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IFCC EMERGING TECHNOLOGIES DIVISION SATELLITE MEETING

23rd GREEK NATIONAL CONGRESS OF CLINICAL CHEMISTRY

ABSTRACT BOOK

Emerging Technologies in Clinical Chemistry and Laboratory Medicine

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Aristotle University Research Dissemination Center (KEDEA)
Thessaloniki, Greece

Organization

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IFCC International Federation of Clinical Chemistry and Laboratory Medicine

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EUROPEAN FEDERATION OF CLINICAL CHEMISTRY AND LABORATORY MEDICINE

IFCC EMERGING TECHNOLOGIES DIVISION SATELLITE MEETING

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Dear colleagues and friends,

On behalf of the Greek Society of Clinical Chemistry - Clinical Biochemistry, we have the pleasure of **welcoming you to** our Annual Scientific Conference, 23rd National Congress of the GSCC-CB on Emerging Technologies in Clinical Chemistry and Laboratory Medicine. This event is scheduled to take place in **Thessaloniki, Greece, from October 30 – November 2, 2025**, which is conducted with the IFCC Emerging Technologies Division (IFCC ETD). The Presentation Title of this event is **"Emerging Technologies in Clinical Chemistry and Laboratory Medicine"**.

This event aims to address new laboratory developments through a special theme chosen for 2025. The conference focuses on providing laboratory professionals and clinicians up-to-date information on the strengths and challenges of emerging technologies and to foster a deep understanding of key aspects related to these innovations — including test standardization, compliance with ISO standards, and their role alongside other technologies currently available in the clinical laboratory.

The Scientific and Organizing Committees has put together an educational program that is up-to-date and focused. This is done by including scientific presentations from experts in the field and presentations of industry activities to promote innovation in our country.

During the conference, distinguished Greek and international scientists will deliver presentations, while the program will also include Symposia, Round Tables, an exhibition of IVD instruments and reagents, as well as Satellite Symposia organized by IVD companies to showcase new methodologies and instruments.

The Organizing Committee is pleased to welcome you to Thessaloniki and looks forward to a scientifically rich and productive congress.

For the IFCC ETD
Damien Gruson

For the GSCC-CB
Michalis Aivaliotis

IFCC

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ABSTRACT INDEX

TITLE PAGE

TITLE PAGE

TITLE PAGE

LECTURES

Emerging Diagnostic Technologies: Shaping the Future of Global Health

Damien Gruson

The global healthcare ecosystem is undergoing a profound transformation driven by the convergence of disruptive diagnostic innovations, precision prevention strategies, and new paradigms in sustainability. At the forefront of this evolution, laboratory medicine is repositioning itself as a central player in shaping equitable and resilient health systems.

Emerging technologies—spanning artificial intelligence, advanced biomarker analytics, wearable biosensors, and point-of-care diagnostics—are rapidly redefining how diseases are detected, monitored, and prevented. These tools enable real-time, decentralized, and personalized care, particularly impactful in underserved and resource-limited settings.

Beyond technology, the integration of exposomics—linking lifelong environmental exposures to disease risk—and multi-omics data (genomics, proteomics, metabolomics) provides an unprecedented lens into the mechanisms of chronic diseases, such as cardiovascular disorders. Coupled with AI, these insights support earlier interventions and more tailored therapeutic approaches.

This keynote will highlight global case studies illustrating the clinical and public health benefits of next-generation diagnostic tools. It will also explore how laboratory medicine can support planetary health by adopting greener practices and circular economy models, while championing health equity through focused programs in women's health and digital access.

Ultimately, the future of global health lies in a multidisciplinary ecosystem where laboratory medicine, technology developers, public health stakeholders, and policymakers co-create scalable and sustainable diagnostic solutions. The IFCC Emerging Technologies Division aims to catalyze this shift—driving innovation not only for what is possible today, but for what is essential tomorrow.

Breaking Silos: Cross-Division Collaboration to Improve Neonatal Jaundice Screening

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INTRODUCTION

The World Health Organization (WHO) and clinical society guidelines recommend treatment decisions for neonatal jaundice based on fixed serum total bilirubin (TBil) cut-offs. Whilst TBil is the "gold standard", it is widely recognized that itsl measurement urgently needs improvement. Furthermore, the plethora of emerging near patient testing and community screening tools must correlate with these standard tests to best support neonatal clinical care.

METHODS

The International Federation for Clinical Chemistry and Laboratory Medicine (IFCC) formed a Working Group for Neonatal Bilirubin (WG-NB) in 2022. The WG consists of members from both the Scientific Division and the Emerging Technologies Division of the IFCC. Importantly 12 industry partners offering neonatal bilirubin testing are members to this WG. The WG-NB have identified four immediate needs to improve TBil measurement. 1) Traceability chain – align methods to give the same result; 2) Commutable EQA materials; 3) Review fitness for purpose of current reference measurement procedures; and 4) Continued cooperation and support from diagnostic manufacturers.

RESULTS

Significant progress has been made towards improving the listing of reference materials and reference measurement procedures on the JCTLM database and to encourage manufacturers to move to NIST916b pure bilirubin calibrator material. Studies looking at bias between instrument platforms using matrix matched neonatal samples and assessment of external quality assurance providers is in progress. Work is also being undertaken to keep abreast of near patient technologies to critically review their performance.

CONCLUSION

The WG-NB will continue to work towards improvement in bilirubin measurement, ensuring more effective linkages between near patient testing and central laboratory testing for the overall benefit of the baby. These advancements will be accompanied by sustained collaboration with clinical societies responsible for developing and refining treatment recommendations.

Standardization process of Continuous Glucose Monitoring: Creating a traceability chain and standards to evaluate performance

K. Makris

Patients with diabetes are required to regularly check their glucose to make therapy decisions. So far, systems for self-monitoring of blood glucose were used, but nowadays minimally invasive continuous glucose monitoring (CGM) systems are increasingly more often employed, and will eventually replace self-monitoring of blood glucose.

Most CGM systems on the market measure glucose concentrations continuously in the interstitial fluid of the subcutaneous fatty tissue. However, CGM has a principle limitation. Collecting interstitial fluid frequently in sufficiently large volumes over short time periods is not easy. As a consequence, no internationally accepted reference measurement procedure is currently available for glucose in interstitial fluid which is a prerequisite to achieve an optimal metrological traceability.

Recent studies indicate that the analytical performance of minimally invasive CGM systems differs not only between manufacturers but also between individual sensors of the same system, sometimes even in the same subject.

Manufacturers do not provide detailed information about the traceability chain and the measurement uncertainty of their systems therefore glucose values obtained with CGM can currently not be adequately traced to higher-order standards or methods. IFCC established a Working Group on Continuous Glucose Monitoring with the aim to establish a traceability chain for minimally invasive CGM systems, as well as to establish procedures and metrics for the assessment of their analytical performance.

Emerging Technologies Division aims to catalyze this shift—driving innovation not only for what is possible today, but for what is essential tomorrow.

Understanding the Exposome: Linking Environment, Biomarkers, and Disease

B. Gouget

The exposome, the comprehensive measure of all environmental exposures across the lifespan, has emerged as a transformative paradigm in laboratory medicine, redefining our approach to complex disease etiology and prevention. In an era marked by global ecological shifts and rising chronic disease burdens, understanding how external exposures interact with biological systems is critical. This presentation explores the exposome as a dynamic interface connecting molecular biomarkers, environmental data, and health outcomes, positioning laboratory medicine as a linchpin of the One Health framework.

By integrating high-resolution biomonitoring, omics technologies, and advanced data analytics, exposomics enables the identification of novel exposure-disease relationships and actionable early-warning biomarkers. We will highlight case studies that demonstrate how exposome-informed diagnostics can support both patient-level precision medicine and population-scale environmental health strategies.

Ultimately, we advocate for a paradigm shift in medical biology: from isolated diagnostics to interconnected health intelligence. This vision redefines the medical laboratory not only as a site of clinical analysis, but as a critical engine for planetary health and sustainability.

The Exposome And Cardiovascular Risk: Emerging Roles For The Clinical Laboratory

S. Stankovic

Cardiovascular disease (CVD) remains the leading global cause of morbidity and mortality, driven by a complex interplay of genetic, lifestyle, and environmental factors. While traditional risk factors such as hypertension, diabetes, dyslipidemia, smoking, and obesity are well-established, they do not fully account for individual variability in disease onset and progression. Therefore, additional contributing factors must be addressed to reduce the burden of CVD further. In this context, research is increasingly focused on non-traditional risk factors present in the built, natural, and socio-economic environments comprising the exposome. The exposome, the youngest member of the widely acknowledged "-ome" family, is defined as “the cumulative measure of environmental influences and associated biological responses throughout the lifespan, including exposures from the environment, diet, behavior, and endogenous processes.”

Clinical laboratories can play a pivotal role in reducing CV risk through comprehensive analysis of the exposome. This approach involves analysing internal biological changes that serve as biomarkers of exposure and effect, including: a) detection of exogenous compounds and genetic expression alterations in blood, urine, tissue samples; b) identification environmental exposure "footprints" in the body using OMICs technologies. Exposure-health association studies also measure key biomarkers such as: stress hormones (e.g., cortisol and catecholamines), oxidative stress biomarkers (e.g., malondialdehyde, oxidized low-density lipoprotein, etc.), inflammatory biomarkers (e.g., cytokines), and circadian rhythm disruption markers (e.g., melatonin). Environmental exposures can act synergistically or additively with genetic predisposition or pre-existing CVD, and can exacerbate detrimental cardiovascular health outcomes (atherosclerosis, heart failure, myocardial infarction, stroke).

Advancements in analytical technologies, combined with artificial intelligence, have enabled clinical laboratories to take a transformative role in exposome research. These tools allow for the detection and quantification of thousands of exposure-related biomarkers, offering new insights into the molecular mechanisms linking environmental factors to cardiovascular pathology. Moreover, the integration of exposomic data with genomic and clinical information supports more precise risk stratification, early disease detection, and the development of personalized preventive and therapeutic strategies. This presentation will explore the emerging roles of clinical laboratories in exposome-based CV risk assessment and outline future directions for research and implementation in precision cardiovascular medicine.

AI in Medical Education: Personalized Learning, Translation and Content Creation.

N. Rifai

Artificial intelligence (AI)-driven learning has been widely used in teaching in colleges and universities in the United States but its utility in medicine has gained prominence only in the past decade. AI utility in medical education can be realized by creating personalized learning tools and in translating and creating de novo content. Adaptive learning approach, which is the closest to personalized education, has been shown to provide users with a higher retention rate of information, greater test score and passing rate, and higher mastery of new information in less time compared to those who use traditional e-learning methods.

In this lecture, the utility of AI in medical education will be explored using the Learning Lab for Laboratory Medicine as an example (https://area9lyceum.com/laboratorymedicine/). This online program is free of charge, to eliminate financial barriers, and consists of 130 Advanced and 103 Medical Laboratory Specialists courses that span across all disciplines of laboratory medicine. Adaptive learning is an ingenious way to communicate information; through AI-driven algorithms, the platform interacts with the learner and identifies the areas in which they are not proficient. It then provides targeted learning materials to remedy the deficiency, thus enabling efficient learning in small blocks of time.
With the assistance of AI and verification by local experts, this program is currently being translated to multiple languages including Japanese, Chinese (traditional and simplified), Bahasa Indonesia, Spanish, Portuguese, French, Korean and Arabic; over 550 translated courses have already been released. Currently, >19,000 individuals from 156 countries are using this program but the numbers are expected to significantly increase as the translated contents become more widely available. The recent integration of GPT4 into the used platform is enabling the creation of de novo educational materials thus accelerating and simplifying the process.

Omics-based biomarkers. Presentation of the current status, market penetration and potential for future application in the clinic.

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Metabolomics show strong increase as the field can offer new insights in disease/health/wellness biochemistry. Liquid Chromatography Mass Spectrometry (LC-MS) takes the largest part of the metabolomics market due to its agility, performance, sensitivity, fit for the analysis of biological samples, direct applicability, large numbers of instruments and practitioners. LC-MS proves superior in the discovery, development of new biomarkers and their application in disease, nutrition, wellness, exposure or safety assessment. Recently LC-MS is also entering the clinical chemistry practice, however its application in the clinic is not problem free. Translational aspects and application of research findings to the clinical practice, proceeds slowly. Metabolomics is still evolving as a technology, so protocols differ between laboratories, in terms of instrumentation, parameters, sample preparation, data handling and informatics tools. These differences hinder harmonization and may result in problems in replication of findings and the adoption of biomarkers. The presentation will highlight constraints that slow the finalization and uptake of LC-MS metabolomics biomarker development.

To illustrate the strong perspective of metabolomics, examples of biomarker discovery will be presented with focus on larger initiatives (i.e. 1200+ cases) where metabolic profiles are associated with genetic, gutmicrobiome data, clinical and anthropometric data to identify associations of omics profiles with diet (CoDiet), or cardiac health (Corlipid). In Corlipid, blood samples from 1500 cases of coronary disease were analysed by untargeted UPLC-TOF-MS lipidomics, untargeted metabolomics, and new targeted methods to quantify ceramides, carnitines (UPLC-MS/MS), and fatty acids (GC-MS). A machine learning algorithm selected 17 parameters (8 metabolites) to predict the coronary angiography results (syntax score the golden standard for quantifying the complexity of coronary artery disease). In Codiet blood and urine samples from four European cohorts were analysed by six UPLC-MS methods (combining targeted and untargeted modes) to map the metabolome and link the obtained profiles with nutrition.

The presentation will emphasize on the needs and the benefits of the development of new analytical methods to effectively map the metabolome. To better illustrate this, we report the development of a new method for the quantitation of aromatic aminoacids and sulphated metabolites. These molecules are important markers in inflammation, cancer and other disorders, however the lack of commercially available standards hinders their quantitation in biological samples. We synthesized 14 sulphated metabolites; after preparative LC purification, NMR and MS verification, we developed a new UPLCMS/ MS that allowed for the quantitation of 30 metabolites in urine, 23 metabolites in blood serum and 28 in feces and the subsequent application in biomarker studies and the analysis of clinicalsamples. The authors acknowledge funding from the Horizon Europe Project 101079370 — BiACEM WIDERATwinning
“Biomic_AUTh, Center of Excellence in Metabolomics research”.

AI for multiomic integration: approaches and case studies

M. Chierici

Multiomics integration, classically defined as the combination of multiple complementary omics layers to model complex traits and phenotypes, has been a longstanding goal in bioinformatics and computational biology, yet there is still no broadly accepted and consolidated approach. The relatively recent availability of large curated resources (e.g., TCGA pan-cancer), which combine multiple omics layers and modalities, has strengthened the need for computational strategies that support robust cancer subtyping and biomarker discovery from multiomics data. In parallel, recent methodological and technological advances in the field of AI, particularly in deep learning, have accelerated the adoption of deep neural network architectures to learn joint representations and patterns from heterogeneous data that traditional approaches may miss. In this talk, after a brief introduction of the conceptual background of integration, we illustrate three complementary case studies. (i) A machine-learning and network-based workflow for integrating gene expression, protein expression, and copy-number variation from TCGA to characterize cancer patient phenotypes; (ii) An integrative analysis of miRNA expression and metabolomics to identify potential predictors of cardiovascular risk; (iii) A deep learning approach to fuse multi-modal data, including whole-slide imaging, copy number variation, and clinical information, in TCGA pancreatic adenocarcinoma. These examples illustrate the versatility and the potential of AI-driven approaches in multiomics and multimodal integration.

Emerging Technologies in Pediatric Laboratory Medicine – Selected Aspects.

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In children, results of clinical laboratory investigations probably play an even larger role than in adult patients for a proper diagnosis, monitoring therapies or establishing the prognosis of disease. During the physiologic development of a child from birth to adolescence, dramatic changes occur resulting in significant modifications in metabolic pathways, reflected in the concentrations of clinical laboratory analytes in the body fluids. Thus, it is indispensable to have access to reference intervals for these analytes which are valid for the respective developmental stage of the pediatric patient under consideration. Ideally, reference interval upper and lower limits would be required, expressed as a continuous function of the actual age of the child.

