P161

Optimization and Determination of the Detection Limit for MicroRNA-155 Sequence Using Laboratory Techniques

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Background: MicroRNAs, as non-coding RNA molecules, play critical roles in gene expression regulation and RNA silencing. They also serve as valuable biomarkers for disease diagnosis. However, current diagnostic methods, such as PCR and ELISA, have limitations, including high costs, the requirement for advanced equipment, and skilled technicians. Therefore, the development of simpler and more cost-effective approaches is essential. Methods: In this study, the optimal conditions for the Enzyme-free toehold-mediated strand displacement (TMSD) reactionwere determined by evaluating parameters such as reaction time (1, 1.5, and 2 hours), temperature (23°C, 25°C, and 27°C), concentration (0.4 to 0.8 µM), and incubation time (30, 45, and 60 minutes). To establish the detection limit of the system, serial concentrations ranging from 0.001 to 1000 nM of the target strand were tested. Results: Based on the signal-to-noise ratio comparison, the optimal conditions were identified as a reaction time of 1 hour, a temperature of 25°C, a Hemin concentration of 0.6 µM, and an incubation time of 60 minutes. Using the equation (ABS = -3.0867C + 0.5244) and calculating the cut off value based on the mean and standard deviation of negative controls, the system's detection limit was determined to be 31 pM with a regression coefficient of 0.99. Conclusion:The designed system, with its suitable detection limit and optimized conditions, offers a simple, accurate, and cost-effective method for detecting miR-155 sequences. It also holds potential for further studies involving clinical research samples. This approach, based on innovative molecular techniques and colorimetric methods, could serve as a practical alternative to complex and expensive existing methods, particularly in resource-limited settings.

Keywords: Non-coding RNA Molecules, MicroRNA-155 (MiR-155), Toehold-Mediated Strand Displacement (TMSD), Colorimetric Methods, Clinical Research

P162

Downregulation of miR-23a-3p in Seminal Plasma: A Promising Biomarker for Non-Obstructive Azoospermia Diagnosis and Male Fertility Evaluation

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IACLD Travel award for attending to QICL & IRAN Lab EXPO, TEHRAN, 2025 Background: Non-obstructive azoospermia (NOA) represents the most severe type of male infertility, with few treatment options currently available. MicroRNAs (miRNAs), which play key roles in regulating spermatogenesis, have gained attention as potential biomarkers for diagnosing NOA and assessing the likelihood of success in assisted reproductive technologies. This research focuses on analyzing the expression levels of miR-23a-3p in the seminal plasma of NOA patients, comparing these levels to those in individuals with reduced sperm quality and normozoospermic controls. Methods: The study included 35 normozoospermic individuals, 35 individuals with impaired spermatogenesis, and 15 patients with NOA. RNA was extracted from seminal plasma, and complementary DNA (cDNA) was synthesized. Quantitative real-time PCR (qRT-PCR) was employed to measure the expression levels of miR-23a-3p across the groups. Results: The analysis of miR-23a-3p expression revealed a statistically significant threefold reduction in the NOA group compared to the control group. In contrast, the NOP group showed no significant difference in expression levels relative to the control group, indicating no change in expression. However, a significant difference was observed between the NOA and NOP groups, with the NOA group exhibiting lower expression levels than the NOP group. Conclusion: The seminal plasma expression of miR-23a-3p has the potential to serve as a biomarker for diagnosing NOA and evaluating male fertility, offering important insights for developing personalized approaches to manage male infertility.

Keywords: Infertility, Seminal Plasma, Non-Obstructive Azoospermia, miRNA, miR-23a-3p

P163

The Relationship between SARS-CoV-2 Antibody Titer and the AI Value in Covid-19 Patients

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Background: A significant factor in the humoral immune response to COVID-19 is avidity. Additionally, Antibody levels are crucial for protection during the disease. Given that avidity values and antibody titers are linked to infection symptoms and severity, we investigated the relationship between AI values and antibody concentrations. Method Forty patients with symptomatic COVID-19 and forty asymptomatic carriers of SARS-CoV-2 were enrolled in our study from September to December 2021. We measured anti-S and anti-N IgG avidity indices (AI) using a modified ELISA that employs urea as a chaotropic agent. Serum concentrations of anti-S and anti-N IgG were measured using specialized ELISA kits. Results AI values for both anti-S and anti-N IgG were lower in symptomatic groups than in asymptomatic cases, with only the difference in anti-N IgG reaching statistical significance. However, the titers of both anti-S IgG and anti-N IgG were significantly elevated in symptomatic patients. In our analysis for correlation, we did not find any significant association between AI and antibody titers; however, the correlation between anti-S AI values and anti-S titers was significant in both groups. Conclusion Our research underscores the important roles of both anti-S IgG and anti-N IgG avidity and titers in protecting against symptomatic COVID-19. Keywords Covid-19, avidity index, antibody titer, symptomatic, asymptomatic.

Keywords: Covid-19, Avidity Index, Antibody Titer, Symptomatic, Asymptomatic

P164

Impact of Vitamin D Deficiency on Platelet Parameters in Patients with COVID-19

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Introduction: There is limited information about the relationship between platelet parameters and vitamin D levels in patients with COVID-19. This study aims to explore the connection between serum vitamin D levels and platelet parameters in COVID-19 patients, comparing these parameters between patients with and without vitamin D deficiency. Additionally, it examines the prognostic significance of these parameters in cases of vitamin D deficiency. Methods: A total of 743 patients diagnosed with COVID-19 were included in the study. Participants were categorized into two groups: those with vitamin D deficiency and those without. The relationship between platelet indices and vitamin D levels was assessed using Pearson's correlation analysis and one-way ANOVA testing. Results: Patients with vitamin D deficiency showed significantly higher platelet counts and mean platelet volume (MPV) compared to those without deficiency. A significant negative correlation was found between vitamin D levels and both platelet count ($r = -0.835$, $P = 0.001$) and MPV ($r = -0.324$, $P = 0.042$) in patients with vitamin D deficiency. These findings suggest that vitamin D levels can influence platelet count and MPV in COVID-19 patients. Discussion: The results indicate that maintaining adequate vitamin D levels in COVID-19 patients is crucial, as it is linked to a reduction in MPV. Lower MPV levels may decrease the risk of developing conditions such as coronary artery disease, highlighting the importance of managing vitamin D levels in these patients.

Keywords: Platelets, COVID-19, Vitamin D, Thrombocytosis, Mean Platelet Volume

P165

The Effect of Static Magnetic Field on Gene Expression of THP1

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Background: AML is a bone marrow-related disease. It results from a disorder of hematopoietic stem cells due to genetic changes in blood cell precursors that result in the overproduction of neoplastic myeloclonal stem cells. In AML, the 5-year overall survival rate is 44%. Despite the advancements achieved in treatment modalities, challenges persist, including drug resistance, side effects, and relapse of the disease. Recent investigations into the use of static magnetic fields for AML treatment have demonstrated potential antitumor efficacy. Methods: The THP1 was exposed to a static magnetic field and after 24 hours of exposure, the expression of genes related to apoptosis, cell cycle, and the autophagy pathway was examined using Real time-PCR. The results were finally analyzed using statistical methods. Results: The results of gene expression analysis by the Real time-PCR showed that after 24 hours of exposure of THP1 to the static magnetic field, the expression of apoptotic genes including Caspase9, Bax, NOXA increased and the expression of anti-apoptotic genes Bcl2 decreased. This indicates an increase in apoptosis by magnetic fields. The static magnetic field severely inhibited the proteins related to autophagy pathway ATG7 and ATG10. Cyclin-B1, Cyclin-A2, Cyclin-D1, CDK-1. CDK-2, CDK-4, and CDK-6 also decreased expression, while P53 and P21 expression increased, indicating an arrest in the cell cycle. Conclusion: Static magnetic fields have antitumor effects, increasing apoptosis, inhibiting autophagy, and arresting the cell cycle. As a result, we can consider static magnetic fields as a candidate for supplementary AML therapy.

Keywords: Static Magnetic Field, Apoptosis, THP1, Cell Cycle, Autophagy

P166

Targeting Ferroptosis in Multiple Myeloma: Mechanisms and Therapeutic Strategies

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Targeting Ferroptosis in Multiple Myeloma: Mechanisms and Therapeutic Strategies Fatemeh Karimian1*, Nader Vazifeh Shiran1 1-Department of Hematology and Blood Banking, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran Ferroptosis is a distinct type of cell death that is dependent on iron and is primarily induced by lipid peroxidation. This phenomenon has emerged as a crucial element in numerous pathological states, particularly in relation to cancer. Recent studies have elucidated the core mechanisms that regulate ferroptosis, emphasizing the vital roles played by iron metabolism, oxidative stress, and lipid peroxidation in its regulation. Knowing the mechanism of factors that promote ferroptosis, such as erastin and RSL3, and inhibitors such as ferrostatin-1, not only enhances our comprehension of ferroptosis but also opens avenues for innovative strategies in cancer therapy and beyond. In the treatment of multiple myeloma as a hematological malignancy, we face challenges such as recurrence of the disease and drug resistance. In the context of multiple myeloma, the combined application of ferroptosis inducers, including artesunate and bortezomib, presents encouraging strategies for addressing drug resistance and improving the effectiveness of chemotherapy. Critical signaling pathways, notably the PI3K/AKT and Nrf2/HO-1 pathways, as well as processes such as ferritinophagy, offer valuable mechanistic understanding of how ferroptosis facilitates cellular death. It is essential for future research to focus on discovering novel ferroptosis modulators and enhancing combination therapies to exploit the vulnerabilities of this pathway. These approaches present considerable potential for meeting the unfulfilled requirements in cancer therapy and other medical fields.

Keywords: Ferroptosis, Multiple Myeloma, Iron-Dependent Death, Lipid Proxidation

P167

CMV Infection in Patients with Active Ulcerative Colitis: Prevalence and Underlying Factors of Pathogenicity

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Background: Cytomegalovirus (CMV) infection has garnered increasing attention in the context of active ulcerative colitis (UC), a chronic inflammatory bowel disease (IBD), characterized by periods of remission and relapse. Exploring the interplay between CMV and UC highlights the need for heightened awareness of viral infections in gastrointestinal disorders, particularly among patients with Active UC, to improve patient management and therapeutic strategies. Methods: In this cross-sectional study, serum samples from 82 patients with UC were assessed for CMV serological markers (IgG and IgM antibodies) using the chemiluminescent immunoassay (CLIA) method. Following this, polymerase chain reaction (PCR) was employed to detect CMV DNA in plasma samples. The clinical findings along with demographical collected data were analyzed using SPSS version 16 software. Results: Among 82 patients with active UC, 12.2% were diagnosed with active CMV infection, and 48% had a history of previous CMV infection (IgG+ and IgM-). No significant differences in clinical symptoms or demographic variables among the three patient groups were observed (P>0.05). However, there was a significant difference in weight loss between patients with active CMV infection and those with IgG+ and IgM- (P = 0.040). Additionally, patients with active CMV had significantly higher corticosteroid consumption compared to the other two groups (P = 0.020). Conclusions: The prevalence of CMV in patients with active UC highlighted the necessity of accurately diagnosing the presence of latent or active CMV infection before initiating treatment. Furthermore, the role of corticosteroid use in CMV reactivation and the severity of colitis should not be underestimated.

Keywords: Cytomegalovirus, Ulcerative Colitis, Inflammatory Bowel Disease, Viral Infection

P168

Investigation and Comparison of Hospital Bacterial Contamination of Environmental Surfaces and Medical Instruments in Special Departments of Medical Training Centers and Government Hospitals in Mazandaran Province between 1402 and 1403

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Backcgrand: Hospital Contamination is considered one of the important health problems of medical communities, whose successful control requires awareness and the implementation of documented measures and plans in this field. Methods: This descriptive study was first conducted in 1402 from 10 medical training centers and hospitals in Mazandaran province. Sampling was done confidentially and without prior notification of the centers in the early hours of the morning shift and before the first surgery in the operating room and also before the start of routine work in the ICU departments. In the continuation of this study, similar to last year's method in 1403, it was conducted on the same special departments of ten selected hospital centers in the province, and after performing various diagnostic steps, the results and the obtained data have been examined and compared with the previous year. Resulte: The results obtained in the comparison of two different years are significantly different and in general, the amount of pollution in 1403 has decreased compared to 1402, which is very promising. Among the 10 studied centers, The average percentage of contamination of bacteria that can potentially cause hospital infection in 1402 and 1403, respectively, the contamination from microbial samples in the operating room was 26.8% and 12.7% and in the ICU This amount was 41.2% and 22.3%. conclusion: According to this study it is suggested that measures similar to this study of microbial sampling from the centers and hospitals of the province should be carried out without notice during annual programs and the obtained report should be presented to the centers in order to follow up more on the implementation of infection control programs and to reduce them as much as possible The level of hospital infection.

Keywords: Hospital Contamination, Bacterial Contamination, Medical Instruments, Mazandaran

P169

Integrating Convolutional Neural Networks with Machine Learning for Advanced Diabetes Diagnosis and Management

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Diabetes mellitus is a widespread metabolic disorder associated with severe complications such as cardiovascular disease, nephropathy, and neuropathy. Early detection and effective management are essential to mitigating disease progression. Traditional diagnostic methods, including HbA1c measurements and oral glucose tolerance tests, are often invasive, time-consuming, and less sensitive in detecting early-stage diabetes. Convolutional neural networks (CNNs), a subset of machine learning specializing in image and pattern recognition, offer a revolutionary approach to diagnosing diabetes and predicting its complications. CNNs have been applied to diverse datasets, such as retinal fundus images, skin lesion photographs, and histopathological slides, to detect diabetes-related abnormalities with high accuracy. For instance, CNNs can identify diabetic retinopathy by analyzing retinal microaneurysms and hemorrhages, achieving sensitivity rates above 90%. These models also integrate electronic health records (EHRs) to assess clinical parameters like glucose trends and lipid profiles for better risk stratification. Additionally, CNNs process continuous glucose monitoring (CGM) data to predict glucose variability and hypoglycemia risks in real time. Furthermore, their application in multi-omics analysis has uncovered novel biomarkers, enabling personalized diabetes management. CNN-based models have demonstrated superior accuracy compared to traditional methods, reducing diagnostic variability and improving complication prediction. They have been particularly effective in identifying early kidney damage and cardiovascular risks by integrating clinical and imaging data. Moreover, CNN-driven multi-omics analysis has facilitated personalized treatment strategies, including tailored glucose-lowering therapies and lifestyle modifications. Despite these advancements, challenges such as data availability, privacy concerns, and model interpretability remain. The "black-box" nature of CNNs hinders their clinical adoption, necessitating explainable AI (XAI) solutions. Future developments, including integration with wearable devices, quantum computing, and precision medicine, will further enhance CNNs' role in diabetes care, requiring collaborative efforts among researchers, clinicians, and policymakers.

Keywords: Convolutional Neural Networks, Machine Learning, Diabetes Diagnosis, Diabetic Retinopathy, Personalized Medicine, Multi-Omics Analysis, Explainable AI

P170

Understanding Ferroptosis: From Cancer to Brain Diseases and Inflammation

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Ferroptosis, an iron-dependent form of regulated cell death characterized by the accumulation of lipid peroxides and depletion of glutathione, has emerged as a pivotal player in diverse disease pathologies. This paper provides a comprehensive review of the molecular mechanisms underlying ferroptosis and its implications across various diseases. significant strides have been made in unraveling the intricate pathways governing ferroptotic cell death. Key factors including iron metabolism, lipid peroxidation, and antioxidative defense mechanisms have been elucidated. Iron catalyzes the Fenton reaction, leading to lipid peroxidation and eventual cell demise. Concurrently, the depletion of glutathione, a crucial antioxidant, further exacerbates cellular susceptibility to ferroptosis. Understanding these mechanisms provides crucial insights into the potential targets for therapeutic interventions. ferroptosis has been implicated in the pathogenesis of a myriad of diseases spanning from cancer to neurodegenerative disorders. In cancer, dysregulated iron metabolism and heightened lipid peroxidation promote tumor progression and therapy resistance. Conversely, in neurodegenerative diseases such as Alzheimer's and Parkinson's, ferroptosis-induced neuronal death contributes to disease exacerbation. Additionally, ischemia-reperfusion injury, characterized by oxidative stress and inflammation, has been linked to ferroptosis-mediated tissue damage. Furthermore, mounting evidence suggests a pivotal role of ferroptosis in driving inflammatory responses, thereby implicating it in the pathophysiology of inflammatory disorders. Exploring the therapeutic potential of targeting ferroptosis presents exciting prospects for disease management. Strategies aimed at modulating iron metabolism, enhancing antioxidative defense mechanisms, or directly inhibiting lipid peroxidation hold promise in mitigating ferroptosis-associated pathologies. Furthermore, combination therapies targeting ferroptosis alongside conventional treatments may offer synergistic benefits in overcoming treatment resistance and improving patient outcomes. this review underscores the role of ferroptosis in pathogenesis and highlights the therapeutic avenues it presents across various disease contexts. By elucidating molecular intricacies of ferroptosis, we pave the way for innovative therapeutic strategies aimed at tackling complex diseases with unmet clinical needs.

Keywords: Ferroptosis, Iron Metabolism, Lipid Peroxidation, Antioxidative Defense, Disease Pathogenesis

P171

Investigation of the Prevalence of Helicobacter pylori Infection and Antibiotic Resistance to Clarithromycin in Tehran, Iran

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Background: Helicobacter pylori is adapted for colonization in the human stomach and is present in approximately half of the human population. Failure of the eradication could cause gastritis, duodenal ulcers, gastric cancer, and mucosa-associated lymphoid tissue (MALT) lymphoma. Although clarithromycin, a broad-spectrum antimicrobial drug from the macrolide class, is well-known for its effectiveness against H. pylori and is commonly used as a primary treatment in triple therapy regimens, the rapid rise in its resistance is a growing concern. Therefore, the primary objective of this study is to investigate the prevalence of H. pylori infection and the resistance of H. pylori isolates to clarithromycin in Tehran, Iran. Methods: A total of 764 antral gastric biopsy samples were collected from gastritis patients in the endoscopy unit of Firouzgar Hospital, Tehran. These samples were transported to the laboratory in a transport medium and cultured on supplemented Columbia agar under microaerophilic conditions for 3 to 5 days. The confirmed isolates using both biochemical and molecular tests were preserved at -80 oC for further analysis. Antibiotic resistance to clarithromycin was assessed using the Epsilometer test (E-test). The minimum inhibitory concentration (MIC) values for clarithromycin were interpreted based on CLSI standards. Results: Overall, in the present study, out of 764 collected samples, 162 Helicobacter pylori isolates were identified (21.5%). The highest prevalence was measured in women (61.7%) and the age range of participants was 11-87 years (mean age: 43.7 years). Among the isolates with optimum growth for MIC test, resistant to clarithromycin was detected in 67.9% of them (15/22). Conclusion: The results of this study highlight the increase in resistance to clarithromycin in Tehran. Clarithromycin-containing treatment regimens should not be used in the absence of a demonstrated clarithromycin susceptibility test or in patients with persistent infection who have history of a PPI-clarithromycin triple regimen.

Keywords: Helicobacter Pylori Infection, Clarithromycin Resistance, Tehran

P172

Examine the Impact of Burdock on HDL-C and LDL-C Levels in Stein-Leventhal Syndrome

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Background: Stein-Leventhal Syndrome, commonly known as polycystic ovary syndrome, is a prevalent endocrine disorder in women. It is primarily caused by a combination of genetic predisposition, oxidative stress, and environmental factors. This condition impacts lipid metabolism, leading to a decrease in HDL-C and an increase in LDL-C. Given the potential of herbal medicine to mitigate complications of this syndrome, Burdock, a plant rich in antioxidants such as chlorogenic acid, has been considered a promising candidate. This study aims to investigate the effects of Burdock on HDL-C and LDL-C levels in individuals with Stein-Leventhal syndrome. Methods: This clinical trial involved 60 women with Stein-Leventhal syndrome. Participants were randomly allocated into two groups: the intervention group, receiving Burdock root, and the control group, receiving placebo. Fasting blood samples were obtained from all participants at baseline to assess HDL-C and LDL-C levels. Both groups underwent their respective treatments daily over a 12-week period. Following the intervention, post-treatment blood samples were collected, and HDL-C and LDL-C levels were re-evaluated to determine the effects of Burdock on lipid profiles. Results: Daily consumption of Burdock root for 12-weeks significantly reduced serum levels of LDL-C ($p < 0.05$) and increased serum levels of HDL-C ($p < 0.05$) in the intervention group compared to the control group. Conclusion: This study showed that Burdock is effective in controlling the lipid profile in women with Stein-Leventhal syndrome and probably does this through its antioxidants. Therefore, the use of this plant can be effective in improving Stein-Leventhal syndrome.

Keywords: Stein-Leventhal Syndrome, Burdock, High-Density Lipoprotein, Low-Density Lipoprotein

P173

The Use of MgSO4 in the Diagnosis of EDTA-Dependent PTP Using Vacuum and Aspiration Methods of Blood Collection

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IACLD Travel award for attending to QICL & IRAN Lab EXPO, TEHRAN, 2025 Introduction: EDTA, a common hematology preservative, can, in rare cases, cause EDTA-associated pseudothrombocytopenia (PTCP). Calcium ion binding alters platelet glycoprotein IIb-IIIa, leading to platelet aggregation and falsely low platelet counts on automated analyzers. This can be misinterpreted as true thrombocytopenia. Adding magnesium sulfate (MgSO4) to EDTA prevents this in vitro phenomenon. Blood collection methods vary, including vacuum and aspiration, especially in patients with hematological conditions. This study lacked prior research comparing vacuum systems with MgSO4. Methods: Fifty patients with unexplained thrombocytopenia underwent parallel whole blood analysis using EDTA tubes and EDTA tubes with MgSO4, using two vacuum systems (2- and 3-component). Platelet counts (PLT) were determined using a Sysmex XN1000 analyzer. Morphology was assessed using Papenheinm staining. Results: Forty-one patients (82%) showed true thrombocytopenia confirmed by morphology. Nine patients (18%) exhibited EDTA-associated PTCP. MgSO4 corrected platelet counts to the reference range. For instance, EDTA tubes showed counts of 8 and 58 x 109/L, while EDTA + MgSO4 showed 192/188 and 176/168 x 109/L, respectively. Platelet counts were nearly identical (within 5%) across both vacuum systems when MgSO4 was used. Conclusion: Adding MgSO4 to EDTA blood collection tubes is a promising approach for diagnosing EDTA-associated PTCP, allowing its detection regardless of the vacuum system used during initial patient assessment.

Keywords: Pseudothrombocytopenia, Magnesium, EDTA, Citrate, Platelet Aggregation

P174

Neglected Dermoparsitic Diseases in Khuzestan Province (Pathology, Diagnosis and Treatment)

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Background: Demodicosis is a chronic dermoparasitic disease caused by Demodex folliculorum and D. brevis. Clinical manifestations of demodicosis are varied. The infestations may be free of symptoms or the lesions might be as rose- red pustules and the most typical features of rosacea is characterized by the presence of an erythematous papule- pustule rash, mainly in the face and inflammation in acute and chronic forms may occur. Scabies is a dermoparasitic disease caused by Sarcoptes scabiei (var. hominis). Factors such as crude population, poor economic and sanitation and immunosuppression in individuals can be considered as risk factors. Norwegian scabies is a severe clinical form observed in immunocompromised patients (e.g., IDS, leukemia, diabetes, transplants and immunosuppression therapy) cases characterized by the presence of a large number of parasites in the horny layer of the skin in all stages (ova, larvae and adults), hyperkratinization and thick crusts in many parts of the body. Methods: For diagnosis, scraping from the skin of lesions of patients and smear preparation with 20% KOH and microscopic examination indicated the Demodex folliculorum or sarcoptes scabiei. Results: 6 mg of ivermectin taken orally twice daily at 2-weeks intervals and 1% cream reduced the average number of Demodex mites in chronic demodicosis. For scabies administration of 5% permethrin ointment for two weeks is effective. Conclusion: Local and systemic corticosteroids are contraindicated in any patient diagnosed with demodicosis or scabies. Secondary bacterial infections must be treated aggressively with an appropriate antimicrobial. Keywords: Demodicosis, scabies, neglected diseases.

Keywords: Demodicosis, Scabies, Neglected Diseases

P175

Challenges in Diagnosing Strongyloides Stercoralis and Advances in Detection Methods Introduction

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Introduction Strongyloides stercoralis is a soil-transmitted helminth responsible for strongyloidiasis, a neglected tropical disease. The parasite can persist asymptomatically for decades, but in immunocompromised hosts, it may cause life-threatening hyperinfection. Traditional diagnostic methods often lack sensitivity, necessitating improved diagnostic strategies. Methods This review synthesizes recent studies evaluating different diagnostic techniques, including parasitological, serological, molecular, and next-generation sequencing (NGS) approaches. Microscopy, seroassays (e.g., ELISA), immunochromatographic rapid tests, and polymerase chain reaction (PCR)-based methods were compared for their accuracy, sensitivity, and applicability. Results Parasitological methods such as stool microscopy remain widely used but are insufficient due to intermittent larval shedding. Serological assays, particularly ELISA, show higher sensitivity but lack specificity in endemic area. Molecular approaches, such as real-time PCR and sequencing, have demonstrated superior sensitivity and specificity. Novel methods, including metagenomic NGS, have successfully identified Strongyloides stercoralis in patients where conventional tests failed. Rapid diagnostic tests (RDTs) using recombinant antigens have shown promise for field use, particularly for prevalence studies. Conclusion Accurate diagnosis of Strongyloides stercoralis remains challenging due to the parasite's unique life cycle and low larval excretion. Combining multiple diagnostic methods enhances detection rates. Recent advancements, particularly molecular and antigen-based techniques, offer promising solutions for timely and reliable diagnosis, crucial for treatment and disease control.