Examples for thoroughly validated reference intervals resulting from studies recently performed in population-based investigations, studying large cohorts of healthy children in Europe, North America and some other countries will be presented. Furthermore, up-to-date information on patient-based reference intervals will be given and their advantages and disadvantages will be presented.

Additionally, other emerging technologies arising in special aspects of pediatric laboratory medicine will be discussed, such as preanalytical considerations, e.g., overcoming the problem of microliter-range sample volumes by micro-sampling techniques.

Newborn screening for metabolic disorders has gained increasing importance, and examples for screening programs including the methodology will also be shown.

A final consideration will be given to upcoming new analytical approaches, such as NMR spectrometry for metabolome analysis.

Multi-omics and systems biology in personalized diagnostics in the era of precision medicine

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In the era of precision medicine, the integration of multi-omics approaches and systems biology holds immense potential for revolutionizing personalized diagnostics. By simultaneously analyzing genomic, transcriptomic, proteomic, metabolomic, and other omics data, multi-omics provides a comprehensive understanding of the molecular mechanisms underlying disease heterogeneity. This holistic view, when coupled with systems biology frameworks, facilitates the creation of dynamic models that capture the intricate interactions within biological networks. These models enable the identification of biomarkers, prediction of disease progression, and tailoring of therapeutic strategies to individual patients. The application of these advanced technologies not only improves diagnostic accuracy but also accelerates the development of personalized treatment regimens, offering a more precise, targeted approach to healthcare. However, challenges remain in data integration, interpretation, and clinical implementation, highlighting the need for robust computational tools, standardized protocols, and cross-disciplinary collaboration. As we move towards more personalized care, the fusion of multi-omics and systems biology will be instrumental in advancing precision medicine, offering the potential for improved patient outcomes and more effective therapies.

Frontotemporal Dementia (FTD) genes: the "actionable" case of progranulin

Kroupis Christos

Neurodegenerative dementias are becoming an increasingly significant burden in the developed world; a battery of clinical, imaging, psychological and laboratory tests are used to diagnose cognitive impairment and mood/behavioral/language disturbances and differentiate from other non-degenerative causes. They comprise a spectrum of diseases; mainly, are classified in one of four categories such as Alzheimer's (the majority of cases ~60-70%), Frontotemporal dementia (FTD), Lewy-body dementia and Vascular dementia (although mixed cases are not uncommon).

Key events in these diseases are the extracellular deposition of amyloid plaques and the presence of neurofibrillary tangles of p-tau protein that lead to neurotoxicity and neuronal cell death. They form the basis for the latest AT(N) 2018 classification that evaluates amyloid aggregation, tau aggregation and neurodegeneration. Additional biomarkers are being examined in CSF in order to increase diagnostic accuracy (such as neurogranin, neurofilaments etc.) and nowadays even in blood, in order to provide earlier detection in a less-invasive way.

FTD is as common as Alzheimer's disease in patients <65y and concerns about 5-15% of the total dementia patients worldwide. FTD spectrum includes bvFTD (behavioral variant), PNFA (Primary non-fluent Aphasia) and SV (semantic variant), FTD-ALS and the atypical Parkinsonian syndromes PSP (Progressive Supranuclear Palsy) and CBD (Cortico-basal Degeneration). For FTD, genes such C9orf72, PGRN, MAPT, TARDBP, FUS etc. are being investigated. With the advent of Next Generation Sequencing, a panel of 25-30 genes can be examined simultaneously and genetic causes of all dementias can be detected.

PGRN encodes for a secreted factor of 593 amino acids, named progranulin that enhances neuronal survival, protects cells from cellular stress and is important for proper lysosomal function of neurons. Progranulin levels can be easily measured in plasma where significantly lower levels can assist in identifying candidates for loss of function (null) GRN mutations. This low-cost screening test can allow them to be included in novel Precision Medicine treatments such as intracisternal PGRN gene therapy or intrathecal anti-sortilin antibodies. However, there is need for an international IFCC effort in order to harmonize these assays with a certified reference material and establish universal cutoffs not only for null mutations' carriers but also for those patients with intermediate plasma progranulin protein levels due to either hypomorphic mutations or epigenetic or other genetic factors; they could also benefit by therapeutic "action" on their progranulin level.

Introduction to Intraoperative Cytometry

G.S. Markopoulos

Intraoperative flow cytometry (iFC) has emerged over the past decade as a novel and versatile technique that addresses one of the key challenges in surgical oncology: the need for fast, accurate, and reproducible tissue assessment during surgery. This introductory presentation will outline the fundamental principles of iFC, including cell preparation directly from fresh tumor samples, rapid staining with DNA- or protein-targeting dyes, and multiparametric analysis through flow cytometry platforms adapted for operating room conditions. Emphasis will be placed on the workflow, highlighting how tissue dissociation and labeling can be completed within minutes, generating results that are immediately available to the surgical team. Beyond its methodological aspects, we discuss the advantages of iFC particularly in providing objective, quantitative data on cell cycle distribution, tumor index, ploidy status and phenotype, with a prospect on assisting diagnosis, having a golden standard on pathology assessment. The requirements for specialized personnel and integration into clinical workflows, will also be considered. Finally, perspectives on the incorporation of iFC into surgical oncology workflows will be presented, providing clinical applications and translational prospects.

Applications of Intraoperative Cytometry in Surgical Oncology

G. Vartholomatos

The clinical implementation of intraoperative flow cytometry (iFC) has expanded from proof-of-concept studies to real-world surgical oncology applications across multiple tumor types. This lecture will review the most important translational advances and clinical scenarios where iFC has been shown to provide significant added value. Case studies will be highlighted in central nervous system tumors, where iFC has enabled intraoperative determination of tumor grade and guided the extent of resection. Applications in breast-conserving surgery and colorectal cancer will be discussed, focusing on margin status, tumor infiltration, and the detection of residual malignant cells in peritumoral tissue. Special emphasis will be placed on standardized protocols for cell cycle analysis, immunophenotyping using lineage and stemness-associated markers, and evaluation of DNA index, which allow surgeons to obtain a rapid snapshot of tumor biology within minutes. Emerging clinical data will be summarized, demonstrating that iFC has the potential to complement histopathology, reduce reoperation rates, and enhance precision oncology. By presenting practical protocols, reproducible data, and clinical outcomes, the lecture will underline the role of iFC as an evolving bridge between advanced cytometry and the operating theater.

Intraoperative Cytometry and Surgical Oncology

C. Bali

The integration of intraoperative flow cytometry (iFC) into surgical oncology represents a paradigm shift in the way intraoperative decision-making is informed by real-time tumor biology. This presentation will explore how cytometric data—ranging from proliferative indices and tumor cell markers — can be translated into actionable surgical strategies. Clinical examples will illustrate how iFC has supported intraoperative assessment of margins, enabled identification of highly proliferative or therapy-resistant tumor subpopulations, and provided early insights into tumor–immune interactions. The example of iFC integration in colorectal cancer surgery will be discussed, with a potential on assisting diagnosis, prognosis and latter therapeutic interventions. The discussion will also touch upon how iFC aligns with a broader framework that integrates intraoperative molecular, cellular, and clinical data to guide precision surgery. In this context, iFC serves as a cornerstone technology, offering high-throughput, quantitative, and unbiased information that can complement both pathology and imaging. By bridging laboratory advances with intraoperative clinical practice, iFC has the potential not only to improve surgical outcomes but also to assist in personalized oncologic care.

Precision Oncology through Liquid Biopsies: The Emerging Role of ctDNA

A. Magklara

Liquid biopsy refers to the analysis of circulating tumor-derived or tumor-induced material in body fluids, most commonly blood, as a minimally invasive approach to characterize cancer. Unlike traditional tissue biopsies, liquid biopsies allow real-time disease monitoring, capturing spatial and temporal heterogeneity and enabling repeated sampling over the course of treatment. By analyzing circulating tumor DNA (ctDNA), cell free RNA, extracellular vesicles, or tumor-educated platelets, these methods provide a dynamic view of tumor biology and its evolution. ctDNA has emerged as the most clinically advanced liquid biopsy biomarker, moving from exploratory studies toward integration into oncology practice. The development of highly sensitive technologies, such as next-generation sequencing and digital PCR, has expanded the clinical potential of ctDNA, enabling applications ranging from early cancer detection and treatment selection to assessment of minimal residual disease and surveillance of therapeutic resistance. In addition, ctDNA offers unique insights into tumor clonal evolution and mechanisms of acquired resistance, underscoring its role as a real-time companion to therapeutic decision-making. Despite this progress, important challenges remain, including assay standardization, reporting harmonization, validation in large interventional studies, and the establishment of robust regulatory frameworks to ensure widespread adoption. Once these challenges are met, liquid biopsy is expected to become an indispensable tool for precision oncology, complementing and in some contexts potentially replacing conventional tissue analysis, while offering clinicians and patients less invasive and more informative options for cancer management.

Correlation of cancer markers with oxidative stress

M. Trapali

Oxidative stress results from an imbalance between the production of reactive oxygen species (ROS) and the antioxidant defense mechanisms of the body. Excessive ROS can damage cellular macromolecules such as lipids, proteins, and DNA, contributing to carcinogenesis through mutations, genetic instability, and altered signaling pathways. Biomarkers reflecting oxidative stress levels—such as 8-hydroxy-2-deoxyguanosine (8-OHdG), malondialdehyde (MDA), and major antioxidant enzymes (SOD, CAT, GPx, GR)—are present across various types of cancer.

Across multiple malignancies as well as chronic lymphocytic leukemia, 8-OHdG and MDA levels were consistently elevated, while antioxidant enzyme activities were reduced. These alterations correlate with disease stage and progression, suggesting their potential diagnostic and prognostic value. Moreover, the dual role of ROS—promoting tumor growth at moderate levels but inducing cytotoxicity at higher concentrations—highlights the complexity of redox regulation in cancer. Understanding the dual role of ROS—both in promoting and inhibiting tumor development—is essential for designing new therapeutic strategies targeting redox regulation and antioxidant defense enhancement. Moreover, natural polyphenolic compounds show promise as modulators of oxidative stress and epigenetic activity, offering potential anticancer effects.

Keywords: oxidative stress, cancer, 8-OHdG, malondialdehyde, antioxidant enzymes, polyphenols

Clinical (phospho)proteomics for precision medicine

C. R Jimenez

Clinical proteomics aims to disclose disease biology and drive improved diagnostics and treatment. The field has been catalyzed especially over the past decade by developments in sample preparation, mass spectrometry instruments with novel data acquisition modes and bioinformatics, together enabling comprehensive profiling at higher throughput and at lower protein input levels.

I will present our work in cancer and dementia. Highlights include novel screening markers for colorectal cancer discovered by stool proteomics that are in clinical development and cerebrospinal fluid proteomics in dementias showing excellent replication of novel biomarkers for differential diagnosis in own and external cohorts. Large scale pan-cancer tissue proteomics yielded tumor type enriched proteins for multi-cancer classification (http://r2platform.com/TPCPA). Phosphoproteomics of tumor tissue coupled to kinase activity analysis using INKA (ww.inkascore.org) is promising for individualized therapy response prediction, as highlighted using results derived from on-going studies in patient-derived xenografts and needle biopsies.

Altogether, we envision that clinical proteomics powered by precise measurements and dedicated analysis will realize the full potential of multi-parameter diagnostics and personalized medicine.

Towards cancer biomarker discovery: exploring clinical values and emerging technologies

P. Filippou

Early cancer diagnosis increases treatment success and improves survival rates. To improve quality of life for cancer patients there is an urgent need for effective biomarkers. Despite the remarkable progress in diagnostic applications, challenges remain, with existing cancer biomarkers often lack high sensitivity and specificity. Proteomic and/or other biomolecular signatures as cancer biomarkers hold promise for improving diagnosis and management. Established and emerging technologies are hereby summarized, for identifying proteome-based biomarkers that, alone or in combination, could enhance future cancer diagnostics. Key diagnostic approaches are discussed, such as mass spectrometry for biomarker discovery, immunoassays for biomarker validation and molecular Raman spectroscopy, for identifying spectral markers linked and combined to proteomic biomarkers. The examination of different diagnostic tools will focus on aggressive cancers using in vitro cellular models (monolayers and spheroids) and biological samples (such as serum and tissues). In addition, combining bioanalytical tools with computational analysis (i.e. machine learning) could further enhance our understanding of cancer development and progression. Together, these models and diagnostic tools facilitate a more comprehensive understanding of the disease mechanisms, holding great potential for unveiling drivers and biomarkers for cancer monitoring. Finally, a multiplexed biomarker panel, utilizing single or multimodal diagnostic platforms, would offer diverse future applications further strengthening the translational potential in personalized cancer medicine.

Single cell proteomics in translational research and diagnostics

M. Samiotaki

Single-cell proteomics (SCP) represents a critical paradigm shift in biomedical research, moving beyond the limitations of bulk analysis which often obscures crucial functional heterogeneity within complex tissues and cell populations. The high-resolution measurement of thousands of proteins at the individual cell level provides an unprecedented window into cellular signaling, regulatory states, and functional diversity that drives disease onset and progression. In medicine, SCP technologies are proving transformative by enabling the precise identification of rare, pathological cell subpopulations, such as drug-resistant tumor cells or inflammatory immune cells, and tracking their evolution in response to treatment. This capability is essential for discovering novel, cell-state-specific protein biomarkers, understanding complex cell-cell communication networks, and accurately delineating heterogeneous treatment responses in patient samples. By providing a truly individualized molecular view, SCP is poised to accelerate the development of personalized diagnostics and ultra-targeted therapeutics, fundamentally enhancing the realization of precision medicine.

Targeted metabolomics method development for the quantitative analysis of Diabetes Mellitus related serum biomarkers

Olga Begou

Diabetes mellitus (DM) is a chronic, multifactorial metabolic disorder characterized by insufficient insulin secretion, reduced insulin sensitivity, and persistent hyperglycemia. It encompasses several conditions, including prediabetes, type 1 and type 2 diabetes, gestational diabetes, and rarer forms. Sustained hyperglycemia and glycemic fluctuations progressively damage key organs such as the heart, kidneys, eyes, and nervous system. Due to the complex and heterogeneous nature of DM, precise biomarker quantification is essential for early diagnosis, monitoring disease progression, and guiding personalized therapeutic interventions. In this work, a set of clinically relevant DM-associated biomarkers was compiled, leading to the design of a targeted metabolite panel and the development of a validated quantitative method to assess its clinical applicability. A novel HILIC-MS/MS assay was established on a Bruker EVOQ Elite system using an Acquity UPLC BEH HILIC column and a binary gradient of ACN and ACN:H2O (50:50, v/v), both containing 10 mM ammonium formate (pH 9.5). The method enabled quantification of key metabolites, including 1,5-anhydroglucitol, glucose, fructose, mannose, leucine, isoleucine, glutamine, glutamate, phenylalanine, tyrosine, valine, and tryptophan. Validation followed standard bioanalytical guidelines, assessing recovery, precision, linearity, accuracy, and matrix effect. The assay was subsequently applied to serum samples from a multicenter cohort of 300 participants, enabling absolute concentration measurements. The primary aim was to reveal glycemic disturbances that may not be detected by conventional clinical markers such as fasting glucose or HbA1c. Statistical modeling, including covariate-adjusted regression and redundancy analysis, was performed to evaluate their independent associations with metabolic syndrome and diabetes, supported by likelihood ratio tests with false discovery rate correction. Sugars contributed minimally to the overall predictive value, while amino acids, especially glutamine-to-glutamate ratio emerged as a key independent marker of metabolic dysregulation. Moreover, 1,5-anhydroglucitol showed a moderate inverse association with fasting glucose and HbA1c, confirming its sensitivity as a short-term glycemic marker even in non-diabetic individuals, while branched-chain and aromatic amino acids correlated positively with triglycerides and the TyG index, reflecting early metabolic alterations linked to insulin resistance. The robust quantification of these metabolites strengthens precision medicine strategies, supports better clinical decision-making, and provides new insight into the metabolic and inflammatory pathways implicated in metabolic syndrome.