Keywords: Strongyloides Stercoralis, Diagnosis, Molecular Methods, Serology, Next-Generation Sequencing

P176

Review of Novel Methods for Reducing Infection Risk in Blood Transfusion

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IACLD Travel award for attending to QICL & IRAN Lab EXPO, TEHRAN, 2025 Blood transfusion is a critical medical procedure that saves millions of lives worldwide. However, it carries inherent risks, including the transmission of infectious diseases. Ensuring the safety of blood transfusion has been a primary focus of medical research and public health policies. This paper provides an in-depth review of the fundamentals of blood transfusion, its significance, and modern approaches to minimizing infection risks. The implementation of Nucleic Acid Testing (NAT), enhanced donor screening, and pathogen inactivation techniques has significantly reduced transfusion-related infections. This paper also explores the role of next-generation screening technologies and continuous monitoring systems in improving blood safety. With further research and technological advancements, the risks associated with blood transfusion can be minimized, ensuring a safer and more effective transfusion process.

Keywords: Blood Transfusion, Infection Risk, Nucleic Acid Testing, Pathogen Inactivation, Blood Safety

P177

CoQ10 Enhances Therapeutic Efficacy of Adipose-Derived Mesenchymal Stem Cells in a Rat Model of Alzheimer's Disease

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Background: Mesenchymal stem cell (MSC) transplantation shows promise for treating neurodegenerative diseases like Alzheimer's, but poor MSC survival after transplantation limits its effectiveness. This study investigates whether pre-treating MSCs with the antioxidant coenzyme Q10 (CoQ10) can enhance their therapeutic effect in a rat model of Alzheimer's disease. Methods: MSCs treated with CoQ10 were studied in vitro for survival and growth. A rat model of Alzheimer's disease was created by injecting Aβ1-42 into the hippocampus. Rats then received transplants of CoQ10-preconditioned MSCs, and their spatial learning and memory were tested using the Morris water maze. Gene expression related to inflammation, cell death (apoptosis), and nerve growth factors (neurotrophins) in the hippocampus was measured using RT-qPCR. Results: CoQ10 preconditioning boosted MSC growth and survival in vitro by increasing EGF protein levels (Western blot). In Aβ-AD rats, these preconditioned MSCs improved learning and spatial memory. Additionally, they protected the hippocampus by reducing inflammatory cytokines (TNF-α, IL-6, IL-1β) and apoptotic markers (Bax, caspase 3, cytochrome c), while increasing the anti-apoptotic marker Bcl2 and neurotrophins (BDNF, NGF). Conclusions: Preconditioning MSCs with CoQ10 boosted the therapeutic efficacy of these cells. Therefore, it could serve as a targeted strategy for increasing the therapeutic efficacy of MSCs in treating neurodegenerative disorders, including AD.

Keywords: Alzheimer’s Disease, MSC, CoQ10, Preconditioning, Apoptosis, Neurotrophic Factor

P178

The Persistence of Leishmaniasis in the Host: From Host-Parasite Molecular Interactions to the Design of Targeted Therapeutic Strategies

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Introduction: Leishmaniasis, a neglected parasitic disease with diverse clinical manifestations ranging from cutaneous to fatal visceral forms, remains a global therapeutic challenge due to the complex immune evasion mechanisms of Leishmania and the inability to establish long-lasting immunity. Method: This study conducted a comprehensive review of articles from reputable scientific databases, including PubMed, Scopus, and Web of Science, to analyze host-parasite interactions, parasite survival strategies, and innate/adaptive immune responses. Findings: Studies indicate that Leishmania achieves "silent" entry into macrophages via CR3/mannose receptors and inhibits ROS production, thereby evading innate immune responses. Virulence factors such as lipophosphoglycan (LPG), which delays phagolysosome maturation, and GP63, which inhibits MAPK/PKC signaling pathways, facilitate intracellular survival. Additionally, the downregulation of MHC-II and CD80/86 expression on macrophages, coupled with IL-10 and TGF-β secretion, suppresses the Th1 response while activating regulatory T cells (Tregs). Conversely, Th2-driven immune responses promote parasite proliferation by inducing arginase-1 and polyamine production. Furthermore, Leishmania mimics host chemokines, such as MCP-1, to misdirect immune cell migration to non-strategic sites and inhibits the IFN-γ/JAK/STAT1 pathway through phosphatases like SHP-1, ultimately suppressing nitric oxide (NO) production. Notably, humoral immunity is non-protective; antibodies, through FcγR binding on macrophages, facilitate parasite entry via antibody-dependent enhancement (ADE). Conclusion: Disrupting the parasite's immune evasion cycle necessitates simultaneous targeting of virulence factors (LPG/GP63), augmentation of Th1/cytotoxic T cell responses, and suppression of IL-10/TGF-β signaling. Integrating cutting-edge technologies such as mRNA vaccines and nanoparticle-based therapies presents the most promising avenue for achieving durable immunity and ultimately eradicating this pathogen.

Keywords: Leishmania, Leishmaniasis, Host-Parasite Interaction, Immune Response, Targeted Therapies

P179

Prognostic Implications of Platelet Indices in Acute Myeloid Leukemia Patients

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Background: Acute myeloid leukemia (AML), the most prevalent form of leukemia in adults, presents significant clinical challenges due to its heterogeneity, characterized by the clonal proliferation of immature myeloid cells and subsequent bone marrow failure. While substantial progress has been made in elucidating the molecular and cytogenetic factors underlying AML, the prognostic value of platelet indices remains relatively underexplored. This review investigated the role of platelet parameters in AML prognosis and management. Methods: Relevant data were sourced from articles published between 2014 and 2024, identified through a search of databases such as PubMed, Web of Science, and Google Scholar. Results: Emerging evidence highlights the prognostic significance of platelet metrics in AML, particularly in non-M3 subtypes. Pretreatment platelet counts correlate with overall survival, with moderate levels associated with better outcomes. In cytogenetically normal AML, the platelet-to-white blood cell ratio (PWR) inversely correlates with bone marrow blast percentages and FLT3-ITD and NPM1 mutations, predicting overall and event-free survival. PWR also identifies patients at risk of early death in acute promyelocytic leukemia. Lower platelet-to-lymphocyte ratios, decreased MPV, and elevated PDW are also linked to worse outcomes. Notably, PDW increases significantly in patients achieving remission, supporting its role in treatment response monitoring. Conclusion: Collectively, these findings underscore the clinical value of platelet indices as accessible and cost-effective biomarkers for AML prognosis and therapeutic monitoring. To optimize patient outcomes, further research is warranted to integrate these parameters into routine clinical practice.

Keywords: Acute Myeloid Leukemia, Platelet Indices, Prognosis

P180

Investigating the Expression Level of lncRNA-CARMN in Colorectal Cancer Compared to Tumor Marginal Tissue

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Background: Colorectal Cancer (CRC) is one of the deadliest cancers in the world. Using The Cancer Genome Atlas (TCGA), we analyzed RNA sequencing data for CRC. Recently, CARMN Long non-coding RNA (lncRNA) has been discovered, which significantly contributes to the occurrence of various cancers. This study aimed to determine the expression levels of this lncRNA in CRC tissues compared to tumor-adjacent tissues and the relationship of its expression with clinical characteristics. Materials and methods: In this case-control study, RNA-seq analysis of TCGA database was performed in R software and lncRNA-CARMN was identified as one of the important lncRNAs involved in this cancer. Then the expression of lncRNA-CARMN was evaluated in 20 pairs of cancerous and adjacent non-cancerous tissue samples in CRC patients using RT-qPCR. Statistical analysis and graphing of the relationship between RNA level and the clinic-pathological characteristics of CRC was carried out using SPSS and Prism 10 software. Furthermore, the Receiver Operating Characteristic (ROC) curve was drawn to represent the sensitivity and specificity of CARMN expression as biomarkers of CRC. Results: The expression of CARMN was significantly decreased in CRC specimens compared to adjacent tumor samples. Our results showed that the CARMN RNA level in CRC was significantly related to the tumor size and histopathological grade. Moreover, the ROC curve analysis of the CARMN RNA level demonstrated that this lncRNA had an appropriate sensitivity and specificity for the diagnosis goals. Conclusion: Based on the results, lncRNA-CARMN may play critical role in exacerbating and even initiating CRC due to their cellular pathways.

Keywords: Colorectal Cancer, Long Non-Coding RNA, Tumor Marker

P181

Investigating the LY96 Gene Expression in Patients with Liver Cirrhosis

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Background: Cirrhosis is widely prevalent worldwide and can be caused by nonalcoholic fatty liver disease, nonalcoholic steatohepatitis, heavy alcohol consumption, hepatitis B or C infection, autoimmune diseases, and cholestatic diseases. The lipopolysaccharide response pathway is a key pathway involved in the development of liver diseases. Several factors are involved in the response to lipopolysaccharides, one of which is lymphocyte antigen 96 (LY96). Therefore, this study aims to investigate the gene expression of LY96, a part of lipopolysaccharide response pathway in patients with liver cirrhosis. Methods: In this case–control study, the qRT-PCR analyses were carried out to determine the gene expression of the LY96 in patients with liver cirrhosis (n = 38) and control individuals (n = 10). Results: All patients with cirrhosis were etiologically divided into five groups: NASH- (n = 8), HBV/HCV- (n = 8), AIH- (n = 8), PSC- (n = 8), and ALH-related cirrhosis (n = 6). The gene expression of the LY96 was significantly decreased in the NASH group compared to the control group ($P < .05$), whereas in the PSC group, there was a notable increase in the expression of this gene relative to the control group ($P < .05$). No significant changes in LY96 gene expression were observed in the other groups compared to healthy individuals. Conclusion: This study increases our understanding of the response to lipopolysaccharide pathway and the role of related genes such as LY96 in liver cirrhosis.

Keywords: Cirrhosis, Response to Lipopolysaccharide, LY96

P182

Citrullinemia Type 1 Without Orotic Aciduria

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IACLD Travel award for attending to QICL & IRAN Lab EXPO, TEHRAN, 2025 Background and Aim: Citrullinemia is a urea cycle disorder characterized by elevated blood ammonia levels. It has two distinct types. Mutations in the ASS1 gene lead to type 1 citrullinemia, resulting in a deficiency of argininosuccinate synthetase. This deficiency decreases argininosuccinate and increases citrulline levels in patients. Type 1, also known as classic citrullinemia, typically manifests in the first days of life. In contrast, mutations in the ASL gene cause type 2 citrullinemia due to argininosuccinate lyase deficiency, leading to elevated argininosuccinate and citrulline levels. Type 2 is associated with late symptoms, including severe headaches. Notably, some individuals with type 1 mutations remain asymptomatic throughout life. Methods: A 5-day-old newborn was flagged for abnormal citrulline levels during metabolic disease screening using the LC-MS/MS method. The blood ammonia level was normal. The parents were consanguineous and had a healthy child. To confirm the diagnosis, plasma citrulline and blood ammonia levels were periodically monitored for four months. In all cases, citrulline remained elevated while ammonia remained normal. Organic aciduria screening showed normal results. Further genetic testing confirmed type 1 citrullinemia. Results: Initial newborn screening via LC-MS/MS in a dried blood spot (DBS) sample showed a citrulline level of 547 Umol/L (cut off > 26.70 Umol/L). Follow-up tests at several-month intervals revealed citrulline levels of 1712, 2683, and 1876 Umol/L, respectively. Organic aciduria analysis by GC-MS indicated positive orotic acid excretion. citrulline type 1 variant C.40 G>A (AAS1 gene) was confirmed in the whole exome sequencing (WES) genetic test. Conclusion: Newborn metabolic disease screening (2–7 days old) using MS/MS is crucial for early detection of citrullinemia. Citrulline serves as a primary screening marker for the disorder. A milder form may appear later in childhood or adulthood, presenting with neurological symptoms. Early diagnosis through metabolic screening is essential for timely intervention and management.

Keywords: Citrullinemia, Arginosuccinic Acid Synthetase, LC-MS/MS

P183

Can Curcumin Supplementation Reduce Inflammatory and Oxidative Stress Levels in Migraine Patients? Findings from a Randomized Controlled Trial

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Introduction Curcumin is widely recognized for its numerous health benefits, particularly its antioxidant and anti-neuroinflammatory effects, making it a promising candidate for migraine treatment. Despite its therapeutic potential, no previous research has assessed the effectiveness of phytosomal curcumin—a formulation designed to cross the blood-brain barrier (BBB)—in migraine patients. This randomized controlled trial (RCT) investigated the impact of phytosomal curcumin supplementation on oxidative stress biomarkers, including malondialdehyde (MDA), superoxide dismutase (SOD), total antioxidant capacity (TAC), total oxidant status (TOS), nitric oxide (NO), and the inflammatory marker high-sensitivity C-reactive protein (hs-CRP) in individuals suffering from migraines. Materials and Methods This study was a double-blind, placebo-controlled trial involving 70 individuals diagnosed with migraines. Participants were randomly divided into two groups: the intervention group received a daily dose of 250 mg phytosomal curcumin, while the placebo group was given 250 mg of maltodextrin. The intervention period lasted for eight weeks, during which key inflammatory and oxidative stress markers, including hs-CRP, NO, and other relevant biomarkers, were assessed before and after supplementation. Results Compared to the placebo group, the participants who received phytosomal curcumin experienced a significant reduction in blood nitric oxide levels (P=0.003) and total oxidant status (P=0.043). Additionally, a significant increase in total antioxidant capacity (P=0.041) was observed. However, supplementation did not produce a statistically significant effect on hs-CRP, MDA, or SOD levels (P>0.05). Importantly, no adverse effects were reported by any participants throughout the study. Conclusion Phytosomal curcumin appears to reduce nitric oxide (NO) and total oxidant status (TOS) while boosting total antioxidant capacity (TAC). These findings suggest its potential as a therapeutic option for migraine patients. However, additional large-scale, well-structured RCTs are necessary to validate these results.

Keywords: Curcumin, Migraine, Nitric Oxide, Oxidative Stress, Inflammation

P184

Comparison of Two Methods for Acid α-Glucosidase Assays in Dried Blood Spot Samples Using Fluorimetry for Evaluation of Glycogen Storage Disease Type II in Iranian Population

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Background: Glycogen Storage Disease Type II (GSD II), known as Pompe disease, is a life-threatening lysosomal storage disorder, necessitates early and precise detection. Advancing newborn screening improves diagnostic accuracy and clinical efficiency. Methods: The study assessed seven analytical parameters via three enzyme activities in dried blood-spots (DBS) using fluorimetry across two methods: reference method (method I) and developed method (method II), in 141 healthy individuals, 8 GSD II patients, and 10 obligate heterozygotes. Results: Both methods demonstrated strong linearity (R^2 = 0.999). The limits of detection (LOD) and quantification (LOQ) were 0.045 µmol/punch/L and 0.136 µmol/punch/L for method I, and 0.043 µmol/punch/L and 0.129 µmol/punch/L for method II. Intra-day precision was 10.45% for method I and 13.61% for method II, while inter-day precision was 15.99% and 15.43%, respectively. Both methods assessed acid α-glucosidase (GAA), total GAA (tGAA), total neutral α-glucosidase (NAG) activities, NAG/GAA ratio, inhibition percentage, pH ratio, and the percentage of tGAA inhibited by acarbose at pH = 3.8 (method I) or pH = 4 (method II). Receiver operating characteristic (ROC) curves analysis determined cut-off values for NAG/GAA as >17.94 (method I) and >36.04 (method II), and for pH ratio as <9.805 (method I) and <7.113 (method II). Both methods exhibited accuracy, sensitivity, and specificity of 100%. Method II required only 3 hours of incubation, significantly shorter than the 20-hour duration of method I. Conclusions: Both methods effectively differentiated GSD II patients from healthy individuals, with method II offering a more rapid and practical option for clinical implementation.

Keywords: Acid α-Glucosidase, Pompe Disease, Glycogen Storage Disease Type II, Dried Blood Spot Sample (DBS), Iranian Population

P185

Conditioned Medium of Human Umbilical Cord Stem Cells (hMSC-CM) Reduces Oxidative Stress Factors in Blood in CCl4-Induced Chronic Liver Injury

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Introduction: Treatment of rats with CCL4 causes chronic liver damage, and this method is considered one of the models of liver fibrosis and cirrhosis. According to previous studies, the pathogenesis of liver damage induced by carbon tetrachloride is related to the induction of oxidative stress by this toxin. Considering the antioxidant effects of conditioned media derived from mesenchymal stem cells (hMSC-CM) in improving the level of oxidative stress parameters in acute and chronic liver injuries, present study evaluated the effect of this treatment on oxidative stress-related parameters in blood samples of rats treated with carbon tetrachloride. Material and methods: Twenty-five male wistar rats were prepared from Animal Laboratory of Hamadan University of Medical Sciences, Hamadan, Iran. The rats were divided in to five group, including: N (received normal saline), F8 and F12 (received olive oil: CCl4 with 1:1 ratio, 1mg/kg, twice in week for eight and 12 weeks), FC8 (received CCl4 similar with F8 group and hMSC-CM 100µg/kg for four week from fifth week) and F12 (received CCl4 similar with F12 group and hMSC-CM 100µg/kg for eight week from fifth week). Twenty-four hour after last treatment, Total antioxidant capacity (TAC), Total oxidant status (TOS) and Malondialdehyde (MDA) of serum sample of each rats was measured by calorimetric methods. Results: Intraperitoneal injection of CCl4 significantly reduced TAC in both groups treated with this toxin. Injection of CCl4 also increased the levels of two parameters, TOS and MDA, in serum samples prepared from these two groups. Treatment with hMSC-CM significantly prevented the decrease in serum TAC levels and increased serum TOS and MDA levels in the FC8 and FC12 groups. Conclusion: According to finding of present study hMSC-CM treatment improve CCl4-induced oxidative stress.

Keywords: Liver, Oxidative Stress, hMSC-CM

P186

Design of a Novel Multi-Epitope Vaccine Design Against Dengue Virus via Integrated Reverse Vaccinology, Immunoinformatics, and Molecular Dynamics Approaches

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Background: Dengue virus (DENV), a member of the Flaviviridae family, poses a significant global health burden, with an estimated 100–400 million annual infections. The absence of universally effective vaccines and risks associated with antibody-dependent enhancement (ADE) underscore the need for innovative strategies. This study aimed to design a novel multi-epitope subunit vaccine targeting conserved immunogenic regions of DENV structural proteins (C, E, and prM) using an integrated reverse vaccinology and immunoinformatics approach. Methods: Conserved domains of the C, E, and prM proteins were identified and screened for B-cell, MHC-I, and MHC-II epitopes via immunoinformatics tools. Five conserved epitopes were identified between the four dengue genotypes I, II, III, IV. Five selected epitopes were fused with GPGPG, EAAAK and AAA linkers to construct a chimeric vaccine. The construct's antigenicity, solubility, physicochemical properties, and non-allergenicity were rigorously evaluated. A 3D structure was modeled, refined, and validated. Molecular docking with TLR3 and 100 ns molecular dynamics (MD) simulations assessed the vaccine's stability and binding affinity to immune receptors. Immune response predictions were performed using C-ImmSim, while codon optimization and in silico cloning into the pET28a(+) plasmid ensured efficient expression in E. coli. Results: The designed vaccine demonstrated high antigenicity, structural stability, and non-allergenicity. Docking analysis revealed strong interactions with TLR3, and MD simulations confirmed structural stability under physiological conditions. Immune simulations predicted robust humoral and cellular responses, including elevated levels of IgG, IFN-γ, and memory B/T cell activation. Codon adaptation index (CAI) of 0.98 and GC content of 53% indicated high expression potential in E. coli. Conclusion: The proposed multi-epitope vaccine exhibits strong potential to induce protective immune responses against DENV. Its design integrates reverse vaccinology, immunoinformatics, and molecular dynamics, offering a promising candidate for experimental validation and clinical development.

Keywords: Dengue Virus, Multi-Epitope Vaccine, Reverse Vaccinology, Immunoinformatics, Molecular Dynamics

P187

Hypoxic Harmony in Rheumatoid Arthritis: Anemia-Driven HIF-1α/HIF-2α Upregulation Outshines Disease Activity in Systemic Inflammation

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Background: Rheumatoid arthritis (RA), a chronic inflammatory disease, is frequently complicated by anemia, often linked to hypoxia-driven pathways. Hypoxia-inducible factors (HIF-1α and HIF-2α) regulate cellular adaptation to low oxygen, yet their interplay with anemia and disease activity in RA remains unclear. This study elucidates the differential roles of systemic versus local hypoxia in modulating HIF isoforms in RA. Methods: Peripheral blood mononuclear cells (PBMCs) from 100 RA patients (33% anemic, 67% non-anemic) were analyzed. RNA was extracted, reverse-transcribed to cDNA, and HIF-1α/HIF-2α expression quantified via SYBR Green-based real-time PCR. Disease activity was stratified using the DAS28-ESR index (integrating clinical criteria and erythrocyte sedimentation rate), categorizing patients into remission (16%) or active RA (84%). Statistical analyses included Mann-Whitney U, Spearman's correlation, and significance thresholds ($p < 0.05$). Results: Anemic RA patients exhibited significant upregulation of HIF-1α (5.09-fold, $p = 0.003$) and HIF-2α (12.66-fold, $p = 0.009$) compared to non-anemic patients, implicating anemia-driven systemic hypoxia as a dominant regulator. In contrast, active RA patients showed only non-significant elevations in HIF-1α (3.81-fold) and HIF-2α (1.5-fold) versus remission, suggesting localized joint hypoxia may overshadow systemic effects in PBMCs. HIF-1α and HIF-2α expression correlated strongly cohorts ($\rho = 0.603$, $p = 8.22 \times 10{-}10$), reflecting synergistic hypoxic adaptation. Conclusion: This study identifies anemia-associated systemic hypoxia, rather than RA disease activity, as the primary driver of HIF-1α/HIF-2α overexpression. The robust correlation between isoforms underscores their cooperative role in hypoxic responses. Targeting systemic hypoxia pathways may offer novel strategies for managing RA-related anemia, while localized HIF modulation in joints warrants further exploration. Keywords: HIF-1α, HIF-2α, Rheumatoid Arthritis, Anemia, Hypoxia.

Keywords: HIF-1α, HIF-2α, Rheumatoid Arthritis, Anemia, Hypoxia

P188

"Theranostic Nanoparticles and Immune Checkpoint Inhibitors: A Combined Strategy for Cancer Management"

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Cancer remains a significant challenge in modern medicine, with limited treatment options and poor patient outcomes. Recent advances in nanotechnology and immunotherapy have led to the development of innovative strategies, including theranostic metal nanoparticles and immune checkpoint inhibitors. Theranostic metal nanoparticles offer a multifunctional platform for cancer diagnosis, imaging, and treatment, while immune checkpoint inhibitors have shown promise in enhancing anti-tumor immune responses. This presentation will explore the potential of combining theranostic metal nanoparticles with immune checkpoint inhibitors as a novel strategy for cancer management. We will discuss the current state of research in this area, including the mechanisms of action, benefits, and limitations of theranostic metal nanoparticles and immune checkpoint inhibitors. We will also examine the potential of this combined approach to enhance cancer treatment outcomes, improve patient care, and overcome the limitations of current therapies. Our goal is to provide a comprehensive overview of the current research in this area and to discuss future directions for the development of this innovative cancer treatment strategy.

Keywords: Theranostic Metal Nanoparticles, Immune Checkpoint Inhibitors, Cancer Management, Nanotechnology, Immunotherapy

P189

Evaluation of the Frequency and Antibiotic Resistance Pattern of Isolates from Urinary Tract Infection in Patients Referred to Kian Mahallat Laboratory in the First Six Months of 2024

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Introduction: Knowledge of the common bacteria that cause urinary tract infections and their antibiotic resistance patterns is important for prescribing appropriate antibiotics and preventing drug resistance. The aim of this study was to investigate the frequency of bacterial agents of urinary tract infections and to determine antibiotic resistance in patients referred to Kian laboratory in Mahallat city in the first 6 months of 2024. Method: In this descriptive cross-sectional study, urine samples of 1579 patients referred to Kian Mahallat laboratory were examined. The bacteria causing urinary tract infections were identified by standard microbiological methods down to the species level. The antibiotic susceptibility of the isolated bacteria to routine antibiotics was determined by disk diffusion method based on the Standard Institue (CLSI) Clinical & Laboratory Standard and was reported as sensitive, semi-susceptible and refractory. Data were analyzed using SPSS 18 software. Results: Out of 1579 patients, 159 had urinary tract infections. In this study, 75.3% of patients with urinary tract infection were women. Escherichia coli (45.2%), Staphylococcus saperphyticus (28.3%) and Klebsiella pneumoniae (13.8%) were the most common isolated organisms. The highest percentage of antibiotic resistance was obtained in Escherichia coli ciprofloxacin (24.5%). Of the 159 isolates studied, 30 (18.8%) were ESBL positive and 10 isolates (6.2%) showed multidrug resistance (MDR) in addition to ESBL production. Discussion & Conclusions: Escherichia coli and Staphylococcus saprophyticus were the most common causative agents of urinary tract infections. It is necessary to provide resistance information to doctors in order to prescribe the correct antibiotic.

Keywords: Antibiotic Resistance, Urinary Tract Infection, Antibiogram, Mahallat

P190

How Cyclin-Dependent Kinases (CDKs) Take Control of Tumorigenesis, from the Biology of CDKs to Their Participation in the Malignancy Formation

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The discussion on cell proliferation cannot be continued without taking a look at the cell cycle regulatory machinery. Cyclin-dependent kinases (CDKs), cyclins, and CDK inhibitors are valuable members of this system and their equilibrium guarantees the proper progression of the cell cycle. As expected, any dysregulation in the expression or function of these components can provide a platform for excessive cell proliferation leading to tumorigenesis. The high frequency of CDK abnormalities in human cancer together with their druggable structure has raised the possibility that perhaps designing a series of inhibitors targeting CDKs might be advantageous for restricting the survival of the tumor cells. In the present review, we aimed to take a look at the biology of CDKs and then magnify their contribution to the tumorigenesis. Then, by arguing the bright and the dark aspects of CDK inhibition in the treatment of human cancers, we intend to reach a consensus on the application of these inhibitors in clinical settings. Conclusion and future perspective: The latest advances in drug discovery of kinase inhibitors have made it possible to design mono-specific CDK inhibitors, this time by targeting other regions rather than the ATP active-binding sites. Inhibitors could be designed to interact with the allosteric region, target the inactive conformation, create the covalent ligand, and interfere with the binding of substrate. It is postulated that these classes of inhibitors might have lower toxic effects, better pharmacokinetic properties, and higher anti-cancer activities that could reduce the survival of all types of malignancies. Taking advantage of these, CDK inhibitors might have a long way to receive approval for the treatment of human cancers, but, their development could shed a ray of hope for cancer patients, especially those who suffer from chronic malignancies.