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Targeted Metabolomics and Machine Learning for Risk Stratification in Coronary Artery Disease: Insights from the CorLipid Study

O. Deda

Coronary artery disease (CAD) remains a major global health problem and a leading cause of death, increasingly affecting younger adults. Translating biomedical discoveries into clinically useful biomarkers is essential for improving prevention and management. The CorLipid study exemplifies this translation by integrating targeted metabolomics into clinical cardiology to identify and validate biomarkers associated with CAD severity and prognosis 1. Using complementary LC-MS/MS and GC-MS platforms, serum samples from patients with varying disease severity were analyzed for ceramides 2, acylcarnitines 3, fatty acids, and amino acids. Four key serum ceramides, Cer(d18:1/16:0), Cer(d18:1/18:0), Cer(d18:1/24:0), and Cer(d18:1/24:1) were quantified, with elevated levels correlating with increased thrombus burden in STEMI patients 4. Ceramide ratios (Cer16:0/Cer24:0 and C24:1/C24:0) were associated with CAD complexity, while the C24:1/C24:0 and C4/C18:2 ratios predicted major adverse cardiovascular events in diabetic patients 5. Thirteen acylcarnitines were quantified, showing distinct patterns across CAD phenotypes: lower C8, C10, C16, C18:1, and C18:2 in acute versus chronic coronary syndromes, and increased C4 and C5 with disease severity. The C4/C18:2 ratio emerged as a robust predictor of CAD severity 6. Machine learning models (XGBoost) integrating metabolomic and clinical data achieved high sensitivity and negative predictive value for obstructive CAD 7,8, demonstrating metabolomics' potential in early diagnosis and personalized cardiovascular care.

KEYWORDS

Coronary artery disease (CAD); targeted metabolomics; lipidomics; ceramides; acylcarnitines; biomarkers; LC-MS/MS; GC-MS; machine learning; XGBoost; SYNTAX score; thrombus burden; risk stratification; personalized medicine; CorLipid study.

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Cassandra study on pediatric pneumonia. New biomarkers revealed by metabolomics.

C. Virgiliou

Ventilator-associated pneumonia (VAP) remains one of the most frequent and challenging infections in critically ill children, with early diagnosis hindered by subjective clinical criteria and limited performance of current diagnostic methods. In this study, we investigated the potential of metabolomic and lipidomic profiling of blood samples for the discovery of novel biomarkers of VAP. A cohort of pediatric patients (6 months–15 years) admitted to the intensive care unit with suspected VAP was enrolled, and blood samples were collected at four time points (days 1, 3, 6, and 12).

Untargeted lipidomics using UPLC-HRMS (TIMS-TOF/MS) identified 144 lipid species across major classes including glycerophospholipids, glycerolipids, and sphingolipids. Stratification of patients by the modified pediatric clinical pulmonary index score (mCPIS) revealed distinct lipid profiles between high- and low-suspicion groups (mCPIS ≥ 6 vs. < 6). Specific lipid alterations were associated with pharyngeal culture results, notably the detection of Klebsiella pneumoniae and Staphylococcus aureus, highlighting the potential role of lipidomics in both VAP diagnosis and microbial etiology prediction.

In parallel, an untargeted GC–MS metabolomics workflow was optimized with emphasis on derivatization stability and sample storage conditions, ensuring reliable analysis for large-scale studies. Application of this approach to VAP patients yielded 43 identified metabolites, with multivariate and univariate analyses identifying significant associations between disease manifestation and amino acids such as aspartic acid, alanine, and pyroglutamic acid. These metabolites demonstrated strong discriminatory power at the stage of clinical suspicion.

Together, our findings demonstrate that integrated blood-based metabolomic and lipidomic profiling provides valuable insights into the pathophysiology of pediatric VAP. The identified molecular signatures hold promise as biomarkers for early diagnosis and for guiding targeted clinical decision-making, potentially improving outcomes in critically ill children.

New biomarkers in the prognosis and diagnosis of placental disorders of pregnancy.

A. Papapanagiotou

Preeclampsia (PE) is a multifactorial hypertensive disorder of pregnancy that affects approximately 2–8% of pregnancies worldwide and remains one of the leading causes of maternal and perinatal morbidity and mortality. Despite advances in obstetric care, the precise mechanisms underlying its pathogenesis are not fully understood, and reliable early diagnostic tools remain limited.Central to the development of PE is abnormal placentation, which leads to inadequate uteroplacental perfusion and systemic endothelial dysfunction. Angiogenic growth factors, such as placental growth factor (PlGF) and vascular endothelial growth factor (VEGF), along with their tyrosine kinase receptor Flt-1, play a pivotal role in normal placental vascular development. In preeclamptic pregnancies, impaired trophoblastic invasion results in the excessive release of the antiangiogenic soluble fms-like tyrosine kinase-1 (sFlt-1). This circulating receptor binds and neutralizes VEGF and PlGF, disrupting angiogenic balance and contributing to the endothelial damage characteristic of PE.Accumulating evidence highlights the clinical and prognostic relevance of the sFlt-1/PlGF ratio as a biomarker reflecting this angiogenic imbalance. Elevated sFlt-1/PlGF ratios have been shown to precede the onset of clinical symptoms and are valuable in both confirming and excluding PE, particularly in women at high risk. The incorporation of this biomarker into clinical practice has the potential to refine patient stratification, reduce unnecessary hospital admissions, and prevent preterm interventions, thereby improving outcomes and reducing healthcare costs. The purpose of this presentation is to provide an overview of the pathophysiological basis and clinical utility of the sFlt-1/PlGF ratio in the prediction, diagnosis, and management of preeclampsia, and to discuss the cost-effectiveness of implementing this biomarker in routine obstetric care.

Recent data in the diagnosis of plasma dyscrasias.

A. Gargalionis

Plasma-cell dyscrasias constitute a heterogeneous spectrum of clonal disorders defined by the production of monoclonal immunoglobulins or their fragments, encompassing monoclonal gammopathy of undetermined significance, smoldering myeloma, multiple myeloma, and light-chain amyloidosis. Laboratory medicine has traditionally provided the foundation for diagnosis through serum protein electrophoresis (SPEP) and immunofixation (IFE), which remain indispensable for the recognition and isotype characterization of monoclonal components. Recent technological advances, however, have transformed the diagnostic landscape by enhancing analytical sensitivity, resolving therapeutic interference, and enabling earlier recognition of pathological clones. Current International Myeloma Working Group (IMWG) and NCCN updates endorse a laboratory workflow centered on quantitative and proteomic methodologies that complement or supersede conventional gel-based techniques. Serum free light chain (FLC) assays now serve as a major diagnostic biomarker, with an involved/uninvolved FLC ratio ≥100 (and involved FLC ≥100 mg/L) constituting a myeloma-defining event. Furthermore, adoption of age- and renal-adjusted κ/λ reference intervals significantly improves specificity, reducing false positives in elderly and renally impaired patients, especially in the evaluation of systemic AL amyloidosis. Heavy/light chain (HLC) analysis provides isotype-specific quantification and insight into immune paresis, refining risk assessment in MGUS and smoldering disease. The introduction of mass spectrometry (MS)—both MALDI-TOF and LC-MS—represents the most significant innovation in the field. MS achieves superior sensitivity and precision compared with IFE, accurately distinguishing endogenous M-proteins from therapeutic monoclonal antibodies such as daratumumab, identifying light-chain glycosylation linked to amyloidogenic potential, and detecting low-level clones beyond the range of electrophoretic methods. In parallel, rationalization of urine studies based on serum thresholds and renal function now allows many laboratories to omit 24-hour urine electrophoresis without compromising diagnostic accuracy. Finally, minimal residual disease (MRD) assessment using next-generation flow or sequencing and peripheral-blood MS extends laboratory evaluation into the post-treatment phase, correlating molecular clearance with long-term survival. Collectively, these developments redefine the diagnostic paradigm of plasma-cell dyscrasias, shifting from semi-quantitative visualization of monoclonal bands to molecular and proteomic fingerprinting. The integration of MS with FLC and HLC testing establishes a unified, interference-free, and highly sensitive diagnostic strategy that supports precision monitoring, individualized risk stratification, and timely therapeutic intervention in plasma-cell disorders.

Kidney Function Assessment in 2025: Moving Beyond Creatinine to Improve Clinical Decision-Making.

Etienne Cavalier

Accurate evaluation of kidney function is essential for the diagnosis, staging and follow-up of chronic kidney disease (CKD). Serum creatinine, the most widely used marker, remains inexpensive and well validated but presents physiological and analytical limitations, including variability related to muscle mass, diet, and tubular secretion, as well as interferences depending on the measurement method. Cystatin C has emerged as a valuable complementary biomarker, being less affected by muscle mass and demographic factors and recommended by the 2024 KDIGO guidelines in situations where creatinine is unreliable — such as in patients with abnormal body composition, extreme BMI, limb amputation, elderly individuals, or unexplained elevations of serum creatinine. Combining creatinine and cystatin C improves the accuracy of estimated GFR (eGFR) and should increasingly be adopted when clinical decisions depend on precise kidney function assessment. Several equations (CKD-EPI, EKFC) have been developed to refine GFR estimation, with the EKFC approach offering improved performance across all ages and eliminating the need for race adjustment — an important step toward equity in care. Measured GFR using exogenous markers such as iohexol clearance remains the reference method and is clinically necessary in selected situations (e.g., before nephrotoxic treatments, in transplant evaluation, in patients with extreme BMI, amputations, or unexplained creatinine elevation). Its wider implementation in specialized laboratories would significantly improve patient management. Albuminuria, particularly the albumin-to-creatinine ratio (ACR), continues to play a central role in CKD risk stratification and prognosis. Overall, integrating these complementary tools, supported by a clear understanding of their strengths and limitations, enables a more precise and clinically meaningful assessment of kidney function.

Molecular Approaches -Omics in the Diagnosis and Prognosis of Pulmonary Arterial Hypertension.

A. Vassiliou

Pulmonary arterial hypertension (PAH) is a serious condition characterized by increased pressure in the arteries that carry blood from the heart to the lungs. Omics technologies are a fundamental research tool in PAH, offering new approaches to understanding the disease and prospects for early diagnosis. Specifically, genomics identifies mutations in genes associated with hereditary forms of PAH, enabling pscreening of high-risk individuals. Epigenetics and transcriptomics reveal molecular changes that precede clinical symptoms, while proteomics and metabolomics identify biomarkers in the blood, creating multifactorial profiles for more accurate diagnosis and prognosis. Genomics is the most clinically established technology. Genetic testing for mutations (e.g., in the BMPR2 gene) is recommended for patients with a family history, facilitating the early identification of high-risk patients and confirmation of hereditary forms of PAH. The other omics technologies have discovered promising diagnostic biomarkers. However, their use remains primarily experimental due to high costs, technical complexity, and the need for validation in large clinical trials. Furthermore, interpreting the vast amounts of data requires specialized bioinformatics tools. Collectively, these technologies help us better understand the pathophysiology of PAH and enable the development of personalized models for early diagnosis, risk prediction, and customized therapeutic management, aiming to reduce mortality and improve the quality of life for PAH patients.

Lipoproteins and serum miRNAs as Biomarkers for Cardiovascular Disease.

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ABSTRACT

Cardiovascular diseases (CVDs) remain the leading cause of morbidity and mortality worldwide, underscoring the urgent need for early, accurate, and minimally invasive diagnostic strategies. Plasma lipoproteins, including low-density lipoproteins (LDL), very-low-density lipoproteins (VLDL) and high-density lipoproteins (HDL), play a central role in lipid transport with some of them (non-HDL lipoproteins) being causal to atherosclerotic plaque formation. On the other hand, HDL particles exhibit atheroprotective properties, including cholesterol efflux and anti-inflammatory effects. Currently, traditional methods of measuring plasma lipids and lipoproteins continue to be used as biomarkers to determine CVD risk due to their lost cost, standardization, and availability across clinical laboratories, coverage by medical insurance, and validity from many large-scale trials. However, plasma lipoprotein levels are affected by several comorbidities (obesity, diabetes, chronic inflammatory/autoimmune diseases). Moreover, lipoproteins are modified (i.e. oxLDL) and accumulating evidence indicates that the functionality of the particles is a better predictor for CVD than their cholesterol content suggesting the need for more specific diagnostic tests that are not currently used in clinical practice. Another emerging epigenetic CVD risk biomarker is the measurement of circulating miRNAs, small non-coding RNAs that regulate gene expression at the post-transcriptional level in various tissues and exhibit remarkable stability in the bloodstream due to their encapsulation in extracellular vesicles or association with lipoproteins. The expression profiles of miRNAs change in response to pathological states, making them attractive candidates for non-invasive biomarkers. MiRNAs such as miR-126, miR-21, and miR-155 have been detected in coronary syndromes and atherosclerosis reflecting endothelial dysfunction, inflammation, and vascular remodeling, processes central to CVD pathogenesis. Recent advances in high-throughput profiling techniques (omics) have enabled sensitive and specific detection of molecules in plasma (lipids, proteins, metabolites, miRNAs), supporting their use in risk stratification, diagnosis, and prognosis of CVDs. In this context, preliminary miRNA transcriptomics data from the European MCSA-SE project CardioSCOPE using plasma samples from cohorts of patients with Acute Myocardial Infarction (AMI) versus Stable Angina (SA) will be presented. Integrating lipoprotein and miRNA biomarkers into clinical practice could revolutionize CVD management by enabling earlier intervention and personalized therapeutic strategies.

KEYWORDS: lipoproteins; microRNAs; transcriptomics; cardiovascular disease; biomarkers; molecular diagnostics.

From Omics to the Clinic: Bioanalytical Tools Driving NMR-Based Personalized Medicine.

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In recent years, the rapid evolution of -omics sciences has profoundly transformed biomedical research, paving the way for a new era of precision and personalized medicine. Among these disciplines, metabolomics occupies a central position as the functional endpoint of the -omics cascade, directly reflecting the dynamic biochemical status of an organism at the time of sample collection. Through advanced spectroscopic and spectrometric analyses, metabolomics enables the comprehensive characterization of metabolic phenotypes, offering a direct window into disease mechanisms, therapeutic responses, and individual variability.

However, translating metabolomic data into clinically actionable knowledge requires robust, high-throughput, and reproducible bioanalytical tools capable of extracting subtle yet biologically significant signals from complex metabolic profiles. In this context, Nuclear Magnetic Resonance (NMR) spectroscopy has emerged as a powerful and quantitative platform for metabolomics, providing unparalleled reproducibility and minimal sample preparation.

Here, we present recent and ongoing developments of our laboratory in bioanalytical methodologies and computational pipelines based upon AI (artificial intelligence) and ML (machine learning) algorithms designed to enhance the information yield, analytical throughput, and quality control of NMR-based metabolomic studies. We discuss novel strategies for signal optimization, data normalization, all aimed at improving biomarker discovery and clinical interpretation.

Finally, we illustrate the translational potential of these approaches through real-world applications in breast cancer, diabetes and gastrointestinal diseases cohorts highlighting how refined metabolomic profiling can support or in certain circumstances not early diagnosis and monitoring of diseases molecular mechanisms. These advancements underscore the critical role of NMR-driven metabolomics as a bridge between molecular insight and clinical decision-making in the framework of next-generation personalized medicine.

Bioinformatics: Bridging Bench and Bedside.

A. Malousi

Bioinformatics has a transformative impact on modern medicine, bridging the gap between the laboratory and the clinic and providing powerful tools to understand and manage diseases at the molecular level. By integrating and analyzing large-scale biological data — including genomic, transcriptomic, proteomic, and metabolomic profiles— bioinformatics enables the discovery of biomarkers for diagnosis, prognosis, and personalized patient care.