Keywords: Cyclin-Dependent Kinases, CDK, Cyclin, Cell Cycle, Cancer, CDK Inhibitors

P191

The Effect of Vitamin D3 on the Function of Glucantime®-Resistant and Sensitive Leishmania Tropica

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Introduction: Leishmaniasis remains a global health challenge despite control efforts. The search for effective treatments continues, with WHO advocating for novel pharmaceuticals and combination therapies. This study evaluates the effect of 1,25(OH)2-Vitamin D3 on Leishmania tropica-infected macrophages to evaluate treatment efficacy. Materials and Methods:This study investigated the anti-leishmanial effects and toxicity of Vitamin D3 and meglumine antimoniate (Glucantime®), both individually and in combination, at concentrations ranging from 0 to 200 µM. The study was conducted against two isolates of L. tropica: one responsive and one non-responsive to Glucantime®, as well as on mouse macrophage cells infected with these two isolates. Results: Both Vitamin D3 and its combination with Glucantime® reduced promastigotes and amastigotes in macrophages, with more favorable drug profiles observed in responsive isolates. Conclusion: Vitamin D3 and Glucantime® combination effectively treats L. tropica by boosting immune responses, inhibiting parasite growth.

Keywords: Vitamin D, Cutaneous Leishmaniasis, Leishmania Tropica, Drug Resistance, Macrophage

P192

Donor Pre-Transplant IFN-γ/TGF-β Ratio Predicts Graft-Versus-Host Disease-Free Survival in Allogeneic Hematopoietic Stem Cell Transplantation

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Background: Acute graft-versus-host disease (aGVHD) remains a significant complication of allogeneic hematopoietic stem cell transplantation (allo-HSCT). Predictive biomarkers for aGVHD risk, particularly those derived from donors prior to transplantation, are needed to improve risk stratification and donor selection. Objective: To investigate the association of donor pre-Transplantation interferon-gamma (IFN-γ), transforming growth factor-beta (TGF-β) levels and their ratio with the incidence of acute GVHD in allo-HSCT recipients. Methods: We conducted a prospective cohort study of 20 adult allo-HSCT donor-recipient pairs at a single center. Serum IFN-γ and TGF-β levels in donor peripheral blood mononuclear cells were measured before and after G-CSF administration. Graft-versus-host disease-free survival was analyzed using Parametric curves, log-rank tests, and parametric exponential regression. Results: The cumulative incidence of aGVHD at 100 days post-transplantation was 70%. Parametric and log-rank analyses revealed a significant association between higher donor IFN-γ/TGF-β ratio and improved GVHD-free survival (log-rank p=0.026). Parametric exponential regression confirmed a statistically significant inverse association, with a hazard ratio of 0.28 (95% CI 0.09-0.83, p=0.005) for a unit increase in pre-Transplantation IFN-γ/TGF-β ratio. Conclusion: A higher donor pre-Transplantation IFN-γ/TGF-β ratio is associated with improved GVHD-free survival in allo-HSCT recipients and may serve as a potential pre-transplant biomarker for aGVHD risk stratification. These findings highlight the importance of pre-transplant donor immune balance in allo-HSCT outcomes. Further validation in larger, multi-center cohorts is warranted.

Keywords: Allogeneic Hematopoietic Stem Cell Transplantation, Acute Graft-Versus-Host Disease, Interferon-gamma, Transforming Growth Factor-Beta, Donor

P193

Investigation of the Role of Human Herpes Virus in the Occurrence of Pityriasis rosea

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Introduction: Pityriasis rosea (PR) is a common, self-limiting dermatologic condition characterized by pink, scaly lesions, typically resolving within 2 to 6 months. However, some cases become resistant to treatment. Recent studies suggest that PR may be triggered by human herpesviruses, particularly herpes simplex virus type 2 (HSV-2), which can remain dormant and reactivate. The immune system, including pattern recognition receptors (TLRs) and proinflammatory cytokines such as IL-22, may play a significant role in PR's pathogenesis. Methods: A systematic review was performed by searching PubMed, Google Scholar, and Scopus for studies published between 2010 and 2024. Keywords included "human herpesvirus," "pityriasis rosea," "immune system," "TLR receptors," and "proinflammatory cytokines." A total of 27 relevant studies were included for further analysis. Results: The review confirmed that herpesviruses, particularly HSV-2, HHV-6, and HHV-7, are closely linked to PR. Elevated IgM antibody levels suggest active viral infection, and the presence of viral DNA was detected in plasma, peripheral blood mononuclear cells (PBMC), and skin biopsies. Additionally, higher expression levels of TLR2, TLR4, and TLR9, along with increased IL-22 levels, were associated with more severe symptoms of PR. Discussion: The findings suggest that herpesviruses, especially HSV-2, trigger immune responses through TLR receptors, contributing to inflammation and the development of PR. IL-22 plays a key role in amplifying these inflammatory processes. Targeting these immune pathways may offer new therapeutic strategies for managing PR. Moreover, modern diagnostic techniques, including quantitative PCR and antibody testing, can improve the detection and timely treatment of PR, potentially enhancing patient outcomes.

Keywords: Pityriasis rosea (PR), Human Herpesvirus, HSV-2, Virus Activation, Immune Response

P194

The Role of Myrtus Communis L. Compounds against Aspergillus Species through Carboxyaminoimidazole Synthase Pathways: an in Silico Study

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Background: N (5)-Carboxyaminoimidazole ribonucleotide synthetase (N (5)-CAIR synthetase), catalyzes the conversion of aminoimidazole ribonucleotide (AIR) to N (5)-CAIR. This enzyme has been observed only in microorganisms such as fungi. Finding the components that inhibit N (5)-CAIR synthetase is vital for developing novel therapeutic strategies against fungal pathogens. In this study, we aimed to employ molecular docking studies to simulate the binding interactions between bioactive compounds of Myrtus communis L and the N (5)-CAIR of Aspergillus spp., for the identification of optimal binding poses and estimation of binding affinities. Methods: In the study conducted by Thykaer et al, potential targets for exploring anti-Aspergillus effects were identified. These receptor names were then searched within the RCSB Protein Data Bank (https://www.rcsb.org). The molecular structures of bioactive compounds of Myrtus communis L including alpha-pinene, 1,8-cineole, linalool, alpha-terpineol, and (+)-2-carene were obtained from the PubChem database in 3D SDF format and imported into the Molecular Operating Environment (MOE 2019.0102) workspace. Following ligand-target prediction, molecular docking was carried out on the most probable targets to elucidate potential mechanisms of action. Data analysis was conducted using SPSS version 26 software. A confidence interval of less than 0.05 was considered significant in all tests. Results: The corresponding molecular docking scores of bioactive compounds of Myrtus communis L including alpha-pinene, 1,8-cineole, linalool, alpha-terpineol, and (+)-2-carene with N (5)-CAIR were -8.117, -10.935, -11.138, -11.802 and -8.019 7 kcal/mol respectively. Compared to other compounds, the alpha-terpineol with the lowest molecular docking scores (-11.802 kcal/mol) has a stronger binding affinity for N (5)-CAIR. Conclusion: Utilizing molecular docking provided insights into the mechanisms by which these phytochemicals exert their antifungal effects, identifying compounds such as linalool and alpha-terpineol as promising candidates with high binding affinities to key fungal enzymes, N (5)-CAIR (docking score less than -11).

Keywords: Aspergillus Species, Myrtus Communis L, Alpha-Terpineol, Carboxyaminoimidazole Synthase

P195

Pre-Transplant Risk Stratification in Allogeneic HSCT: Prognostic Utility of Liver Enzymes, Donor Thrombocytopenia, G6PD Status, and Disease Subtype

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Background Precise pre-transplant risk stratification is paramount in allogeneic hematopoietic stem cell transplantation (allo-HSCT) to optimize treatment strategies and improve patient outcomes. This study investigated associations between routine pre-transplant laboratory values, clinical factors, and 5-year survival in Iranian allo-HSCT recipients. Methods We conducted a retrospective analysis of 94 patients undergoing allo-HSCT at a tertiary center (2015-2024). Diagnoses included AML (n=57), ALL (n=14), MDS (n=4), myelofibrosis (n=2), aplastic anemia (n=8), and CML (n=3). Using Gompertz proportional hazards modeling (selected via AIC/BIC criteria), we assessed the impact of pre-transplant biomarkers on 5-year overall survival with an exploratory significance threshold of $p<0.1$. Findings Primary disease diagnosis significantly influenced survival, ranging from 415 days median for MDS to 2373 days for ALL. In parametric survival analysis, each 10-unit increase in ALT and AST was associated with increased mortality risk (HR=1.074, 95%CI:0.995-1.160 and HR=1.164, 95%CI:0.992-1.366, respectively). Notably, donor thrombocytopenia (<150,000/μL) strongly predicted poorer recipient survival (HR=20.36, p=0.0047). G6PD deficiency in recipients significantly increased mortality risk (HR=4.95, p=0.009). Pre-transplant recipient neutropenia (HR=2.06, p=0.055) and older recipient age (HR=2.84, p=0.052) showed trends toward higher mortality. Increased donor hemoglobin was associated with higher mortality hazard (HR=1.02, p=0.045). Interpretation Pre-transplant liver enzymes, donor thrombocytopenia, recipient G6PD deficiency, donor hemoglobin, recipient neutropenia, and recipient age emerge as potential prognostic biomarkers for post-allo-HSCT survival. These readily available assessments may contribute to refined risk stratification, potentially informing personalized transplant management strategies. Multi-institutional validation studies are needed to develop robust risk prediction models.

Keywords: Allogeneic HSCT, Risk Stratification, Donor Thrombocytopenia, G6PD Deficiency, Liver Enzymes

P196

Dual Role of Netosis in Parasitic Infections: Protective Immunity or Inducer of Tissue Damage?

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Introduction and Objective: Netosis is an innate immune process carried out by neutrophils to combat parasites. During this process, extracellular traps (NETs) comprise DNA, histones, and antimicrobial proteins that help the body fight off infections. This article aims to look at how netosis affects the immune system in response to helminth and protozoan infections, as well as the damage it causes to tissue. Methodology: We did a study using keywords from databases like PubMed, Google Scholar, and Scopus that had to do with netosis, neutrophil extracellular traps (NETs), parasitic infections, innate immunity, helminths, protozoa, inflammation, and tissue damage. A total of 25 articles from 2009 to 2024 were selected and analyzed. Results: The results indicate that NETs play a significant role in the immune response by trapping and eliminating parasites in the extracellular space. Stimuli such as cytokines can stimulate NET formation and assist in the defense against parasites. In protozoan infections like severe malaria, NETs may contribute to vascular obstruction and blood-brain barrier damage. In other infections, this process can lead to inflammation and tissue destruction. Discussion: Netosis is an active defense mechanism against parasites, but in certain infections, it may cause tissue damage and trigger inflammatory responses. In helminth infections, NETs might have negative effects, while in protozoan infections, they generally serve as an effective defense. The dual role of NETs in parasitic infections requires further investigation to better understand their effects on immune mechanisms and the damage they may cause.

Keywords: Netosis, Neutrophil Extracellular Traps (NETs), Parasitic Infections, Innate Immunity, Inflammation

P197

Platelet-Leukocyte Aggregate (PLA): A Novel Insight into Acute Coronary Syndrome Diagnosis

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Somayeh Yazdanparast 1,2, Mohammad Ghorbani 3,4, Mohsen Hamidpour 3. Background: The rupture of atherosclerotic plaques in coronary arteries is the fundamental pathophysiology of acute coronary syndrome (ACS). The biochemical and cellular phases can be considered the atherosclerosis process. In the cellular phase, leukocytes and platelets in the presence of cytokines trigger platelet-leukocyte aggregate (PLA) formation. Among leukocytes, monocytes and neutrophils play pivotal roles which leads to platelet-monocyte aggregate (PMA) and platelet-neutrophil aggregate (PNA) formation, respectively. In this research, we aimed to investigate PMA and PNA levels in ACS patient samples to discover potential diagnostic markers. Methods: This research included 30 patients diagnosed with ACS and 24 healthy controls. The PLA (PMA and PNA) was evaluated using flow cytometry. Then, the ROC curve was determined to assess their diagnostic value. Results: The results revealed that the average PMA index was significantly higher in the patient group than in the healthy group (P-value < 0.001). Similarly, the average PNA index was considerably higher in the patient group than in the control group (P-value < 0.001). The Pearson correlation coefficient analysis revealed a direct linear but nonsignificant statistical relationship between PMA and PNA (P-value > 0.05). Finally, the under-the-curve (AUC) was 1 for PMA and 0.982 for the PNA variable indicating that PMA and PNA are the most valuable diagnostic markers for ACS. Conclusion: In summary, PMA and PNA can serve as useful diagnostic markers in patients with ACS. Consequently, targeting the formation of PMA and PNA might provide innovative strategies for ACS treatment. Nevertheless, further research is needed to examine these parameters in the clinical diagnosis of ACS.

Keywords: Acute Coronary Syndrome, Atherosclerosis, P Latelet-Leukocyte Aggregate Platelet-Monocyte Aggregate, Platelet-Neutrophil Aggregate, Diagnosis

P198

Naïve T-Cell Depletion: A New Perspective on Preventing Chronic Graft-Versus-Host Disease

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Background: Chronic graft-versus-host disease (cGVHD) is a systemic immunological and fibrotic condition that affects about half of the patients who have received unmanipulated allogeneic hematopoietic cell transplantation (allo-HCT) grafts and remains the leading cause of non-relapse mortality (NRM). Currently, manipulating graft via CD4+ depletion is known as a beneficial approach to reducing cGVHD. In this line depletion of CD45RA naïve T cells and preserving CD45RO memory T cell within graft is an innovative approach. In this narrative review, we aimed to overview on clinical trial conducted based on naïve T cell depletion in allo-HCT patients. Methods: Eligible studies were identified from the clinicaltrial.gov database. Articles in the English language were identified using the following MeSH terms and keywords chronic graft-versus-host disease, hematopoietic cell transplantation, naïve T cells. Finally, the terminated clinical trials in which their results were published are included in this review article. Results: Our comprehensive review identified three clinical trials (#NCT00914940, #NCT01858740, and #NCT02220985) conducted CD45RA naïve T cell depletion before allo-HCT. Totally 138 patients with lymphoid and myeloid hematological malignancies were involved in these trials. All patients received conditioning and GVHD prophylaxis regimens before transplantation. First, the mobilized stem cells undergo CD34+ selection followed by CD45RA depletion. Then, a manipulated graft was injected into candidate patients. The trial results outline that naïve T cell depletion accompanied by HSC engraftment, and relatively rapid immune reconstitution, remarkably decreases both acute and chronic GVHD, reduces relapse, and NRM, increases overall survival (OS), relapse-free survival (RFS), cGVHD-free, relapse-free survival (CRFS), and GVHD-free, GRFS. Conclusion: In summary, this strategy depletes CD45RA T cells as the main mediator of GVHD while preserving CD45RO memory T cells which are needed for the graft-versus-leukemia (GVL) effect. Overall, manipulating allo-HSCT is maximizing patient outcomes after transplantation while minimizing the risks of cGVHD.

Keywords: Chronic Graft-Versus-Host Disease, Hematopoietic Cell Transplantation, T Cell Depletion, Naïve T Cells

P199

Beyond Traditional Markers: Exploring lncRNAs in Saliva and Serum for Breast Cancer Diagnosis

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Objective: Given the need for non-invasive and accessible biomarkers for early breast cancer detection, this study aims to investigate the potential of long non-coding RNAs (lncRNAs) GAS5, MEG3, and HOTAIR as salivary and serum biomarkers for breast cancer and to assess the correlation between their levels in these two biological fluids. Methods: This case-control study enrolled 30 women diagnosed with breast cancer and 30 healthy women as a control group, matched for age and other relevant demographic factors. Saliva and blood samples were collected from all participants. Quantitative real-time PCR (qRT-PCR) was used to determine the expression levels of GAS5, MEG3, and HOTAIR in both serum and saliva samples. The Mann-Whitney U test was employed to compare lncRNA expression between the two groups, and Spearman correlation analysis was used to assess the relationship between serum and salivary lncRNA levels. Results: Our findings revealed a significant downregulation of GAS5 and MEG3 in both serum and saliva of breast cancer patients compared to the control group ($P < .05$). Conversely, HOTAIR expression was significantly upregulated in both serum and saliva of the breast cancer group ($P < .05$). Correlation analysis demonstrated a significant positive correlation between serum and salivary levels of GAS5 ($r = 0.65$, $P < 0.01$), MEG3 ($r = 0.72$, $P < 0.01$), and HOTAIR ($r = 0.71$, $P < 0.01$). Conclusion: This study suggests that GAS5, MEG3, and HOTAIR lncRNAs hold promise as potential biomarkers for breast cancer. The altered expression of these lncRNAs in both serum and saliva may provide a valuable tool for early detection and diagnosis of breast cancer. Further large-scale studies are warranted to validate these findings and to explore their clinical utility.

Keywords: Breast Cancer, Saliva, Serum, lncRNA, GAS5, MEG3, HOTAIR, Biomarker

P200

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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HTLV1 is responsible for two critical diseases in humans: ATLL and HAM/TSP.ATLL is a rare and progressive disease with poor prognosis. Considering the importance of ATLL, in this study, we demand by using and integrating high-throughput microarray data, to identify the most important microRNAs involved in the induction of ATLL disease by presentation of a messaging network model. Materials & Methods After purposeful search and qualitative review of obtained data, the data were processed using R software and miRNAs with different expression (DEMs) were detected based on the value of log fold change. The gene targets of miRNAs were obtained using miRDB online tool. The protein-protein interaction network of gene targets was drawn and analyzed with STRING database. The sub-network was extracted using cytoscape. Pathway analysis was done, 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 were evaluated in 10 healthy participants, 10 ACs and 10 ATLL patients using real-time PCR. Results From the data set (GSE 31629), mir-20a-5p, was identified as an important microRNA with different expression in the patient group in comparison with the healthy and asymptomatic carrier group. It was found that TGF-β signaling pathway is related to HTLV-1 pathogenesis. TGF-β1, TGFBR1 and TGFBR2, which have a key role in regulating the mentioned pathway, were selected. Real-time PCR results showed that the expression level of TGF-β1 and TGFBR2 are decreased and TGFBR1 was increased significantly in ATLL compared to healthy subjects and asymptomatic carriers. Conclusion So by drawing a model of the messaging network and the role of genes in pathogenesis, the pathways involved in carcinogenesis for treatment of patients can be identified.

Keywords: HTLV-1, ATLL, MicroRNA, Adult T Cells Leukemia Lymphoma, Human T-Lymphotropic Virus Type 1

P201

Unveiling the Shared Genetic Landscape of Rheumatoid Arthritis and Systemic Lupus Erythematosus

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Background: Rheumatoid Arthritis (RA) and Systemic Lupus Erythematosus (SLE), two prototypic autoimmune diseases, exhibit striking clinical and immunological overlaps, yet distinct phenotypes. Despite their distinct diagnostic criteria, co-occurrence in patients and shared complications such as arthritis, fatigue, and organ damage, suggest a common genetic foundation. This narrative review synthesizes cutting-edge evidence to explore the shared genetic architecture underlying their pathogenesis, offering novel insights into their coexistence, divergent trajectories, and therapeutic implications. Methods: To map the genetic crossroads between RA and SLE), this review synthesizes evidence from two decades of autoimmune research. We embarked on a multidisciplinary journey, scouring PubMed and Google Scholar for studies that dissected clinical overlaps, immunological paradoxes, and genetic whispers shared by these diseases. Articles were selected if they illuminated shared pathways (e.g., interferon signaling, cytokine dysregulation) or bridged genetic findings to clinical phenotypes. Results: Shared genetic drivers bridge RA and SLE, with STAT4, NFκB, and HLA-DRB1 emerging as key risk loci. These genes orchestrate hyperactive immune pathways (e.g., IFN-γ, NF-κB) common to both diseases. Mechanistically, STAT4 polymorphisms amplify inflammatory cytokines (IL-6, TNF-α), while HLA-DRB1 variants modulate auto-antigen presentation. Clinically, 20–30% of patients exhibit overlapping phenotypes, yet these markers offer diagnostic clarity. Shared pathways suggest therapeutic repurposing potential, such as JAK inhibitors for dual targeting. Unresolved gene-environmental interactions (e.g., smoking, epigenetics) highlight future research priorities. Conclusion: RA and SLE share a robust genetic architecture centered on immune hyperactivation, offering transformative insights into precision medicine. Targeting common pathways may yield dual-purpose therapies, while genetic biomarkers could enhance diagnostic specificity. This synthesis of genetic evidence bridges a critical gap between autoimmune theory and patient-centered care.

Keywords: Shared Genetic Susceptibility, Rheumatoid Arthritis, Systemic Lupus Erythematosus, Autoimmune Comorbidity, Immune Dysregulation

P202

Overview of Celiac Disease Tests

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Introduction: Celiac disease is an autoimmune disorder that occurs due to the body's reaction to gluten, a protein found in wheat, barley, and rye. In this article, common diagnostic tests for celiac disease are reviewed. Background: The diagnosis of celiac disease is based on a combination of clinical symptoms, serological tests, small intestinal biopsy, and genetic tests. Method: 1. Serological tests: Tissue-specific transglutaminase antibodies (tTG-IgA): This test checks for the presence of specific antibodies in the blood. Endomysial antibodies (EMA): This test also checks for the presence of specific antibodies in the blood and is highly accurate in diagnosing celiac disease. Deamidated gliadin antibodies (DGP): This test is especially useful in children under 2 years of age. 2. Small bowel biopsy: Microscopic examination of the small intestine to see the changes that are characteristic of celiac disease. 3. Genetic tests: The presence of the HLA-DQ2 and HLA-DQ8 genes can be helpful and positive in this disease. Results: High levels of specific tTG-IgA and EMA antibodies in the blood, small bowel biopsy results, and the presence of the HLA-DQ2 and HLA-DQ8 genes can increase the risk of celiac disease. Discussion and Conclusion: Serological tests, small bowel biopsy, and genetic tests are all important tools for diagnosing this disease. Combining these tests can lead to a more accurate diagnosis.

Keywords: Celiac Disease, Diagnosis, Serological Tests, Small Bowel Biopsy, Genetic Tests

P203

Importance of Nectin2, NUF2, and Nectin4 Gene Expression in the Pathogenesis of Different Subtypes of Breast Cancer

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Background: The targeted therapy using breast cancer (BC)-associated biomarkers has significantly minimized the side effects of BC treatment. This study aims to elucidate the role of Nectin2, NUF2, and Nectin4 gene expression in the pathogenesis of BC. Method: In this case-control study, the expression of Nectin2, Nectin4, and NUF2 genes was investigated through real-time polymerase chain reaction assay in 46 tumor tissues from BC patients and 46 adjacent non-tumorous tissues as a control group. Data were analyzed using SPSS-21 software, employing independent t-tests and one-way ANOVA. A P-value of <0.05 was considered statistically significant. Results: The results demonstrated a significant increase in the expression of the NUF2 gene in tumor tissues compared with adjacent normal tissues (P = 0.005, fold change = 3.7). No statistically significant difference was observed in the expression of Nectin2 and Nectin4 between the tumor and adjacent tissues. However, higher expression of Nectin2 was noted in the early stages of the disease, particularly in subtypes with estrogen receptor-positive (ER+), progesterone receptor positive (PR+), and human epidermal growth factor receptor 2 negative (HER2-). Furthermore, the expression of NUF2 and Nectin4 was elevated in advanced stages and triple-negative BC (TNBC) subtypes. Notably, the expression of these three genes was higher in patients aged ≤ 45 years. 2 Conclusion: The findings suggest that the expression levels of NUF2, Nectin2, and Nectin4 genes may influence the initiation, progression, and pathogenesis of BC subtypes.

Keywords: Triple Negative Breast Neoplasms, Biomarker, Estrogen Receptor, Progesterone Receptor

Workshop

W1-W30

W1

The Antibiotic Resistance Crisis: The Role of Antibiograms and Impact of Standardized Procedures

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Antimicrobial resistance (AMR) poses a critical global health threat, responsible for an estimated 1.3 million deaths annually. The overuse and misuse of antibiotics in humans, animals, and plants exacerbate this crisis. This workshop focuses on the pivotal role of antibiograms, laboratory tests that identify bacterial susceptibility to antibiotics and standardized procedures in combating AMR. By utilizing antibiograms effectively, healthcare providers can optimize antibiotic therapy, reducing unnecessary prescriptions that drive resistance. Standardized procedures ensure consistency across clinical settings, enhancing the reliability of antibiogram data and informing evidence-based treatment guidelines. The workshop will explore strategies for integrating antibiogram results into clinical decision-making processes and discuss how standardized protocols can improve antibiotic stewardship programs. Participants will engage with experts on best practices for implementing these tools to mitigate the spread of resistant pathogens.

Keywords: Antimicrobial Resistance, Antibiograms, Bacterial Infections, Minimum Inhibitory Concentration

W2

Laboratory Methods for Diagnosing Tuberculosis

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One-third of the world's population is infected with the Mycobacterium tuberculosis, the causative agent of tuberculosis, and the disease is among the top ten killers in the world. Mycobacterium tuberculosis generally affects the lungs, although up to one-third of cases involve other organs, such as the bones and central nervous system. Despite widespread vaccination (BCG) against it and the effectiveness of anti-tuberculosis drugs, this microorganism remains a major killer among infectious diseases worldwide. In this workshop, we will teach laboratory diagnostic methods for tuberculosis to interested parties and laboratory experts.

W3

Developing the Individual Skills of Laboratory Supervisors

Hossein Babaki *

Supervision and personal development, General principles of supervision, A summary of principles related to: Team working, Problem solving, Principles of effective relationships, Time management, Performance management, and basic leadership, Explanation of problemsolving techniques.