This presentation will showcase key applications and technologies, such as predictive models and will analyse significant gaps and challenges in translating big data into clinical practice, including system interoperability and safeguarding patient privacy.

Beyond being a computational tool, bioinformatics serves as a catalyst for precision medicine, turning laboratory insights into actionable clinical solutions and opening new avenues for improved healthcare delivery.

From the Laboratory to Precision Medicine... through the Contribution of Molecular Technology and Artificial Intelligence.

A. Margoni

The modern vision of medicine is its transformation from a generalized, population-based approach into an individualized science, Presicion Medicine. Notwithstanding the wide gamut of drugs, traditional "trial and error" model of treatment has contributed to increased morbidity and mortality over the years. Recent advances in molecular technology have revealed that genetic diversity is mainly inculpated for the variability in therapeutic response and prognosis, establishing molecular diagnostics as a cornerstone of clinical effectiveness. Next-generation sequencing (NGS), automated multiplexed immunoassays and other advanced molecular modalities appear to be the "passkey" for unlocking "evidence-based" therapy by serving as a reliable diagnostic, prognostic and surveillance tool simultaneously. Incorporation of multiple genes, biomarkers, miRNAs and DNA methylation in diagnostic algorithms reassures an accurate stratification in advance of therapeutic interventions, whilst pharmacogenomics may predict therapeutic failure and severe adverse effects by detecting mutations and polymorphisms. Artificial intelligence (AI) offers powerful tools to analyze complex datasets, integrate medical history, and provide standardized interpretations, while ensuring speed and consistency. Coupled with bioinformatics, laboratory medicine increasingly contributes to clinical decision-making, tailored therapeutic strategies and effective screening protocols in high-risk population. However, ultimate responsibility for validation and ethical application lies with the clinician-scientist, whose expertise and intuition remains indispensable in defining the scientific and moral boundaries of medical practice. Ultimately, interdisciplinary collaboration among specialists in biology, genetics, biochemistry, genomics, and bioinformatics is essential. Through such synergy, laboratory medicine can play its pivotal historical role in shaping a more homocentric Medical Science.

ORAL PRESENTATIONS

Reduced Serum Interleukin-2 Levels In Type 2 Diabetes Mellitus: Implications For Age-Related Immune Dysregulation And Therapeutic Targeting.

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BACKGROUND
Type 2 diabetes mellitus (T2DM) is characterized by chronic low-grade inflammation and impaired immune regulation. Interleukin-2 (IL-2) plays a dual role in immune homeostasis, promoting T cell activation while supporting the maintenance of regulatory T cells (Tregs), which are often deficient in metabolic disorders.
OBJECTIVE
To investigate the serum levels of IL-2 in individuals with T2DM and explore its association with clinical parameters such as age, BMI, and gender, aiming to identify potential immunological dysfunctions and therapeutic targets.
METHOD
Serum IL-2 levels were measured using ELISA in 33 participants (13 with T2DM, 10 with type 1 diabetes, and 10 healthy controls). Statistical analysis was performed using SPSS to assess the association between IL-2 levels and diabetes type, BMI, and sex.
RESULTS
IL-2 levels were significantly lower in individuals with T2DM compared to healthy controls ($p=0.012$). A negative correlation was observed between IL-2 levels and age ($p=0.002$), suggesting age-related decline in immune regulation. No significant differences were found in relation to sex or BMI within the T2DM group.
CONCLUSION
The reduced IL-2 levels observed in T2DM patients, particularly in older individuals, underline the potential role of impaired Treg-mediated immunoregulation in disease progression. IL-2 may serve as a useful biomarker or therapeutic target in personalized immunomodulatory strategies for T2DM.

Keywords: Interleukin-2, Type 2 Diabetes Mellitus, Cytokines, ELISA, Immunoregulation, Tregs

The effects of aging and age-related DNA damage on inflammatory and anti-bacterial responses.

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Aging is a complex process associated with accumulation of DNA damage, leading to a gradual decline of immune cell function, known as immunosenescence and dysregulated inflammatory response, known as inflammaging. This contributes to an increased likelihood of chronic and acute comorbidities, including infections. Macrophages are the first line of defense against such infections, as they specifically recognize and uptake pathogens, secrete pro-inflammatory cytokines and facilitate pathogen clearance. Functional biomarkers that can distinguish dysfunctional aged macrophages have not been characterized. Moreover, how ageing and age-related DNA damage affect macrophage responses and pathogen clearance remains unknown.

To address this, we utilized a mouse model of ageing and age-related DNA damage using macrophages from young and aged mice as well as from ERCC1F/+ or ERCC1F/- mice, the latter being defective in DNA damage responses, and mice lacking ERCC1 develop progeria. Bone Marrow-derived macrophages (BMDMs) from these mice were stimulated with a TLR-2 ligand, resembling Gram+ bacterial infection, and differential expression of genes was analyzed by RNA sequencing. Furthermore, we challenged these cells with Group Beta Streptococcus (GBS) and studied the bacterial burden and their ability to activate the antibacterial mechanism of LC3 associated phagocytosis (LAP). The results revealed that macrophages from aged mice displayed a distinct gene expression profile, with increased expression of inflammation-related genes. In cell culture analyses we showed enhanced inflammatory cytokine production and higher expression of the histone demethylases PHF2 and PHF8. In contrast, ERCC1F/- mice display the exact opposite phenotype. Additionally, although macrophages from both aged and ERCC1 F/- mice failed to induce LAP, only ERCC1 F/- macrophages had significantly enhanced GBS load.

Our findings demonstrate that aged macrophages and macrophages from DNA-damage driven aging display altered inflammatory and antibacterial responses, which could be attributed to distinct gene expression profile and expression of epigenetic regulators. In addition, we showed that inflammatory pathways and inflammation related markers are prominent in aged macrophages. Unraveling the complexity of these mechanisms will help us understand macrophage contribution in infection pathology in aged individuals.

This work was supported by a grant from “Hevolution foundation”

Study Of Serum Lipid Profile In Breast Cancer Patients Receiving Adjuvant Therapy.

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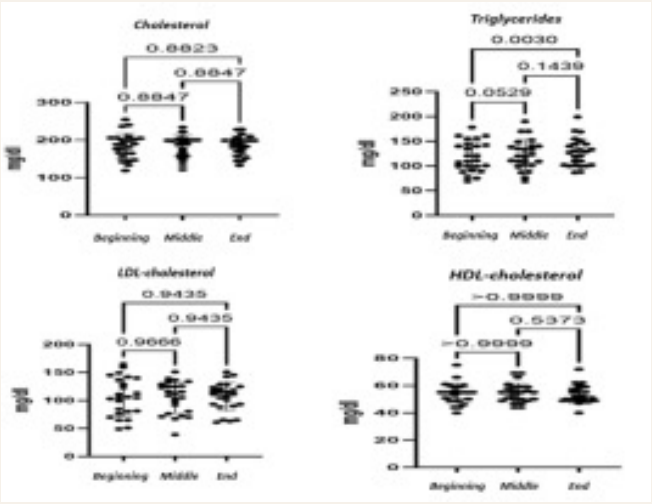
INTRODUCTION
Breast cancer (BC) is the second common cause of death in women. The relationship between serum lipids levels and this type of cancer remains unclear.
AIM
The determination of serum lipid profile (Cholesterol, Triglycerides, LDL-cholesterol, HDL-cholesterol) in BC patients undergoing adjuvant therapy (5FU, cyclophosphamide, doxorubicin, paclitaxel) at three time points of therapy process (beginning – middle – end of therapy).
Material and Method
We carried out photometric measurements for serum levels of parameters, using the Beckman Coulter's automated analyzer AU5800 for each of the 75 blood samples (25 samples for each time point).
RESULTS
The mean values of serum levels of Cholesterol, LDL and HDL between the three time points, no statistical significance is observed. In case of triglycerides, only the comparison between the beginning and end time points shows a statistically significant difference (P=0,003). Box-Plot diagrams depicting the levels of the four lipids at three stages of adjuvant treatment (A: BEGINNING, B: MIDDLE, C: END)
CONCLUSION
TGs level was only significantly increased in breast cancer patients after effective chemotherapy and appears to be a sensitive measurement to determine the effect of adjuvant chemotherapy.

The project is financially supported by ELKE UniWA (Special Account for Research Funds of University of West Attica).



Lost In Translation: How Pre-Analytical Errors Distort External Quality Assessment (EQA) Outcomes.

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The pre-analytical phase of a test remains the most error-prone phase. Improper sampling, use of not recommended tube, handling of samples, deviations from storage requirements can compromise the reliability of test results. In the context of External Quality Assessment (EQA) such errors and the failure to follow reconstitution instructions not only affect laboratory performance but also reduce the educational impact of EQA participation.

This work aimed to raise awareness among healthcare professionals and laboratory staff about pre-analytical errors and the importance of following the urgent instructions of the EQA provider to improve the accuracy and reliability of diagnostic results.

A real-life case study in which, during an EQA distribution, one of the samples provided was found to be unsuitable for analysis due to an error in the manufacturing process. Labs were immediately notified for the sample's replacement via SMS, email, and pop-up notifications on the results entry platform. The notifications instructed to ignore the defective sample and wait for a new one before analyzing and submitting results for that cycle.

Despite the urgent multi-channel notification, 79 out of 245 laboratories proceeded with the analysis and reported results from the compromised sample. Among them, 21 laboratories did not realize their mistake, while 58 requested replacement of their results only after receiving the correct sample and after identifying significant discrepancies with other laboratories. It is worth noting that all laboratories that produced incorrect results performed the analysis after the provider issued the notification.

Also, 26 laboratories responded to the pop-up question regarding whether they understood the replacement instructions. Among them, 13 laboratories responded positively and indeed understood the instructions and recorded correct results, while the remaining 13 recorded incorrect results. Of the latter, 7 responded that they understood the instructions and 6 did not.

Several laboratories reported that they did not receive SMS notifications because their contact information was outdated or missing. Although laboratories are informed about the possibility of receiving SMS regarding deadlines or other relevant updates, some do not consent to the use of their personal mobile phones.

In addition, the large number of laboratories reporting results from the defective sample significantly impacted the statistical analysis. The inclusion of falsely low values disrupted the Gaussian distribution of results, causing a shift in the calculated consensus mean and an artificial increase in the standard deviation (SD). In several cases, extremely low, abnormal results (e.g., glucose = 0) were included in the data set, skewing the results. As a result, valid laboratories were not evaluated correctly while invalid laboratories received a good z-score.

This case shows that human errors, not technical errors, are the main cause of preanalytical mistakes. Improving it requires better communication strategies and compliance monitoring tools from the EQA provider, as well as strong internal process protocols and ongoing staff training specifically focused on preanalytical procedures by the lab.

Molecular Targeting In Schizophrenia: A Pharmacological Evaluation Of Atypical Antipsychotics Using Cadd.

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BACKGROUND: Schizophrenia is one of the most complex psychiatric disorders, arising from a multifactorial interplay of genetic, neurodevelopmental and neurobiological mechanisms. Atypical antipsychotics outperform first generation drugs, yet they are ineffective against cognitive and negative symptoms and carry significant adverse effects.

OBJECTIVE: The present study employed Computer-Aided Drug Design (CADD) to evaluate the molecular binding affinities of four atypical antipsychotics, namely Risperidone, Aripiprazole, Clozapine, and Quetiapine, at the dopamine D2 receptor (DRD2).

MATERIALS AND METHODS: Docking simulations were performed in ArgusLab, with each ligand docked twice using grid boxes of 15 Å and 20 Å along the X, Y and Z axes. The GADock engine was used, with the parameter of Max Generations set to 10^4, while all other parameters were kept at default values. Lowest energy poses were selected and visualized in UCSF Chimera. Notably, the crystal structure of DRD2 used in this study was co-crystallized with Risperidone, which was removed prior to performing docking simulations to validate the reliability of the computational protocol.

RESULTS: The results of the study demonstrated that Risperidone and Aripiprazole, exhibited the highest affinities for DRD2, with ΔGRisperidone = -11.3441kcal/mol and ΔGAripiprazole = -10.9505kcal/mol.
The values presented are consistent with the known clinical effectiveness of the preceding antipsychotics in alleviating positive and extrapyramidal symptoms. Quetiapine demonstrated intermediate binding (ΔGQuetiapine = -10.9401kcal/mol), reflecting its transient receptor occupancy, whereas Clozapine displayed the lowest affinity (ΔGClozapine = -10.7639kcal/mol), in accordance with its broad and non-selective pharmacological profile.

CONCLUSION: Our analysis presents the utility of CADD as a cost-efficient and reliable tool in psychopharmacology. By elucidating receptor/drug interactions, computational approaches can support the design of optimized antipsychotic therapies, aiming to improve efficacy and minimize adverse effects. Future therapeutic strategies in schizophrenia may also be guided by the predictive power of CADD.

Synthetic Neurosteroids As Modulators Of Psoriatic Inflammation.

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Psoriasis is a chronic inflammatory skin disease influenced by both genetic and environmental triggers, with an unclear pathogenesis. The disease is characterized by alterations in skin homeostasis and a pronounced immune response, with notable infiltration of antigen-presenting cells that contribute to the initiation and progression of the disease. Clinical studies have proposed a correlation between the neurosteroid dehydroepiandrosterone (DHEA) and dermatological conditions. Reduced serum levels of DHEA have been observed in patients with psoriasis. However, its therapeutic application is limited due to rapid metabolic conversion into active androgens and estrogens. BNN27, a synthetic analogue of DHEA, has been shown to exert significant anti-inflammatory and immunomodulatory effects. Importantly, BNN27 exhibits a delayed metabolic profile compared to DHEA, thereby enhancing its therapeutic potential. The present study aimed to investigate the role of BNN27 in the context of psoriasis, utilizing the well-established imiquimod (IMQ)-induced murine model.

METHODS

Wild-type male mice (8–12 weeks old) were used in this study. Psoriasis-like skin inflammation was induced via daily topical application of imiquimod (IMQ) cream on their back skin and right ear. BNN27 was administered intraperitoneally at doses of 10, 50, and 100 mg/kg for seven consecutive days. At the end of the treatment period, mice were euthanized, photographs of the skin lesions were taken, and blood and tissue samples were collected for further analysis. Disease severity was evaluated using a modified Psoriasis Area and Severity Index (PASI) scoring system, assessing erythema, scaling, and thickness.

RESULTS

Administration of BNN27 at a dose of 10 mg/kg resulted in a marked decrease in PASI score by the sixth day of treatment compared to vehicle-treated mice. Histological evaluation of the affected area of BNN27-treated mice revealed that BNN27 administration led to a reduction in epidermal thickness, normalization of rete ridge architecture, decreased immune cell infiltration in the dermis, and reappearance of the granular layer. In contrast, flow cytometry analysis showed no significant changes in the immune cell populations following treatment. Furthermore, protein expression analysis indicated that levels of pro-inflammatory cytokines remained unchanged. However, a significant downregulation of AKT2 protein levels was observed in mice treated with BNN27 at both 10 mg/kg and 100 mg/kg doses.

CONCLUSIONS

These findings suggest that BNN27 may exert anti-inflammatory effects in psoriasis. However, further investigation of protein expression pathways following BNN27 treatment may serve as a valuable tool for monitoring disease progression and therapeutic response.

GC-MS metabolic fingerprints of Dried Blood Microsamples in comparison to Plasma.

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Blood microsampling (BμS) has emerged as a promising approach in the analysis of endogenous metabolites, especially for its minimally invasive sample collection and simplified analysis logistics. Different BμS devices are currently available; although they share similar concepts for sample collection, matrix variations might impact the analytical outcomes. The aim of the present work was to evaluate the global metabolic profiles obtained from different BμS devices, namely Dried Blood Spots (Whatman), Volumetric Absorptive Microsampling (Mitra), and Capitainer cards, compared to plasma.
For this purpose, venous blood was collected from 10 healthy, overnight-fasted individuals and loaded onto the devices. Plasma was produced from the same blood samples, and analysis was performed using a GC-MS method with methoxyamine and trimethylsilane derivatization. The metabolite extraction protocol was optimized and methanol was selected as the optimum extraction solvent. The different matrices were compared regarding the number, intensity, and annotation of features. Furthermore, blood microsample metabolic profiles collected from the fingertip of three individuals were compared against paired plasma and blood.
BμS, mainly from Mitra and Capitainer devices, provided equivalent or greater information than plasma, considering the number and intensity of features, precision, and annotated metabolites intensity. Overall, the results suggest that BμS is a viable alternative for untargeted blood metabolomics, providing comparable information to conventional matrices. Capillary blood collected using Mitra devices exhibited variations when compared to venous whole blood and plasma, with distinct trends observed across several metabolites. Consequently, further research is necessary to determine the applicability of this approach in specific contexts.

KEYWORDS: GC-MS, Microsampling, Untargeted Metabolomics.
The work has been Funded by the European Union under the HORIZON-MSCA-2021 project 101073062 : HUMAN – Harmonising and unifying blood metabolic analysis networks.

A Comparative Analysis Of Zoonotic DiseasesIn Albania And Europe.

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ABSTRACT
Zoonotic diseases, which are transmitted from animals to humans, present significant public health challenges worldwide. Albania, with its diverse ecosystems and agricultural practices, faces unique risks compared to other European countries. This study aims to:
- Identify the prevalence, transmission patterns and control measures of zoonotic diseases in Albania, comparing these trends with those seen across Europe.
- Underscore the necessity for integrated approaches in managing zoonotic diseases, fostering regional cooperation, and enhancing surveillance and response mechanisms.
Key zoonotic diseases such as bovine brucellosis, bovine tuberculosis, anthrax, leptospirosis are major concerns in Albania, primarily due to close human-animal interactions in rural communities. Limited surveillance and diagnostic capabilities contribute to underreporting, posing a challenge in assessing disease burden accurately. In contrast, European countries generally benefit from advanced monitoring systems, coordinated veterinary and public health policies and widespread vaccination programs that effectively reduce the occurrence of outbreaks.
This presentation will analyze epidemiological data, highlighting Albania's challenges, including gaps in biosecurity, veterinary healthcare, and public awareness. Additionally, it will explore successful strategies implemented in European nations that could be adapted to Albania's context.
Strengthening cross-border collaboration and improving disease prevention strategies are crucial for reducing zoonotic transmission risks.

KEY WORDS: zoonosis, infection, prevalence

Circulating miRNA Risk Score for bladder cancer prognosis: Insights from Patient-Derived Xenografts and Clinical Cohorts.

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The heterogeneity of bladder cancer (BlCa) prognosis necessitates patients' lifelong surveillance, emphasizing the need for modern molecular tools development towards tailored therapeutics. In the present study, by employing a miRNA-seq approach, we explored the circulating miRnome of BlCa aiming to provide new insights towards their potential clinical utility. miRNA-seq was performed in 15 BlCa patient-derived xenograft (PDX) mouse model tumors and their corresponding plasma samples, while the most strongly deregulated miRNAs were assessed in 216 BlCa patients' circulation following 3'-end polyadenylation & RT-qPCR. Cox proportional hazards regression analysis was applied to establish a circulating miRNA-based non-muscle invasive and muscle invasive BlCa (NMIBC & MIBC)-specific risk scoring system (miRisk-score). miRNA-seq identified concurrent upregulation of miR-1290, miR-193b, miR-375, miR-4488, miR-100 & miR-1246 in both PDX tumors and plasma, strongly linked to advanced stage/grade and worse PDX outcome. Our screening cohort validated their association with unfavorable prognostic features, while elevated pre-treatment circulating miR-375/miR-4488 and miR-1290/miR-193b resulted in worse NMIBC and MIBC outcome, respectively. Following, we established a prognostic NMIBC-specific (miR-375/miR-4488) and MIBC-specific (miR-1290/miR-193b) circulating risk-score that outperformed the prognostic utility of each circulating miRNA alone. High NMIBC miRisk score was associated with increased early relapse and progression while multivariate models incorporating miRisk-score improved T1/high-grade patients' stratification. In addition, higher MIBC miRisk-score was associated with worse T2-T4 patients' overall survival, while its integration with tumor stage enhanced risk prediction. NMIBC-specific and MIBC-specific circulating miRisk-score evaluation provides a minimally invasive tool to complement biopsies, reducing unnecessary follow-up invasive procedures and guiding personalized treatment.

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Investigation of the effect of modifying polymorphisms to clinical and biochemical characteristics of APOE4 dementia patients.

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INTRODUCTION

APOE4 is an established genetic risk factor for the development of late-onset Alzheimer's disease (AD) and a detrimental factor for other dementias; however, there is a substantial variation in disease onset and progression, even among 4/4 homozygotes. Many polymorphisms in other genes are being examined as APOE4 risk modifiers. Klotho, a longevity membrane-bound secreted factor and ECM protein fibronectin are postulated to exert neuroprotective effects when up-regulated and their role is examined extensively in demented brains.

AIM

To develop methods for accurate genotyping of two missense polymorphisms in KLOTHO and FN1 (fibronectin) genes that affect their expression and investigate their impact on clinical and biochemical characteristics of dementia APOE4 carriers.

PATIENTS-METHODS

Eighty (80) consecutive Greek APOE4 dementia patients with available data in CSF biochemical markers (amyloid b42, tau, p-tau181 and their ratios) were recruited and genotyped in this pilot study (BRAIN Precision TAEDR-0535850 funding). The Fujirebio INNOTEST ELISA kits were used for the biomarkers' measurements. The reagents for genotyping of the two SNPs (rs140926439, FN1 NG_012196.1:g.16777G>A, p.Gly357Glu and rs9536314, KLOTHO NG_011485.2:g.42760T>G, p.Phe352Val) were provided by Roche Diagnostics Hellas (ELKE NKUA #19635 funding). Statistical analysis was carried with the SNPStats tool and the SPSS vs.30 software (IBM).

RESULTS-CONCLUSION

Real-time qPCR genotyping methods with melting curve analysis were developed in the LightCycler 480 platform (Roche) and validated adequately. The 80 patients were ascertained either as AD (n=20), AD mixed with other dementia (n=36) or other dementia according to their biochemical profile and clinical characteristics (presentation age range 52-85y). Twenty of the patients were homozygotes APOE4/4. No fibronectin alteration was detected. The KLOTHO G alteration was detected in 14 (22%) of APOE3/4 heterozygotes and in 5 (29%) APOE4/4 homozygotes (Hardy-Weinberg p>0,05). The carriers' presentation age and p-tau didn't differ while amyloid and tau indices were slightly worse in KLOTHO carriers' vs the rest of the whole dementia population (mean values±SE were 470±39 vs 538±29 pg/ml for amyloid and 556±130 vs. 448±41 pg/ml for tau) without reaching statistical significance (most probably due to the limited population size). The same trend is being observed when analyzing AD only or AD-mixed subpopulations. Due to conflicting data with other literature reports on these modifying SNPs, further functional studies are needed to corroborate the postulations on APOE4 dementia patients.

ABSTRACTS OF POSTER PRESENTATIONS

Heterozygous Lepore Hemoglobin: A Case Presentation.

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Introduction: Hb-Lepore is a structurally abnormal hemoglobin that results from in-frame fusion between the 5' end of the δ-globin gene and the 3' end of the β-globin gene, formed by unequal crossover or gene conversion events during meiosis. The aim of this study is the presentation of an Hb-Lepore heterozygote case.
Materials and Methods: Female patient, aged 28 years, was presented at the laboratory for prenatal testing. Among other tests, whole blood count (Sysmex XN-550 hematology analyzer), iron profile (Siemens Advia 1200 Biochemistry Analyzer) and Hb electrophoresis (Sebia Hydrasys 2 Electrophoresis Analyzer) were performed.
Results: Test results were as follows: hematocrit 35.3 %, Hemoglobin 11.8 g/dL, RBC 5.24 M/μL, MCV 67.0 fL, MCH 22.5 pg, MCHC 33.6 g/dL, serum iron 120 μg/dl and ferritin 5 ng/mL. The patient presented hypochromia, anisocytosis and poikilocytosis. Hb electrophoresis in agarose (pH 8.6) showed an abnormal pattern with mild elevation in HbA2 (3.1%), mild reduction in HbA (85.5%), normal HbF (0.5%) and Hb Lepore (10.9%). Sickling test was negative. Electrophoresis at acid pH (6.2) showed a prominent HbA band and a faint band in the F region. The presence of Hb Lepore was confirmed by means of High Performance Liquid Chromatography (Arkray Adams HA 8160 HPLC automated analyzer).
Discussion: Hb Lepore is a common abnormal hemoglobin seen in the Mediterranean region, especially in Central Portugal and in the Spanish Alta Extremadura. The heterozygous form of Hb Lepore is asymptomatic and has a pattern resembling minor thalassemia. Electrophoresis pattern shows aberrant Hb-Lepore fractions at a rate of 5–10% and a decreased percentage of HbA. The homozygous state is clinically similar to beta thalassemia intermedia or major. Hb-Lepore identification at the laboratory includes whole blood counts, red cell indices, hemoglobin electrophoresis at alkaline and acid pH, as well as hemoglobin analysis by HPLC. A correct diagnosis is essential for proper clinical management and genetic counseling.

Hereditary Persistence Of Fetal Hemoglobin (HPFH).

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INTRODUCTION

Hereditary Persistence of Fetal Hemoglobin (HPFH) is a rare benign asymptomatic genetic disorder where the Hb-F persists in adult life. Usually, it is discovered on screening for other hemoglobinopathies or glycosylated hemoglobin measurement. The aim of this study is to describe a case of HPFH.

CASE REPORT

A 32-year-old Caucasian female was referred to the Biochemistry Laboratory for routine antenatal tests. Whole blood count results were as follows: RBC 6.21 M/μL, HB 10.9 g/dL, MCV 62.4 fL, MCH 17.6 pg, MCHC 28.2 g/dL, anisocytosis ++, microcytosis++ and hypochromia++. Agarose hemoglobin electrophoresis on alkaline pH 8.6 showed elevated levels of HbF (44.1 %), elevated levels of HbA2 (4.1 %) and reduced levels of HbA (51.8 %). Sickling test was negative. Serum iron was 30,2 μg/dl and ferritin 6,0 ng/mL. HPFH was further confirmed with high performance liquid chromatography (measurements were performed by Sysmex XN-550 hematology analyzer, Siemens Advia 1200 Biochemistry Analyzer, Sebia Hydrasys 2 Electrophoresis Analyzer and Arkray Adams HA 8160 HPLC automated analyzer

DISCUSSION

HPFH is inherited in a Mendelian way, caused either by large deletions in the human beta globin subunit gene or by point mutations in the promoters of the gamma globin genes. An incidental finding of HbF with or without a family history should be further investigated, as it could be due to HPFH or other underlying conditions, such as leukemias (juvenile chronic myeloid leukemia acute myeloblastic leukemia, lymphoblastic leukemia, chronic myeloid leukemia) and bone marrow failure syndromes (Diamond-Blackfan anemia, dyskeratosis congenita, Fanconi anemia, Shwachman-Diamond syndrome). Moreover, patients with beta thalassemia have a variable increase in HbF determined by the degree of beta chain deficiency and co-inheritance of alpha thalassemia. Trisomy 13 is associated with the delayed switch of HbF to HbA and persistently elevated HbF levels. HPFH can also be drug-induced by drugs like hydroxyurea (ribonucleotide reductase inhibitor) and the thalidomide analog pomalidomide (immunomodulatory drug).

Reference Intervals For Serum Concentrations Of Tartarate Resistant Acid Phosphatase-5b For Greek Adult Population.

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BACKGROUND-OBJECTIVE
Bone turnover markers (BTMs) reflect the metabolic activity of bone tissue and can be used to monitor osteoporosis therapy. Tartrate-resistant acid phosphatase, isoform 5b (TRACP-5b) is a bone resorption marker not influenced by renal function or food intake and can be measured in serum by immunoassays. We aimed to determine reference intervals (RI) for serum concentrations of TRACP5b for the Greek adult population.
METHODS
We collected samples from 431 apparently healthy Greeks (142 men as well as 149 pre- and 140 post-menopausal women), who volunteered to participate in our study. Data on socio-demographic characteristics, medical histories and medications were collected and subjects with conditions or receiving medications that affecting bone metabolism were excluded. Dual-energy x-ray absorptiometry (DXA) used to measure bone mineral density (BMD) in all participants. All blood collections were performed in the morning after overnight fast. Serum TRACP5b concentrations were measured by an automated immunoassay on the ISYS analyzer (Immunodiagnostic Systems,Boldon,UK). The RI was defined as the central 95% range. We determined RI according to CLSI guide C28-A3 and using the MedCalc Software.
RESULTS
The median age of men, pre- and post-menopausal women were 49, 42 and 57 years respectively. DEXA results revealed that 342 participants had normal BMD, 79 were osteopenic and 10 had osteoporosis which excluded from analysis. Since our data were not normally distributed (Shapiro-Wilk test) in any group and after testing for outliers (Tukey test), we used the non-parametric method suggested by the CLSI guide in order to determine the RI. Multiple regression analysis revealed that age, sex, menopausal status and BMD were fectors significantly affecting TRACP-5b levels. Spearman rank correlation (rho) between TRACP-5b levels and age and BMD was 0.296 and -0.315 ($p<0.0001$ in both cases) suggesting that TRACP levels increase with age and there is an inverse relationship between BMD and TRACP-5b levels. Subjects with osteopenia exhibited significantly higher values for TRACP5b compared to those with normal BMD [median(25,75percentiles)] 3.22U/L(2.71-3.37) vs 2.40U/L(1.95-3.08). Post-menopausal women exhibited significantly higher values 3.19U/L(2.63-3.83) compared to pre-menopausal 2.19U/L(1.75-2.68) and men 2.48U/L(2.07-3.13). Separate RI are calculated and suggested for subjects with normal BMD (1.11-4.92U/L), with osteopenia (1.33-6.95U/L) as well as for men (1.30-4.50 U/L), pre-menopausal (0.85-4.24U/L) and postmenopausal women(1.29-6.92U/L).
CONCLUSION
We provide RI for TRACP5b concentrations in serum for the Greek adult population using an automated immunoassay. Our data may aid to interpret bone turnover in the Greek adult population.

Assessment of Precision and Accuracy of the SD GlucoNavii Glucometer Compared with a Central Laboratory Reference Method.

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OBJECTIVES
The point-of-care (POC) glucometers for blood glucose measurement have gained increasing attention due to their ability to provide rapid results at or near the patient, thereby reducing turnaround times and supporting timely clinical decisions. The objective of this study was to evaluate the precision and accuracy of the GlucoNavii (SD Biosensor, Suwon, Republic of Korea) POC glucometer and to compare its performance with values obtained from the central laboratory reference method.
METHODS
Precision and accuracy studies of the glucometer were assessed using a single POC device operated by a trained researcher. Within-day and between-day precision were determined by repeated measurements using the manufacturer's two-level quality control sera. A total of 115 lithium heparin (BD Barricor) whole blood samples were analyzed with the glucometer. The plasma, rapidly separated from the same tube, was analyzed on the Beckman Coulter AU5800 central laboratory analyzer for comparison. Data was evaluated in accordance with ISO 15197:2013 guidelines for glucometer performance.
RESULTS
The within- day coefficient of variation (CV%) ranged from 2.5% to 3.1%, while between-day CV% ranged from 5.2% to 7.2%. Of the 115 samples, 69 (60%) were hyperglycemic and 46 (40%) were euglycemic; hypoglycemic samples (<70 mg/dL) were not available. A moderate correlation was observed for samples <100 mg/dL (r=0.49, p=001), while a strong correlation was demonstrated for samples ≥100 mg/dL (r = 0.92, p<0.001). Also, fewer than 95% of results at <100 mg/dL fell within ±15 mg/dL of the reference method, whereas >95% of results at ≥100 mg/dL fell within ±15% of the reference.
CONCLUSION
SD GlucoNavii glucometer demonstrated acceptable within-day precision; however, inter-day imprecision indicates limited reproducibility. While the device fulfilled ISO 15197:2013 accuracy requirements in the hyperglycemic range (≥100 mg/dL), its performance at glucose concentrations <100 mg/dL requires further validation. Importantly, hypoglycemic samples were not represented in this study, and additional investigations are needed to confirm the device's reliability in patients with low glucose levels.