Keywords: General Principles of Supervision, Team Working, Problem Solving, Principles of Effective Relationships, Time Management, Performance Management, Basic Leadership

W4

Designing a Risk-Based Quality Control Plan According to CLSI EP23:2023

Narges Babadaie *

The CLSI EP23:2023 standard examines and establishes quality control procedures in clinical laboratories. It is designed to enhance the accuracy and reliability of test results and includes the following concepts and methods: 1. Definition of Quality Control: Clear definitions of quality control and its significance in laboratory processes. 2. Risk-Based Approach: Identification and assessment of risks associated with laboratory processes, along with management strategies to address them. 3. Documentation: Emphasis on the importance of documentation and the accurate recording of procedures and results. 4. Development of a Quality Plan: Guidance for creating and implementing a comprehensive quality plan within the laboratory. 5. Continuous Improvement: Encouragement for ongoing review and enhancement of processes and systems. The primary goal of this standard is to improve the quality of laboratory services and ensure patient safety by providing accurate and reliable results.

Keywords: CLSI EP23, Quality Control (QC), Risk Assessment, Quality Plan

W5

Intra-Laboratory Integration of Allowable Errors

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Evaluation of characterstics and performance monitoring of a given measurement procedure (MP) is performed by a type of judgement by using statistical criteria which may determine concurrently or are predetermined. Standard deviation derived from double testing or reported results in an extra assessment program for a peergroup, and calculated confidence interval during verification of bias or measuring interval of a given MP in a medical laboratory, are examples of statistical criteria which are determine concurrently by using of data of related study. In this case, judgement is highly affected by data derived from study. So that when fluctuations due to random errors are low, standard deviation and confidence interval become narrow and judgment will be stricter. In contrast, when these fluctuations are high, standard deviation and confidence interval become wide and judgment will be less strict. To solve this challenge, in is recommended to use predetermined criteria, such as monthly, six-month or allowable standard deviation which will result in more consistent judgement and without consideration of study random error. The ultimate judgment will be according to allowable errors which are predetermined criteria. Selection of appropriate basic allowable error for a given MP from different resources, which is for basic condition, is paramount. In addition, for different conditions which may occur during different studies, such as imprecision, bias, measuring interval, reagent lot change, and duplicate test studies, it is recommended to use modified allowable errors (mAE), which can be calculated according to factors, such as MP sigma (z), number of repeats or samples (n), considering or not considering of bias (uB), and risk factor (R). This results in integration and harmonization of judgment during studying characterstics and performance of a given MP.

Keywords: Allowable Total Error, Allowable Error, Modified Allowable Error, Integration, Harmonization

W6

Integrated Quality Management System: Knowledge and Tools

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The goal of an effective and efficient laboratory is to consistently provide the appropriate examinations with accurate results in a timely manner and with the most judicious use of resources. So, each laboratory with any size and complexity needs a quality management system (QMS) which consists an organizational structure, responsibilities, policies, processes, procedures, and resources to direct, control, and improve an organization, such as a medical laboratory, with regard to quality in a systematic and process-oriented manner. In a QMS, activities fall into two main categories, including 12 quality system essentials (QSEs) and path of workflow (POW). Each of 12 QSEs, including organization and leadership, customer focus, facilities and safety, personnel, supplier and inventory management, equipment management, process management, documents and records, information management, nonconformity event management, assessments, and continual improvement, is a building block to quality that is necessary to support any laboratory's POW from preexamination to examination to postexamination. An integrated QMS (IQMS) is needed to deliver consistent, high-quality, and cost-effective laboratory services. Using such a system, results in simplicity of ensuring laboratory-wide compliance with regulatory and accreditation requirements. NIKAQMS.com Web Application is a useful tool for medical laboratories which facilitates and simplifies designing, implementation and maintenance of an IQMS through effective coordination and integration of the 12 QSEs as a balanced system to manage the quality of the laboratory's POW.

Keywords: Quality Management System, QMS, Integrated Quality Management System, IQMS, Quality System Essentials, QSE, Integration, Harmonization

W7

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 false-negative 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

W8

Sustainability on Medical Laboratory

Mojtaba Ehtiyat *

Sustainability in labs involves a multitude of considerations, from turning off lights and equipment when not in use to minimizing water consumption. The impact of such measures accumulates over time, leading to significant energy savings and a reduced environmental impact. ISO/IEC 42001 is the world's first AI management system standard, providing valuable guidance for this rapidly changing field of technology. It addresses the unique challenges AI poses, such as ethical considerations, transparency, and continuous learning. For organizations, it sets out a structured way to manage risks and opportunities associated with AI, balancing innovation with governance. Benefit: Framework for managing risk and opportunities Demonstrate responsible use of AI Traceability, transparency and reliability Cost savings and efficiency gains.

W9

Emergence of Drug Resistance in Dermatophytes (Diagnostic and Therapeutic Problems and Challenges)

Mahsa Fattahi *, Zahra Mousavi, Navid Neyshabori Nejad

Superficial mycoses are common fungal infection among vertebrates induced by dermatophytes. Dermatophytosis involve about 20-25% of world population. Dermatophytosis is getting to be a concern since of the growing recurrence of recalcitrant cases. Aliteraturereview on dermatophytosis reports unprecedented changes in global epidemiology, length of infection, and response to medication. There are reports of increasing treatment failure and acquisition of drug resistance are alarming, especially because of limited alternative therapies. Breaking the resistance chain requires global attention to assembled management programs are requiring to improve treatment outcomes and reduce antifungal resistance. Traditional available treatments for dermatophytosis : Traditional available treatments for dermatophytosis : recent manifestations of fungal infections during thecoronavirus pandemic in the past 4 years, such asCOVID-19 associated aspergillosis and mucormycosis, demanded broad implication of antifungals, which may have had a role to do with further aggravation of resistancepossibly due the extensive exposure of the susceptible fungi to these chemicals .These limitations are challenged even more by drug–drug interactions, adverse toxicities, andimpediments in administration routes. An important notion on this matter is the importance of timely prescription by preferably using AST, caseselection and precise follow up. we believe that AST is a helpful step for strategic treatment of recalcitrant dermatophytosis, if performed by an expert mycologist and according to surveyed guidelines protocols.

Keywords: Drug Resistance, Dermatophytes

W10

Detection of Cell-free DNA in Serum and Plasma by Optimied a Nested PCR Asay for Diagnosing Patients Suspected of Hydatid Cyst

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Cystic Echinococcosis (CE) is a disease caused by the larvae of the Echinococcus granulosus worm. Ingesting the eggs of these worms, which are excreted in the feces of infected dogs, can lead to the formation of cysts in the liver or lungs of humans or herbivorous animals. Although ultrasound is commonly used for diagnosing these cysts, hydatid cysts are often misdiagnosed as cystic lesions of different origins. Therefore, faster, more accurate, and non-invasive diagnostic methods remain essential. In this workshop, an special PCR assay will be conducted for the sensitive detection of cell-free DNA (cfDNA) specific to Echinococcus granulosus in serum or plasma samples from patients suspected of having echinococcosis. The modified phenol-chloroform method will be used to extract cfDNA. For the amplification of specific cell-free DNA, a semi-nested PCR targeting the NADH dehydrogenase subunit will be performed, followed by standard agarose gel electrophoresis for analysis. This workshop aims to enhance laboratory-based diagnostic accuracy while also improving the participants' diagnostic skills, making it a valuable learning experience.

Keywords: Echinococcosis, Cell-free DNA, Seminested PCR, Diagnosis

W11

Harmonizing Laboratory Reports with Clinical Needs: Challenges and Solutions

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The workshop, titled "Harmonizing Laboratory Reports with Clinical Needs: Challenges and Solutions," is designed to enhance the quality and usability of antibiogram reports and antibiotic susceptibility testing (AST) in clinical laboratories. This workshop will address the challenges in providing accurate and standardized reports that are directly applicable to clinical decision-making by infectious disease specialists. The primary goal is to create a common and standardized language in laboratory reports, ensuring results are clearly, comprehensively, and practically presented to clinicians, enabling them to make more confident treatment decisions. In addition to examining current issues, the workshop will provide practical solutions to overcome these challenges and standardize laboratory procedures. Participants will learn about modern methods for interpreting laboratory data and reporting them in a way that meets clinical needs. This initiative will foster greater coordination between the laboratory and clinical settings, ultimately helping to improve patient treatment and reduce antibiotic resistance. This workshop will empower laboratory and clinical specialists to play a more effective role in patient care. The program will emphasize the importance of standardized reporting for better communication, effective treatment strategies, and improved patient outcomes. Through this interactive and educational approach, attendees will develop the necessary skills to achieve more harmonized results in AST reporting.

Keywords: Harmonization Laboratory Reports Clinical Needs Antibiogram Antibiotic Susceptibility Challenges Solutions Clinical Communication Quality of Laboratory Services Antibiotic Resistance

W12

Antibiogram Update According to CLSI2025

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In this workshop, new and practical points of the latest Antibiogram guidelines (CLSI2025) will be explained to update the Antibiogram. This update will include, including the following- the steps of performing the standard Antibiogram- Antibiogram of bacteria and related points- How to correctly read zones of non-growth and exceptions- How to perform and report antibiotic resistance using phenotypic methods-How to perform and report antibiotic resistance using genotypic methods. Also, the correct and standard method of reporting the Antibiogram with interpretation recommendations that are very important in accurate patient treatment will be explained, and the quality control section of the Antibiogram will also be provided with up-to-date information.

Keywords: CLSI2025, Antibiogram, Antimicrobial Susceptibility Testing, Interpretation Recommendations, Quality Control

W13

Artificial Intelligence and Medical Laboratory

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Artificial intelligence is a widely-used subject of computer science which talk about human-like machines in area such as learning, reasoning and understanding language. The goal of AI, is to design computer program which is able to imitate human actions. Human processing of large data is time-consuming and error-prone, therefore the scope of AI is constantly expanding. Due to production of millions of data daily, medical laboratory is a good area for exploiting AI. AI in Medical laboratory, has resulted to improvement in patient results quality, diagnosis efficacy and personalized patient care. Some branches of AI includes machine learning, deep learning, neural networks, natural language processing and computer vision, each has some applications in medical laboratory. AI has been successfully applied in different areas of medical laboratory. These includes usage in instrument automation, error detection (inappropriate sample quality, QC plots), autoverification of related test results and transfer to LIS, predicting laboratory tests values (GGT from ALT and ALP or ferritin based on other chemistry and full blood count), multiple test interpretation (urine amino acid profile and serum protein electrophoresis), benefit from genetic testing (familial hypercholesterolemia based on lipid profile), improving laboratory information systems and genomic analysis. Computer vision is used in automated image analysis for neoplastic tissue diagnosis and grading, AF bacilli investigation in stained smears, monoclonal band detection in SPE. In addition to discuss some examples of application of AI, we point out to required qualifications to work in the field of AI in medical lab, during this workshop.

Keywords: Artificial Intelligence, Medical Laboratory, Machine Learning, Computer Vision

W14

Basics and General Rules of Quality Control in Clinical Laboratories

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Considering the importance of the role of clinical laboratories in identifying the disease in the early stages and guiding the treatment, the accuracy and correctness of the laboratory results is very important, which requires all laboratory personnel to master the quality control of the clinical laboratory apart from scientific laboratory information To avoid any errors in the results. Therefore, by holding this workshop, we intend to familiarize students and laboratory personnel with the rules of quality control and the principles of work in quality control in order to provide the basis for improving the quality of laboratory results.

Keywords: Quality Control

W15

Platelets: From Cell Counter to Interpretation

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The workshop "Platelets: From Cell Counter to Interpretation" is designed to enhance participants' knowledge and skills in platelet analysis. This comprehensive workshop covers various scientific and clinical aspects of platelets. Participants will first become familiar with the biological characteristics of platelets and their critical role in coagulation and wound healing processes. Next, it will explore the methods and techniques for counting platelets using cell counters, focusing on key points related to sample collection and preparation. A significant section of the workshop involves the analysis of platelet histograms and the interpretation of errors and unusual results. Participants will learn how to analyze test results and identify the relationship between platelet count variations and common hematological disorders such as thrombocytopenia and thrombocytosis. Finally, through practical examples and interactive Q&A sessions, participants will have the opportunity to share their experiences and discuss various challenges related to the diagnosis and treatment of hematological disorders. The overall aim of the workshop is to improve the accuracy and quality of laboratory diagnosis in the field of platelets, empowering participants to enhance clinical outcomes in their practices.

W16

Practical Biochemical Formulas in Medical Laboratory

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In modern medical diagnostic laboratories, particularly in the biochemistry department, mathematical calculations and the application of laboratory formulas constitute an integral component of daily operations. It is essential for all laboratory personnel, from the technical director to staff across various sections, to possess a comprehensive understanding of the principles, applications, and interpretation of these formulas. This workshop will provide a structured and concise review of essential formulas utilized in clinical biochemistry, including solution preparation calculations, blood glucose assessments, lipid profile analysis, enzymatic ratio determinations, iron metabolism calculations, urine and clearance evaluations, and other relevant computations, which will be discussed in a summarized and categorized manner.