Comparison Of Whole Blood Hba1c Measurements Obtained From K3-Edta Tubes Versus Wasserman Tubes.

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INTRODUCTION-AIM

Glycated hemoglobin (HbA1c) testing is a health indicator for pre-diabetes identification or diabetes detection and follow-up. HbA1c is typically measured in whole blood sample collected in tubes containing ethylene-diamine-tetra-acetic acid (EDTA) as anticoagulant. Simplifying collection and transport of blood samples for HbA1c measurement remains of great interest. In this study, we collected blood samples in K3-EDTA tubes and Wasserman tubes to assess their comparability for HbA1c measurement.

MATERIALS AND METHODS

A total of 41 subjects were enrolled in the present study. For HbA1c testing, whole blood samples (N=41), obtained from the subjects, were collected in K3-EDTA-containing tubes (appropriate volume: 2.0 mL) (kept at 4 ± 2 °C to be analyzed within 24 h). Afterwards, 1 ml of whole blood sample from each K3-EDTA tube, was transfused into a Wasserman tube (kept at room temperature to be analyzed within 2 h) and Hb1Ac was measured again. The Tosoh G8-90SL (Japan) Ion-Exchange High Performance Liquid Chromatography (IE-HPLC) Analyzer was used to obtain HbA1c measurements, in all samples. HbA1c data were classified in 2 groups. Group A included HbA1c measured in whole blood samples collected in K3-EDTA tubes, while Group B consisted of HbA1c measurements of whole blood samples, which were transfused from K3-EDTA tubes to Wasserman tubes. Data analysis was performed using the JASP 0.95.1 software. The paired samples t-test was applied. Results were expressed as Mean ± Standard Deviation. P-value < 0.05 was considered to be statistically significant.

RESULTS

There was no significant difference in HbA1c values between A and B Group (p=0.058). (Group A: 6.385±1.526 vs Group B: 6.366±1.538 % -p=0.058).

CONCLUSIONS

In conclusion, when assessing the whole blood HbA1c levels of the same subjects, between samples using K3-EDTA tubes and Wasserman tubes (blood transfusion from the K3-EDTA tubes), no statistically significant difference was found. It appears Wasserman tubes could be used for HbA1c measurement with blood transfusion from the K3-EDTA tubes into Wasserman tubes. However, further investigation needs, with a larger number of samples.

Investigation Of The Role Of microRNAs In Infection-Related Neuropathy: A Systematic Review And Meta-Analysis.

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INTRODUCTION

Peripheral neuropathy (PN) is a common and debilitating condition that can arise from infectious etiologies, including viral agents such as Human Immunodeficiency Virus and Varicella-Zoster Virus. Despite its clinical burden, infection-induced PN remains underdiagnosed. MicroRNAs (miRNAs), small non-coding RNAs that regulate gene expression, have emerged as promising diagnostic biomarkers and therapeutic targets in neuropathology. This systematic review and meta-analysis aimed to synthesize data from observational studies assessing the diagnostic and mechanistic role of circulating miRNAs in infection-induced PN.

METHODS

Following PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) and MOOSE (Meta-analysis of Observational Studies in Epidemiology) guidelines, a comprehensive literature search was conducted in PubMed, Web of Science, and Cochrane Library up to April 2025. Inclusion criteria comprised studies comparing circulating miRNA levels between patients with infection-related PN and infectious controls without PN. Diagnostic accuracy was assessed using the area under the ROC curve (AUC), while heterogeneity was quantified with the I^2 index.

RESULTS

Three high-quality observational studies with a total of 233 participants (103 with PN) met the inclusion criteria. Seven miRNAs (miR-455-3p, miR-34c-5p, miR-107, miR-892b, miR-486-3p, miR-127-5p, and miR-7), targeting pathways related to neuronal survival, inflammation, and neuroimmune regulation, showed significant differential expression. The meta-analysis demonstrated moderate to high diagnostic accuracy (AUC range: 0.788–0.896), with minimal heterogeneity (I^2 = 0%).

CONCLUSIONS

Circulating miRNAs exhibit consistent diagnostic potential in distinguishing infection-induced PN and may mechanistically contribute to its pathogenesis. A multifactorial miRNA panel could enhance early diagnosis and guide personalized therapeutic strategies. However, further prospective and multicenter studies are warranted to validate these findings and establish clinical utility.

Comparative analysis of chemiluminescent immunoassay outcomes for anti-HCV antibodies and HCV core antigen.

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BACKGROUND

Hepatitis C virus (HCV) infection is a major public health issue, causing severe complications such as cirrhosis and hepatocellular carcinoma. Diagnostic methods usually rely on the detection of anti-HCV antibodies, reflecting past exposure, and HCV core antigen tests, which indicate ongoing infection.

OBJECTIVE

The aim of this study was to perform a paired comparison of anti-HCV and HCV-Ag positive samples and further explore their association. Specifically, we investigated whether anti-HCV values could serve as a predictive marker for HCV-Ag positivity and assessed the diagnostic performance of this correlation.

MATERIALS AND METHODS

A total of 93 anti-HCV-positive patients were enrolled over a 12-month period at the Blood-Borne Pathogens Laboratory of the Blood Donation Department. Anti-HCV antibodies were quantified using the ARCHITECT i12000 SR analyzer (CMIA; cut-off >1.00 S/CO), and positive samples were additionally tested for HCV-Ag on the same system (positivity threshold: 3.00 fmoL/L). The statistical analysis was carried out using Pearson correlation, ROC curve analysis, and logistic regression. The study protocol was approved by the Research Committee and Scientific Council of Tzaneio General Hospital (Prot. No. 4055/18-03-2025).

RESULTS

Results demonstrated a mild positive trend between anti-HCV and HCV-Ag values; however, Pearson's correlation was weak ($r = 0.342$) and non-statistically significant ($p = 0.069$). ROC analysis demonstrated an AUC of 0.783, suggesting good diagnostic proficiency. Logistic regression revealed that anti-HCV levels were a statistically significant predictor of HCV-Ag positivity ($p < 0.001$), where each unit increase in anti-HCV was associated with a 36.6% increase in the odds of HCV-Ag detection (OR: 1.366, 95% CI: 1.163–1.605).

CONCLUSION

The study highlights that, despite the absence of a strong direct correlation between anti-HCV and HCV-Ag levels, anti-HCV values demonstrated significant predictive capacity for HCV-Ag positivity. These findings reinforce the diagnostic relevance of anti-HCV antibodies, not only as a marker of past exposure but also as a potential indirect indicator of active infection, particularly in contexts with limited access to molecular testing. Importantly, the results warrant further validation in larger, multicenter cohorts to strengthen the generalizability of these observations. Future research should also consider incorporating additional clinical and virological parameters to refine predictive models and optimize diagnostic algorithms for HCV infection.

Homeostasis Model Assessment Of Insulin Resistance In Tranfusion Dependent Patients.

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INTRODUCTION

B-thalassemia(BT) and Sickle cell Disease(SCD) are genetic blood disorders characterised by reduction or absence of Hb A β-globulin chains-Hb A (α2 β2), leading to hemolysis and anemia. Worldwide, incidence is 0.3–0.4 million persons/year, who carry different types of mutations, resulting in variable phenotypes ranging from unremarkable symptoms to severe anemia. Treatment involves regular transfusions at standard intervals. Nevertheless, multiple transfusions have adverse events due to iron overload(IO). So transfusion-dependent patients (TDP) require continuous monitoring. The side effects of IO include significant endocrine disorders, such as, hypogonadism, growth retardation, hypothyroidism, hypoparathyroidism, adrenal insufficiency and glucose intolerance(GI). Insulin resistance(IR) is the underlying cause of GI. Homeostasis model assessment of insulin resistance(HOMA-IR) is the best way to evaluate insulin resistance(IR) because it discriminates individuals with IR at early stage and individuals with metabolic syndrome.

AIM

To Determine insulin(INS), calculate HOMA-IR in BT and SCD patients and compare with a control group.

METHODS

67 TDP patients (Group A) were studied, 34 male, median age 42(67-12)years. 26 healthy controls (Group B), 10 male, median age 43(20-91)years. Patients with diabetes mellitus were excluded. INS was determined on Beckman Coulter's UniCell DXI800 Access Immunoassay analyzer by enhanced chemiluminescence (CMIA). HOMA-IR was calculated. The SPSS version 29 and the non-parametric Mann-Whitney U-test compared results between Group A and B. Statistical significance threshold was set at $p<0.05$.

RESULTS

Regarding Group A, median HOMA-IR was 1.1(0.4-4.2). In Group B, median HOMA-IR was 1.2(0.4-2.1). No statistically significant difference was found in HOMA-IR between the two groups, $p=0.327$.

CONCLUSIONS

BT and SCA are common genetic disorders in Greece, yet the national Prevention Programme(NPP) has controled the birth of children with the above-mentioned diseases. The NPP prioritised the development of strategies to help increase patient survival rates and improve quality of life. Several complications leading to acute or/and chronic diseases are due to IO, caused by multiple transfusions, which are, however, an effective treatment. The pathogenesis of IR in BT and SCD is mainly attributed to transfusion IO. IO in pancreas impairs b-cell function and decreases INS production, in liver, impairs glycogonolysis, neoglycogenesis and INS sensitivity, in muscles generates IR. Continuous patient follow-up, iron status monitoring and extensive chelating therapy contributed to alteration of these deregulations. This study's results are consistent with these data. Until now, the usual way of patients IR monitoring was to determine fasting blood glucose and OGTT. HOMA-IR is the best way of monitoring IR by successfully discrimminating IR and prediabetes, suitable for the above group of patients. Furthermore, IR detected with HOMA-IR is reversible. HOMA-IR incorporation into TDP's monitoring is also recommended because it is easier than OGTT, as the results are obtained from a single blood sample, which is extremely important for this group of patients who are under considerable stress.

Assessment And Correlation Of Vitamin D, Vitamin B12, And Folate Levels In Patients Of Kozani General Hospital.

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INTRODUCTION
Vitamin D has been shown to affect folate absorption in vitro and may also influence vitamin B12 absorption. The aim of this study was to assess serum levels of vitamin D, vitamin B12, and folate in patients at the Kozani General Hospital and to evaluate potential correlations among them.
METHODS
A total of 1453 patients (41.3% men and 58.7% women; median age: 55 years) who visited the hospital between July 2023 and June 2025 were included in the study. Serum levels of 25(OH) D (VD), vitamin B12 (VB12) and folate (FOL) were measured concurrently using a fully automated Roche Cobas Pro analyzer. Based on their vitamin D levels, patients were categorized into three groups: Group 1 (≤20 ng/mL; n = 927, 63.8%), Group 2 (21–29 ng/mL; n = 400, 27.5%), and Group 3 (≥30 ng/mL; n = 126, 8.7%). Descriptive statistics and the Mann–Whitney test were used to compare vitamins levels. Correlations between vitamin D and vitamin B12/folate levels were analyzed using Spearman's correlation test.
RESULTS
The median levels of vitamin D, vitamin B12, and folate among all participants were 18.7 ng/mL, 348 pg/mL, and 5.05 ng/mL, respectively. A very weak but statistically significant positive correlation was observed between vitamin D and vitamin B12 ($r = 0.14$, $P < 0.001$), as well as between vitamin D and folate ($r = 0.17$, $P < 0.001$). Vitamin D deficiency (≤20 ng/mL) was observed in 63.8% of patients, vitamin B12 deficiency (<197 pg/mL) in 7%, and folate deficiency (<3.89 ng/mL) in 31.5%. No significant sex-based differences were found in the median levels of vitamin D (19.3 ng/mL in males vs.18.4 ng/mL in females) or vitamin B12 (342 pg/mL in males vs. 355 pg/mL in females) ($P > 0.05$). However, median folate levels were significantly higher in females (5.21 ng/mL) compared to males (4.83 ng/mL) ($P = 0.008$). Finally, comparison of median vitamin B12 and folate levels across the three vitamin D groups (Table 1) showed that vitamin B12 levels were significantly lower in the vitamin D deficiency group ($P < 0.016$), whereas folate levels increased significantly with increasing vitamin D levels ($P < 0.016$)."

Table 1: B12 and FOL levels at different VD levels.

VD levels (ng/mL)	Median B12 level (pg/mL)	Median FOL level
≤20	339	4.84
21-29	353	5.26
≥30	383	6.24

CONCLUSIONS
Based on the results of the present study, it can be concluded that vitamin D is positively associated with serum levels of both vitamin B12 and folate, although the correlations are weak. A high prevalence of vitamin D deficiency was observed in the study population. Finally, significant sex-based differences were found for folate levels, but not for vitamin D or vitamin B12.

Metabolomic Profiling Reveals Triple Negative Breast Cancer Subtype-Specific Nutrient Dependencies And Resistance-Associated Rewiring.

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Triple-negative breast cancer (TNBC) is an aggressive and highly heterogeneous disease characterized by early relapse, limited targeted therapeutic options, arise of drug resistance, and poor prognosis. Six TNBC molecular subtypes have been reported -two basal-like (BL1, BL2), an immunomodulatory (IM), a mesenchymal (M), a mesenchymal stem–like (MSL) and a luminal androgen receptor (LAR)- each defined by distinct gene expression profiles and ontologies. Metabolic reprogramming, a hallmark of cancer, enables cancer cells to sustain their high energy demands and withstand cytotoxic stress thereby promoting drug resistance. TNBC cells exhibit enhance glycolysis, but also rewire fatty acid oxidation, glutaminolysis, and amino acid metabolism, highlighting the metabolic complexity of the disease.

Comprehensive metabolomic analyses of TNBC subtypes, and of their alterations during the development of chemoresistance, remain limited. To address this, we investigated the extracellular metabolite profiles of parental and paclitaxel-resistant (PTX-res) TNBC cell lines representing three subtypes (MDA-MB-468, BL1; BT549, M; SUM159, MSL). Conditioned media were collected after 24 h from cells at 60% confluency, filtered, and analysed by 1H NMR, with cell-free medium serving as baseline control.

A total of 26, 22, and 25 metabolites were identified and quantified with high confidence in MDA-MB-468, BT549, and SUM159 cells, respectively, using the Chenomx software. BT549 parental cells showed the strongest glycolytic signature, with highest glucose consumption and lactate secretion compared to the MDA-MB-468 and SUM159 parental cells. Amino acid uptake and secretion patterns also varied across subtypes. Partial-Least-Squares-Discriminant Analysis (PLS-DA) demonstrated clear separation of parental and PTX-res cells for all cell lines. The top ranked metabolites accounting significantly for this separation were creatinine for MDA-MB-468, glutamine for BT549 and 2-phosphoglycerate for SUM159. KEGG enrichment analysis revealed distinct pathway signatures, with aminoacyl-tRNA biosynthesis consistently represented across all TNBC lines by the largest number of metabolites. Resistance-associated shifts in metabolite levels further suggested remodeling of shared metabolic pathways.

The above results demonstrate that extracellular metabolite profiling not only captures subtype-specific metabolic programs but also reveals their dynamic rewiring during the acquisition of chemoresistance. The observed differences in metabolite uptake and secretion further highlight candidate biomarkers of TNBC heterogeneity and therapy resistance. Together, our findings underscore the potential of metabolomics to inform precision therapeutic strategies tailored to TNBC subtypes.

Retrospective Analysis of Vitamin D Serum Levels in the Elderly Population of the Epirus Region.

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AIM OF THE STUDY
The primary aim of this retrospective study was to evaluate the serum concentrations of vitamin D over a four-year period in an elderly population in Epirus (Western Greece). Vitamin D, also known as calciferol, encompasses vitamin D2 (ergocalciferol), derived primarily from dietary intake, and vitamin D3 (cholecalciferol), endogenously synthesized in the skin upon exposure to ultraviolet B (UVB) radiation acting on 7-dehydrocholesterol. The cutaneous synthesis of vitamin D declines progressively with age, decreasing by approximately 13% per decade. At the age of 70, synthesis capacity is reduced by nearly 50% compared to that at 20 years of age (Chalcraft et al., 2020).
METHODS
Between January 2020 and October 2023, serum vitamin D concentrations were measured in a total of 5,496 people aged ≥70 years. The serum samples were analyzed using the radioimmunoassay (RIA) technique at the Laboratory of the Nuclear Medicine Department, University Hospital of Ioannina. The influence of age, sex, and calendar year on the serum vitamin D levels was assessed using parametric statistical methods. The Data are presented as mean ± standard deviation (SD). Statistical significance was set at $p<0.05$.
RESULTS
The total number of the patients was 5496 and the mean age was 77,5 ± 6,2. The cohort comprised 3,387 females (61.7%) with a mean age of 77.6 ± 6.2 years, and 2,109 males (38.3%) with a mean age of 77.5 ± 6.3 years. The analysis showed revealed persistently suboptimal serum vitamin D levels throughout the study period. However, a statistically significant upward trend was observed over the four years ($p<0.001$). Mean concentrations increased from 15.8 ± 8.0 ng/mL in the year 2020 to 25.2 ± 10.0 ng/mL in year 2023. Despite this improvement, the prevalence of vitamin D sufficiency (defined as serum levels ≥30 ng/mL) remained low: 5.4% in 2020, 13.4% in 2021, 21.4% in 2022, and 22.4% in 2023. Two-way ANOVA revealed no statistically significant differences in vitamin D levels between men and women across the study years ($p=0.274$). Furthermore, no significant variation was observed among different age subgroups within the elderly population.
CONCLUSIONS
The findings of this retrospective analysis demonstrate a gradual improvement in serum vitamin D levels among the elderly population over the studied period. Nonetheless, the overall prevalence of vitamin D sufficiency remains markedly low, with the majority of individuals exhibiting levels below the recommended threshold of ≥30 ng/mL. Chronic vitamin D deficiency in older adults has been associated with an increased risk of musculoskeletal disorders (e.g., osteoporosis, osteomalacia, fragility fractures) and non-skeletal conditions such as diabetes, cancer and cardiovascular diseases (Giustina et al., 2023). Public health strategies should include targeted interventions such as routine screening, dietary fortification, supplementation, and safe sun exposure practices to address hypovitaminosis D in this vulnerable population group.

Correlation Of High Sensitivity Troponine With Parathormone Stat And 1-84 And With Egfr In Haemodialysis Patients With Chronic Kidney Disease.

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INTRODUCTION

In patients with chronic kidney disease (CKD), elevated levels of high-sensitivity troponin T (TNT-HS) may be observed due to subclinical cardiac injury from uremic toxicity or left ventricular hypertrophy, as well as reduced renal clearance.

AIM

The aim of this study was to investigate the correlation of TNT-HS concentration with eGFR and serum PTH STAT and PTH 1-84 levels in hemodialysis patients with CKD.

MATERIALS AND METHODS

In 55 serum samples from hemodialysis patients with CKD (38 men and 17 women), with a mean age of 67±15 years, TNT-HS, PTH STAT, and PTH 1-84 concentrations were measured by electrochemiluminescence (ECLIA) using two automated immunoassay analyzers (ROCHE Diagnostics). Serum creatinine concentration was also determined in the same samples by a photometric method using an automated biochemical analyzer (ROCHE Diagnostics), and the estimated glomerular filtration rate (eGFR) was calculated. Statistical analysis was performed using SPSS Statistics v.25.

RESULTS

In the overall patient cohort, a significant negative correlation was found between TNT-HS and eGFR (rs = -0.268, p = 0.048), with no correlation with gender. No significant correlation was observed between TNT-HS and PTH STAT (rs = 0.123, p = 0.369) or between TNT-HS and PTH 1-84 (rs = 0.119, p = 0.388).In the 36 patients aged ≥65 years, a significant negative correlation was found between TNT-HS and eGFR (rs = -0.373, p = 0.025), but no significant correlation was found between TNT-HS and PTH STAT (rs = 0.011, p = 0.947) or between TNT-HS and PTH 1-84 (rs = -0.024, p = 0.890). In contrast, among the 19 patients aged <65 years, a significant positive correlation was observed only between TNT-HS and PTH 1-84 (rs = 0.455, p = 0.05). Moreover, troponin levels did not differ significantly between the two age groups.

CONCLUSIONS

As renal function deteriorates, in patients with CKD aged ≥65 years, there is a significant increase in serum TNT-HS levels, with no association with gender. Additionally, in patients aged <65 years, a significant positive correlation was found between TNT-HS and PTH 1-84. Therefore, in younger individuals with CKD, it may be important to monitor troponin, as CKD may be accompanied by subclinical cardiac injury, as well.

Is Thyroid Affected In The Context Of Acute Kidney Injury?

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INTRODUCTION

Acute kidney injury(AKI) refers to a decline in kidney function that occurs over a few hours or 5-6 days. It is a multicausal disease. The diagnosis is based on elevated serum creatinine(Cr) level and/or urine output drop. There is limited information regarding the prevalence of AKI in Greek hospitals, but it is relatively frequent, particularly among ICU patients. In a multicentre prospective study, AKI occurred in 16% of ICU patients. Worldwide, AKI affects 10-15% of hospitalized patients and more than 50% of ICU patients. AKI may be reversible but also, a serious condition requiring prolonged hospitalization and may lead to chronic kidney disease with dialysis need and in high risk of hospital-acquired infections, associated with elevated hsCRP and Procalcitonine(PCT). In severe disease, such as AKI, thyroid gland alterations often occur. Low FT3 occurs very often. Less frequently, FT4 and TSH remain normal or slightly decreased. This is the non-thyroidal illness syndrome(NTIS). Renal function is indirectly involved and metabolism and excretion of TSH, FT3, FT4 may be affected. Thyroid hormones transport proteins, such as TBG, albumin are altered in renal failure, affecting total T3 and T4, but not necessarily FT3 and FT4. Medications administered to AKI patients, such as corticosteroids or heparin may affect TSH levels or suppress T3 and T4 secretion.

AIM

Investigating the impact of AKI on TSH, FT3, FT4 and probable correlation between the severity of renal damage (Cr) and concomitant inflammation (PCT) with thyroid function.

METHODS

135 hospitalised patients were studied. 39 with AKI, 13 male, median age 80(57-94)years, (Group A). 96 healthy controls, (Group B), 47 male, median age 52(17-87) years. TSH, FT3, and FT4 were determined by enhanced chemiluminescence on the DXI800 analyser (Beckman Coulter). SPSS version 29 and Mann-Whitney U-test compared Group A and B. In Group A, TSH, FT3, FT4 were correlated with Cr and PCT with Spearman correlation test. The level of statistical significance was set at $p<0.05$.

RESULTS

In Group A, median TSH levels were 1.472(0.154-47.155)mIU/L, median FT3:1.97(1.13-3.1)pg/ml, median FT4:1.12(0.62-1.49)ng/dl. In Group B, median TSH was 1.80(0.456-4.562)mIU/L, median FT3:3.26(1.77-4.56)pg/ml median FT4:0.94(0.68-1,46)ng/dl. FT3 was statistically significantly lower in Group A($p<0.05$). In Group A, FT3 was negatively correlated with Cr and PCT, r=-0.431 and -0.521, respectively, $p<0.05$.

CONCLUSIONS

AKI can cause temporary alterations in thyroid gland function. A prospective study of 147 patients with AKI revealed that 77.5% exhibited some sort of thyroid dysfunction. Another study which compared AKI patients with healthy subjects showed that low FT3 was the most common disorder in AKI (40-100% depending on severity). Low FT3 is the main finding of NTIS. The more severe the AKI, the more severe the disorder is. TSH and FT4 may also be affected. Similar findings occurred from the data collected. FT3 was lower in the AKI Group. The more severe the disease (elevated Cr) or complicated (elevated PCT), the lower the FT3. In stress or severe disease, such as AKI, human body adapts its metabolism to save energy. This is a normal body response to severe stress or inflammation. In daily practice, many laboratory tests are prescribed by clinicians leading to huge medical expenses. Alterations of TSH, FT3, FT4 in AKI are temporary in terms of NTIS and no treatment is required, so the relevant laboratory testing is not generally suggested for these hospitalized patients, unless in already known or suspected thyroid disease, electrolyte or heart rate dyregulation.

Computer-Aided Drug Design Against Huntington's Disease Using Psychedelic Compounds.

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Huntington's disease (HD) is a progressive, hereditary neurodegenerative disorder caused by CAG repeat expansion, an abnormal increase of cytosine–adenine–guanine triplet repeats in the huntingtin (HTT) gene, resulting in the formation of mutant huntingtin (mHTT) and subsequent neuronal dysfunction (McColgan and Tabrizi, 2018). Current treatments, including VMAT2 inhibitors, SSRIs, and atypical antipsychotics, provide only symptomatic relief without altering disease progression. Psychedelic compounds have recently gained attention for their ability to promote neuroplasticity and attenuate neuroinflammation, two critical mechanisms disrupted in HD (Jimenez-Sanchez et al., 2017). In this project, Computer-Aided Drug Design (CADD) was employed to evaluate the binding interactions of both established pharmacological agents and psychedelic molecules with key HD-related proteins (HTT, BDNF, Drp1, GABA(A), NMDA, PGC-1α, and TrkB). Molecular docking simulations performed with UCSF Chimera and ArgusLab demonstrated that psychedelics such as Cannabidiol, Cannabinol, Brorphine, Tetrahydrocannabivarin, and Tetrahydrocannabinol exhibited strong binding affinities, particularly with TrkB, NMDA, HTT, GABA(A), and Drp1, in some cases surpassing the interactions observed with conventional drugs like Tetrabenazine, Deutetrabenazine, Risperidone, and Sertraline. A three-dimensional representation of the molecular docking of Cannabidiol with the TrkB receptor revealed the most favorable binding affinity (-13.41 kcal/mol) (Figure 1) among the psychedelic compounds tested, indicating a particularly stable complex. These findings suggest that psychedelics may represent viable multi-target candidates for future drug design and therapeutic intervention in HD, meriting further validation through in vitro and in vivo studies.

Topic: Neurological Diseases

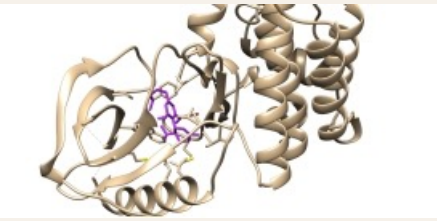

Figure 1. Three-dimensional representation of the molecular docking of Cannabidiol with the TrkB receptor. The compound showed the strongest binding affinity (-13.41 kcal/mol) among the psychedelic substances tested, indicating a particularly stable complex. The colored (purple) region in the figure corresponds to the ligand molecule — in this case, Cannabidiol — within the active site of the receptor (protein).

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Precision in Practice: Applying Sigma Metrics Framework to Enhance Quality and Reliability in the Clinical Chemistry Laboratory of a Tertiary Care Cancer Centre.

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BACKGROUND
The sigma metrics approach is a well-established method for assessing laboratory performance, offering a quantitative measure of process quality by identifying variations and assessing error rates. This study aims to evaluate the performance of key quality indicators in a clinical chemistry lab within a tertiary care cancer hospital using sigma metrics.
METHOD
A retrospective analysis was conducted using data from a clinical chemistry laboratory over a 12 months' period. Key quality indicators were analysed in the Pre- analytical, Analytical & Post Analytical areas. Indicators with sigma values of ≥6 were classified as excellent, 3-6 as acceptable, and <3 as requiring improvement.
RESULT
The analysis revealed that a number of indicators achieved sigma values of between 5 to 6, indicating high performance and reliability. However, a considerable number of indicators were found within acceptable sigma values i.e. 3-6, indicating areas where quality improvement measures are necessary.
CONCLUSION
The sigma metrics approach effectively identified the strengths and weaknesses in the performance of quality indicators in the clinical chemistry lab. The study highlights the need for continuous monitoring and improvement. Implementing corrective measures in areas with lower sigma scores will help the lab maintain its critical role in supporting accurate cancer diagnostics and treatment planning.

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Computational Drug Design For Alzheimer's Disease Through Drug Repurposing Approaches.

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Alzheimer's disease (AD) is a progressive neurodegenerative disorder affecting primarily the cerebral cortex and hippocampus and is also the most prevalent form of dementia. Pathologically, it is defined by extracellular deposition of insoluble β-amyloid (Aβ) peptides in plaques, intracellular aggregation of hyperphosphorylated tau into neurofibrillary tangles and widespread neuronal loss (Masters et al., 2015). Current pharmacological treatments provide only symptomatic relief, underscoring the urgent need for novel and safer therapeutic strategies (Cummings et al., 2025). This study employed Molecular Docking to evaluate the binding affinities of FDA-approved and investigational AD drugs, as well as antihypertensives, antiretrovirals and compounds targeting Apolipoprotein E ε4 allele (APOE4) and the M1 muscarinic receptor. Docking calculations predicted the affinities of the above compounds against major AD-related proteins, namely, Aβ1-42, BACE1 (Beta-site APP Cleaving Enzyme 1), gamma secretase, tau, PSEN1&2 (Presenilin 1&2), APOE4, AChE (Acetylcholinesterase) and BChE (Butyrylcholinesterase). Docking simulations were conducted using UCSF Chimera and ArgusLab, with Gibbs free energy (ΔG) as the primary measure of interaction strength. Computational analyses revealed that Candesartan, an angiotensin II receptor blocker, exhibited exceptional binding properties across four of the above-mentioned proteins (BChE, APOE4, tau, AChE), achieving the strongest interaction with BChE (-17.267 kcal/mol) (Figure 1), outperforming FDA-approved AD drugs such as Donepezil and Memantine. This favorable binding was principally developed through hydrogen bonding and hydrophobic interactions. Thus, these computational results reinforce drug repurposing as a promising therapeutic paradigm for AD and identify Candesartan as a strong candidate for further experimental and clinical validation.

Topic: Neurological Diseases

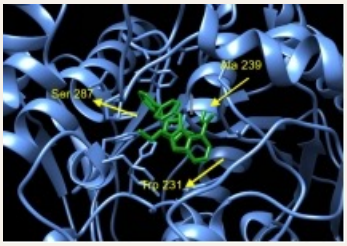

Figure 1. Three-dimensional representation of the Candesartan - BChE complex, as obtained from Molecular Docking. The drug Candesartan is depicted at its active site in green, while the BChE protein is shown in blue. Important binding amino acids are highlighted in yellow.

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NLR as a Systemic Inflammation Marker In Covid-19 Patients: A Pilot Study In A Greek Tertiary Hospital.