Keywords: Biochemistry Formulas, Biochemical Calculations and Urine Calculations

W17

Laboratory Giagnosis of Onychomycosis

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Nowadays one of the commonest problems in dermatology is onychomycosis (fungal infection of nail) and based on this one of the reasons of refer to dermatology clinic is nail disorder due to mycotic infection. Clinical diagnosis of onychomycosis is very difficult therefore a good and correct diagnosis need to laboratory diagnosis that make by an expert man. In this work shop we try to describe the clinical signs, sampling, direct examination and culture the specimens with a standard and correct report.

Keywords: Onychomycosis, Nail Dermatophytosis, Nail Candidiasis, Nail Mold Infection

W18

Introduction of Common Non-Conformity and Errors along with Corrective Actions in the Clinical Laboratory

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It is estimated that >70% of clinical decisions are based on information derived from laboratory test results. This indicates that medical laboratory error is potentially high. Error definition is use a wrong plan to achieve an aim, occurring at any part of the laboratory cycle, from ordering examinations to reporting and interpreting the results. Any defect in various steps that lead to a deviation of the reported value from the actual (accepted) value. Non-compliance means any event that has a negative impact on an organization. This impact can be on employees, product, equipment or environment. Continuity of non-compliance leads to its repetition and the possibility of its occurrence in the future, the final result of which will be the impact on customers, therefore, every center should take steps to prepare non-conforming work management instructions. Grading of non-compliance includes major and minor cases. Major cases include the lack of documentation of a requirement or its complete non-implementation. Minor cases include the lack of a part of the documentation of a requirement or the non-implementation of a part of a standard requirement. All laboratory employees should take the necessary training to identify non-compliance cases. Identified cases should be reflected to the relevant official and appropriate corrective or preventive measures should be taken and implemented. Monitoring non-conformities provides laboratory managers with valuable information for decision-making. The clinical laboratory management must answer the question of how to determine, measure and monitor the optimal performance point of each activity in the laboratory. The implementation of this mechanism is one of the most difficult tasks of the middle and senior managers of a laboratory. Any partial or main activity in the laboratory that leads to a defect in the partial or the entire process of producing test results and affects the visible or invisible quality of the results should be recorded as non-conformity working and corrected. The consequences of laboratory error are incomplete care of patients, threat of health and death, disproportionate action at the level of community health, epidemic of an undiagnosed infectious disease, and waste of resources.

Keywords: Clinical Laboratory, Error, Non-Conformity

W19

Performance Standards for Antimicrobial Susceptibility Testing Based on CLSI M100

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Antibiotic susceptibility testing (AST) is an in vitro measure to assess the likelihood that a particular antimicrobial agent will treat an infection caused by a particular organism. Treatment of an infection is directly due to data from this laboratory test. It is commonly utilized to monitor recent antimicrobial resistance patterns in order to guide empirical antimicrobial therapy selection. CLSI is the global standard for antibiogram. The main purpose of this training workshop is to guide the instruction details in disk selection, the correct procedure of test QC and the corrective action due to identifiable errors, and to rectify reading and reporting patient results.

Keywords: Antimicrobial Susceptibility Testing, Disk Diffusion, Antimicrobial Resistance, Antibogram QC, Antibiotic, CLSI M100

W20

Diagnosis of Myeloid and Lymphoid Malignancies: From Hematomorphological Features to Molecular Alterations

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Hematomorphology is an essential tool in the diagnosis and classification of blood disorders, especially leukemias. In this context, the development of the FAB classification for acute leukemias and gradually for other leukemias and related disorders is one of the most important diagnostic strategies that has so far been able to make significant progress in the diagnosis and uniform classification of patients by accurately determining the differential criteria. However, in recent years, this classification has been gradually supplemented by the WHO classification, which, in addition to morphology, also widely uses immunophenotyping, cytogenetic analyses, and molecular genetics. Furthermore, since 2022, the recent ICC classification, in combination with other conventional classifications, has introduced a multi-parametric approach with greater clinical relevance to improve the treatment of affected patients. Despite recent advances, the FAB classification continues to be used as a valuable tool in describing morphological subtypes. In addition, in the early stages of evaluation, where access to immunophenotyping and genetic analyses is limited, the use of cytochemical techniques will also be important, which should not be overlooked. However, it is important to understand the differences between the FAB and WHO classifications, due to the differences in diagnostic criteria. Therefore, the use of these classifications should be done with full awareness of the limitations and strengths of each to maximize diagnostic accuracy and quality of patient management. In this regard, holding relevant specialized workshops is a valuable and important solution that can provide a unique opportunity to increase diagnostic capabilities through comprehensive training in hematomorphology of blood malignancies and its relationship with genetic and molecular findings. This will be effective in improving and updating laboratory and clinical services.

Keywords: Classification (WHO and ICC), Genetics, Hematomorphology, Leukemia, Lymphoid,Myeloid

W21

Molecular Diagnostics Laboratories Requirements

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The results of medical diagnostic tests influence approximately 70% of clinical decisions made by physicians in various fields, including diagnosis, treatment, and disease monitoring. In medical laboratories, molecular tests have gained increased importance, particularly since the onset of the COVID-19 pandemic in late 2019. Given the crucial role that diagnostic test results play in physicians' decisions, these results must consistently exhibit sufficient accuracy and precision. Otherwise, there can be significant repercussions for patient safety and disease management. Before the COVID-19 pandemic, molecular diagnostic laboratories in Iran were limited to a few specialized centers. However, since the outbreak, the number of molecular diagnostic laboratories has rapidly increased to meet the country's needs. These laboratories have been conducting molecular diagnostic tests for COVID-19, achieving significant successes in the timely diagnosis of suspected COVID-19 patients. Nevertheless, the rapid development of molecular laboratories has also resulted in challenges, such as the inability to establish all quality assurance requirements and the failure to fully implement safety and biosecurity principles in the molecular sector. Furthermore, molecular diagnostic technologies and methods are advancing at a rapid pace. Many new high-throughput molecular tests are now commercially available, impacting the infrastructure of numerous diagnostic laboratories. This workshop will explain the principles and operational requirements essential for molecular diagnostic laboratories.

Keywords: Molecular Methods, Requirements, Molecular Diagnostics Laboratories

W22

Interpretation of Flow Cytometry Graphs 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

W23

Fundamentals and Technical Challenges in Coagulation Laboratory: A Summary of International Guidelines

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Coagulation laboratories play a key role in the diagnosis and monitoring of bleeding and thrombotic disorders. To achieve accurate and reliable results, adherence to international standards is essential at all stages, including pre-analytical, analytical, and post-analytical phases. International guidelines such as CLSI, ISTH, and BSH emphasize that sample collection, transportation, and storage must be performed under standardized conditions. Factors such as the use of appropriate anticoagulants, the correct blood-to-anticoagulant ratio, and the prevention of hemolysis and lipemic samples directly impact result accuracy. Technical challenges include internal and external quality control, drug interferences (such as warfarin and heparin), standardization of calibration methods, and limitations related to diagnostic equipment and reagents. Additionally, biological variations among patients, including genetic factors and underlying diseases, can influence test results. Guidelines recommend that laboratories use calibration and quality control methods based on international reference materials and regularly assess instrument performance. Adopting standardized approaches in result interpretation, utilizing advanced techniques, and providing continuous staff training are key strategies to enhance accuracy and minimize laboratory errors. Adhering to these principles not only improves patient diagnosis and treatment but also prevents misinterpretation of results and serious clinical consequences.

Keywords: Coagulation Laboratory, Bleeding and Thrombotic Disorders, International Standards, Quality Control

W24

The Essential Guide to Vitamin D3, Magnesium and Zinc

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Vitamin D3, magnesium, and zinc play vital roles in the body's metabolic processes. deficiencies in these nutrients can have numerous negative impacts on health condition. Vitamin D3 is crucial for the of calcium and phosphorus absorption, thereby maintaining bone and skeletal health. Additionally, vit dD3 supports the immune system and help regulating nervous system function. A deficiency in vitamin D3 can lead to conditions such as osteoporosis, muscle weakness, joint disease, cardiovascular diseases, and even depression. Magnesium is among the essential minerals for maintaining the proper function of the nervous system, musculoskeletal, and cardiovascular system. Magnesium deficiency can result in symptoms such as muscle cramps, chronic fatigue, anxiety, sleep disturbances, and even heart disease. Zinc is also crucial for the proper functioning of the immune system, tissue repair, and cellular growth. A deficiency in zinc can lead to weakened immune system, delayed wound healing, hair loss, growth disorders, and nervous system dysfunction. Ultimately, developing a healthy life style that can help preventing disease through a balanced diet, adequate sleep, regular physical activity, and routine check-ups can reduce healthcare costs and improve individuals' quality of life. Vitamin D3, magnesium, and zinc are essential nutrients for maintaining body health, prevention of diseases and as treatment protocols. This workshop will address metabolism, methods of measurement and monitoring, as well as interpretive points and clinical considerations.

Keywords: Hypovitaminosis D3, Mg, Zn, Tests Interpretation and Monitoring

W25

Lowering Overall Laboratory Testing Costs Through Result Validation and Integrative Interpretation

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Validation and interpretation of laboratory results in various ways leads to significant reductions in overall laboratory costs and increases in turnaround time. Key points of this process are reviewed and recommended by presenting real cases.

Keywords: Integrative Interpretation, Recheck Decision

W26

Statistical Quality Control with a Sigma Metric Approach

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Physicians need accurate laboratory reports and other paraclinical services in making decisions about treating a disease. And making any wrong decision in this direction may cost the patient's life. Therefore, it is necessary for the laboratory to play its essential role in this field by relying on the power of tools, materials, and the efficiency of all those involved in the laboratory. Purpose of quality control: - Providing accurate information in order to diagnose and help the doctor. - Identifying errors with the aim of improving methods, reducing errors, and gaining awareness and knowledge to eliminate them. - Communication and belief between the Physician and the patient in presenting the results and performance of the laboratory. - Increasing scientific power and more awareness, and as a result, observing the above. - Identify and eliminate those errors that are within the laboratory's responsibility The purpose of the statistical quality control program is to determine scientific indicators and monitor them in improving the quality of laboratory results, which ensures the use of new sigma metric methods instead of traditional methods, and provides the laboratory and physicians with improved quality of output results with modern methods. Quality assurance is to create trust in 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, 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 and 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.

W27

Introducing Application of New Gel Technilogy (FardAvar Glory 90) in Immunohematology and Hospital Blood Banking in Iran

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Current developments in methods available in the transfusion services, Tube conventional method and Gel techniques FardAvar Glory 90 are discussed and their advantages and application in terms of equipment, procedures, test reactions, sensitivity, specificity, stabilities, endpoint reproducibility, and quality control will be compared and shared with attendees at the workshop.

Keywords: Column Agglutination Technique (Gliry 90), Conventional Tube Technique, Blood Bank, Immunohematology

W28

The Role of Artificial Intelligence (AI) in Semen Analysis

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Artificaial Intelligence (AI) is transforming semen analysis by providing more accurate, efficient, and objective assessments of male fertility. Traditional methods of semen analysis are prone to variability and subjectivity. AI algorithms, particularly those based on machine learning and deep learning, mitigate these issues by analyzing vast datasets to identify patterns and predict outcones. A significant application of AI in semen analysis includes the automatic measurement of sperm concentration, motility, and morphology, reducing human error and enhancing consistency. AI driven image analysis techniques offer precise evalution of sperm morphology, detecting subtle abnormalities that may be overlooked during manual assessments. In summary, AI is enhancing the accuracy and accessibility of semen analysis. These advancements hold great potential for improving the diagnosis and treatment of male infertility, contributing to better reproductive heaith outcomes.

Keywords: Artificial Intelligence, Machine Learning, Semen Analysis, Sperm Selection

W29

Methods of Identifying Phenotypic Intestinal Pathogens, Aeromonas, Salmonella, Shigella

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The workshop is aimed at how to properly perform diagnostic tests and how to properly diagnose intestinal pathogen bacteria. In this training course, in addition to practical techniques in identifying and identifying bacteria, we will address the challenges in performing tests. In many cases, inter ventional factors will change the results of diagnostic test in the microbiology. The ability to separate and report the pathogens from the stool sample is important because the pathogen colonies must be identified and detected from the normal gastrointestinal floral colonies.

W30

The Role of Systems Thinking in Medical Laboratory Management - Clauses 3, 5, and 8 of ISO 15189-2022 Standard

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For establishing a dynamic, reliable, and responsive system in a medical laboratory, it is essential to define and solidify quality management, objectives, policies, and risk management (Clauses 4-5, 5-5, 6-5,and Clause 8 of ISO 15189:2022).Familiarity with systems thinking and its application is a fundamental necessity for laboratory management and successfully driving the system across temporal and spatial horizons. A lack of systems thinking exposes a medical laboratory, like any other system, to superficial perspectives, rushed solutions, a reactive firefighting culture, and the acceptance of persistent problems when planning and dealing with crises. Systems thinking teaches us to expand the system's boundaries slightly beyond conventional limits to cultivate a broader perspective. By considering the system from the viewpoint of a greater number of stakeholders, we can institutionalize pluralism. For every planning and problem-solving approach, it is crucial to account for both temporal and spatial dimensions. We must always remember the inherent resistance of systems to management policies and acknowledge that the objective within a system or laboratory is in order to accurately describe the current reality of the medical laboratory system.

Keywords: ISO 15189:2022 Standard, Accreditation, Systems Thinking, Medical Laboratory Management

Authors Index

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