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INTRODUCTION
Neutrophil to lymphocyte ratio (NLR) is a marker of systemic inflammation and has recently been considered a possible predictor of prognosis in COVID-19 patients.
OBJECTIVE
This pilot study aimed to assess the NLR and its relationship to C reactive protein (CRP) and D-dimers (D-D), also used as indicators of disease severity, in patients with COVID-19.
MATERIALS AND METHODS
Electronic records of 38 patients admitted to a Greek tertiary public general hospital in Athens from December 2021 to February 2022 were reviewed retrospectively. Statistical analyses were executed by IBM SPSS 20.0.
RESULTS
Upon admission, mean NLR, CRP and D-D were 5.7, 65.8 mg/L and 2322.1 μg/L respectively. NLR correlated with CRP ($p=0.02$, $r=0.36$) and was higher, though not significantly, when the latter exceeded 100mg/L (7.3 versus 2.5 and 5.7 in case of negative and <100 mg/L CRP levels respectively). Mean CRP levels of patients with NLR>9 were significantly higher than those with lower ratio (104.9 versus 56.7 mg/L, $p=0.04$). The ratio did not correlate with D-D levels nor with other available parameters (fibrinogen, hemoglobin, platelets, total white blood cells).
CONCLUSIONS
Although previous studies have reported its correlation with CRP and D-D levels in COVID-19, the present study only demonstrated an association of NLR with the former. The study was designed as a pilot analysis of data collected from an electronic medical database and included a small sample size, without clinical data such as patient outcomes. Nevertheless, NLR is readily available as part of the full blood count analysis routinely performed and could provide useful, individualized information.

The Mayer stool test as a valuable indicator of the reliability of laboratory measurement of fecal Calprotectin.

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PURPOSE
Calprotectin is a calcium-binding protein secreted primarily by neutrophils and monocytes. Fecal calprotectin is increased in Inflammatory Bowel Disease IBD (Crohn's disease CD and ulcerative colitis UC) and contributes to the differential diagnosis between irritable bowel syndrome and Crohn's disease or ulcerative colitis. In case of a normal result, we are moving away from the possibility of inflammatory bowel disease and a colonoscopy is not necessary to rule out inflammation. The Mayer stool test is a diagnostic test that can detect small amounts of blood in the stool through the detection of hemoglobin. The purpose of the study is to investigate the value of the Mayer stool test as an indicator of the quality of the laboratory measurement of fecal Calprotectin but also as an indicator of confirmation of IBD.
METHODS
Patient stool samples were submitted to the laboratory, and extracted and diluted according to the instructions of the fCAL turbo Buhlmann Laboratories AG kit for automated turbidimetry on the Roche Cobas Integra 400 plus analyzer. The Mayer stool test was performed on the same stool samples using the FOB Rapid Test Cassette ALL TEST rapid chromatographic immunoassay.
RESULTS
Positive and negative Mayer stool tests are recorded per group of normal, gray zone, and pathological patients according to Calprotectin measurements. It is clear that the number of Mayer positive tests increases as the concentration of Calprotectin increases. This observation is confirmed by a Chi-Square Test (GraphPad Prism5) and a statistical significance of $p=0.0007$ within the pathological group and of $p<0.0001$ between the normal and pathological groups.

Group	Calprotectin Value Range	Number (N)	Positive Mayer	Negative Mayer
Normal	0-80 μg/g	37	5	32
Gray zone	81-160 μg/g	4	0	4
Pathological	161-10000 μg/g	62	36	26
	Analysis of the range 161-10000 μg/g			
Pathological	161-1000 μg/g	31	11	20
	1001-10000 μg/g	31	25	6

CONCLUSIONS
The analysis indicates that there is a statistically significant agreement. Descriptive statistics show excellent agreement in the groups of normal (prevalence of negative Mayer), gray zone and pathological patients (statistically significant prevalence of positive Mayer). For the pathological patient group, the presence of positive Mayer increases as the concentration of calprotectin increases. This reinforces the value of calprotectin in confirming inflammatory bowel disease, a condition that leads to blood loss in the stool and chronic inflammation that affects red blood cell production.

Comparative analysis of the implementation of biosafety measures in clinical laboratories of Health Centers and Hospitals in Greece.

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INTRODUCTION
Biosafety in clinical laboratories is a fundamental prerequisite for the protection of personnel, patients, and the wider community. Despite its importance, available data on the level of biosafety implementation in laboratories of Health Centers and Hospitals in Greece, as well as their comparative assessment, remain limited.
METHODOLOGY
A mixed-methods study was conducted using structured questionnaires completed by laboratory personnel (n = 158 in Health Centers; n = 415 in Hospitals) and standardized checklists completed by a certified biorisk management consultant (n = 35 and n = 36, respectively). The analysis focused on four domains: (A) Facilities and Engineering Controls, (B) Administrative Measures, (C) Personal Protective Equipment (PPE), and (D) Emergency Preparedness. Percentage differences (Δpp), 95% confidence intervals (CI), and significance levels ($p < 0.05$) were calculated.
RESULTS
Hospitals consistently recorded higher compliance rates compared to Health Centers across all domains. The largest discrepancies were observed in infrastructure and engineering controls, where Health Centers demonstrated more severe deficiencies (e.g., access restriction, autoclaves, biosafety cabinets). In administrative measures, substantial gaps were identified in both categories, particularly in risk assessment, the availability of SOPs, biosafety manuals, and the designation of a biosafety officer, with Health Centers showing the greatest shortfall. PPE availability was generally high, with Hospitals outperforming due to stronger institutional structures (written policies, occupational physician), although both settings lacked formal policies on the donning and doffing of PPE. In the domain of emergency preparedness, Hospitals had more structured plans and reporting systems, while significant gaps were evident in Health Centers.
CONCLUSIONS
Hospital laboratories in Greece demonstrate more developed and organized biosafety systems compared to Health Centers; however, in both laboratory settings significant deficiencies were identified in infrastructure, administrative procedures, and preparedness. These findings highlight the need for an overall strengthening of biosafety systems, with particular emphasis on Health Centers, in order to achieve full alignment with national and international standards and to enhance the protection of personnel, the community, and the environment.

KEYWORDS: Biosafety, Biorisk management, Clinical laboratories, Health Centers, Hospitals
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Correlation Of Immunochemiluminescence And Real-Time PCR Results In HBsAg Positive Samples: An Experimental Approach.

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BACKGROUND

Accurate diagnosis of Hepatitis B Virus (HBV) infection is crucial for treatment and viral transmission control. While the detection of Hepatitis B surface antigen (HBsAg) is a common serological marker, molecular detection of HBV DNA by Real-Time PCR allows for earlier identification and provides quantitative data on viral load, which is essential for monitoring disease progression and treatment response. The potential correlation between these two key diagnostic parameters remains a relevant scientific question.

OBJECTIVE

To experimentally evaluate the relationship between qualitative HBsAg detection using a Chemiluminescent Microparticle Immunoassay (CMIA) and quantitative HBV DNA determination via Real-Time PCR in a cohort of HBsAg-positive samples.

MATERIALS AND METHODS

This study included 26 samples, positive for HBsAg. Qualitative HBsAg determination was performed using the CMIA technique on the Abbott Architect i2000SR analyzer, while quantitative analysis of HBV DNA was carried out by RT-PCR on the Abbott m2000rt platform. Data were statistically analyzed using the Microsoft Excel and the SPSS v29.

RESULTS

Statistical analysis revealed a very weak, non-significant linear correlation between the two parameters (R2=0.078, p=0.0209). ROC analysis yielded an Area Under the Curve (AUC) value of 0.200, indicating poor predictive performance. These findings suggest that HBsAg detection via CMIA is not a reliable indicator of viral load as determined by RT-PCR in this sample set.

CONCLUSION

The present study indicates that the qualitative/semi-quantitative measurement of HBsAg by immunochemiluminescence demonstrates only a weak correlation with the quantitative measurement of HBV DNA, without statistical or predictive significance. This finding may be attributed both to the biological characteristics of the virus, such as the overproduction of HBsAg regardless of HBV replication, and to parameters including disease phase, treatment status, viral mutations, or the immune condition of the individual. Therefore, assessing the relationship between the two methods requires future studies with larger sample sizes and more advanced statistical approaches, while taking into account the aforementioned parameters, in order to obtain more reliable and generalizable conclusions.

Vitamin D Deficiency in Greece: Seasonal Dynamics Based on Two Years Data from IN VITRO LABS Reference Laboratory.

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BACKGROUND
Vitamin D plays a key role in calcium homeostasis and bone metabolism, while also contributing to immune and muscle function.
Low vitamin D levels are associated with bone fragility, increased risk of osteoporosis, and a higher susceptibility to infections and chronic diseases.
Deficiency rates are strongly influenced by latitude and season, with high prevalence reported in the Eastern Mediterranean and Europe especially in latitudes 20-40° North, despite abundant sunlight. Contributing factors may include local cultural practices, extensive body coverage, dietary habits, supplementation in terms of limited Vitamin D fortification of basic goods, socioeconomic status, and skin pigmentation.
MATERIALS AND METHODS
Data from 46,471 patient results (June 2023–August 2025) were collected and categorized by gender and month of analysis using the Siemens Atellica system. Results were assessed for seasonal variation, in terms of observed mean annual fluctuation and categorized as severe (<10 ng/mL), moderate (10–20), or mild deficiency (20–30) in order to demonstrate their relative occurrence per season and among gender.
RESULTS
Lowest mean values were observed in February–March, while highest averages seem most strongly related to late summer months in August–September. Men showed greater seasonal variation with lower averages in winter and considerably higher in summer than women. Severe deficiency fluctuated dramatically (<1% in September vs. >18% in March), with women slightly more affected. Moderate deficiency displayed the strongest seasonal dependence, particularly in men (annual range up to 49%). Mild deficiency remained relatively stable (30–50% year-round) with minimal sex differences.
CONCLUSIONS
Moderate deficiency is the most season-sensitive, whereas mild deficiency shows minimal seasonal impact. In contrast, severe deficiency, though less common and with the lowest annual variation, exhibits the sharpest seasonal shifts, with steep proportional increases from winter to summer.

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Neutrophil To Lymphocyte Ratio As A Simple, Inflammatory Marker In The Emergency Department. A Preliminary Report.

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INTRODUCTION

A promising hematological parameter of systemic inflammation and stress, is the Neutrophil to Lymphocyte Ratio(NLR). A Full Blood Count(FBC) is all that is needed to calculate NLR. NLR reflects the dynamic relationship between innate cellular immune response that neutrophils induce and adaptive cellular immune response induced by lymphocytes in the context of various disorders. In adults NLR's reference range is 1.0-2.0. NLR higher than 3.0 and below 0.7 is pathological. Nevertheless, there is a grey zone 2.0-3.0, which may serve as early warning of disorders such as cancer, infection, inflammation and atherosclerosis. Atherosclerosis is initiated and progresses as a result of inflammation1. Inflammation promotes coronary atherosclerotic plaque rupture, leading to thrombosis and in Acute Myocardial Infarction(AMI). AMI is a leading cause of death worldwide and includes ST-segment elevation myocardial infarction(STEMI) and non-STEMI(NSTEMI). b-natriuretic peptide(BNP) is the most promising biomarker for routine use as a supplement to Troponin-I. hsCRP is a classic, yet non-specific inflammation marker regarding diagnosis, prognosis, and therapeutic strategies in AMI.2 Another non-specific inflammation marker in AMI may be the NLR. Nevertheless, data regarding NLR and AMI are limited.

AIM

To determine FBC, calculate and evaluate NLR in patients diagnosed with AMI on admission, compare with a control group and correlate with BNP.

METHODS

244 patients admitted to a tertiary Greek hospital were evaluated. 199 suffered AMI, STEMI and NSTEMI, median age 65(42-92)years-Group A. 45 were healthy controls with median age 47(19-75)years-Group B. Patients with hematological, inflammatory, infectious or cardiovascular diseases, including atrial fibrillation, were excluded. FBC was determined by the UniCell DXH800 analyser (Beckmann-Coulter), which is routinely used in the hospital's core laboratory. BNP was determined by enhanced chemiluminescence on UniCell DXI800 analyser (Beckmann-Coulter). The SPSS version 29 and the non-parametric Mann-Whitney U test compared NLR levels between the two groups. NLR was correlated with BNP with Spearman correlation test, ρ correlation coefficient was calculated. The statistical significance level was set at $p<0.05$.

RESULTS

Regarding Group A, median NLR was 4.3(0.6-31.4). In Group B, median NLR was 1.8(1.0-4.0). NLR was statistically significantly higher in Group A($p<0.001$) and correlated with BNP($\rho=0.23$, $p<0.05$).

CONCLUSIONS

NLR's calculation is a simple process. Novel studies demonstrated that NLR may be a prognostic marker for several diseases with inflammatory pathophysiology. NLR determined by dividing the absolute number of neutrophils by the absolute number of lymphocytes in FBC is an inflammatory marker for cardiovascular risk stratification, associated with worse outcomes in patients with AMI. In accordance with international data, the data collected showed that patients with AMI had higher NLR compared to the control Group and that NLR was correlated with BNP. NLR is a nonexpensive and easily accessible marker for AMI on admission. It can be calculated very quickly. It is suitable for use in remote health care units, where only essential screening tests for patient management are available. Further research on prognosis, outcome and risk stratification regarding NLR and AMI is required.

Comparison Of PTH (1-84) and Intact PTH Levels in a Group of Oncologic Patients.

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BACKGROUND

Measurement of circulating levels of parathyroid hormone (PTH) is crucial for the diagnosis and therapeutic management of several diseases. Determination of PTH levels in serum can be confusing because of the different molecules that are detected. A third generation immunoassay was developed in order to overcome previous limitations, and improve the determination of biologically active PTH by selectively detecting the full-length active hormone PTH (1-84) and excluding inactive fragments.

OBJECTIVES

The aim of this study was to compare and identify possible correlations and differences of PTH (1-84) and intact PTH (iPTH) levels in a group of oncologic patients.

METHODS

Serum samples were collected from 94 oncologic patients. Determination of iPTH and PTH (1-84) levels were performed by a second and third generation electrochemiluminescence "ECLIA" assay in the Cobas Pro (e801) analyzer (ROCHE). Further investigation of the influence of patients' baseline laboratory parameters, including renal function serum biomarkers, was conducted to identify risk factors associated with assay performance and observed levels of the two PTH measurements. Serum biochemical markers were determined in Cobas Pro (c503) analyzer (ROCHE). eGFR was calculated using the eGFR MDRD equation.

RESULTS

Analysis of results showed that serum iPTH values were significantly higher than those of PTH (1-84) ($p < 0.001$). Despite this finding, both results demonstrated a very strong linear relationship with a Pearson correlation coefficient of $r=0.99$ ($p<0.0001$), indicating that they follow an almost identical pattern of change. Out of 94 patients, 19% had a high difference in the levels of the two assays, with 27% of them showing impaired renal function (eGFR < 60 mL/min/1.73m2).

CONCLUSIONS

Measured PTH (1-84) levels were lower than those of iPTH, but they showed great correlation. The differences were greater in patients with impaired renal function, especially in patients with low eGFR value. This suggests that PTH (1-84) may offer greater specificity for monitoring parathyroid function in patients with renal impairment. However, more studies are needed in order to investigate the correlation and clinical value of different PTH molecules.

Biomarker SuPAR as a prognostic tool in proper management of patients in emergency departments.

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INTRODUTION

SuPAR (soluble urokinase plasminogen activator receptor) is a biomarker of systemic chronic inflammation (SCI). It has been found to be a broad prognostic biomarker associated with incident disease and adverse clinical outcomes across both general and patient populations. It represents a common underlying disease-process shared by many diseases such as kidney disease, sepsis, cardiovascular disease, and inflammatory disorders.

AIM

The aim of this study is to find out the role of SuPAR in the evaluation of patient's condition in emergency departments, in association with other inflammatory biomarkers such as CRP, FIB, D-DIMMERS and white blood cells concentration.

METHODS

The concentration of SuPAR was measured in the EDTA plasma of 39 patients using suPARnostic TurbiLatex Reagents by ViroGates, and for these patients was also measured the concentration of white blood cells and CRP, FIB and D-DIMMERS.

RESULTS

SuPAR		CRP >10	FIB>400	D-DIMMERS >500	WBC >10.5
<4 low risc	2	-	-	-	-
4-6 intermediate risc	5	3	2	4	2
>6 high risc	32	31	20	25	21

As it is shown from the table above, the patients who belong to the low risc group, they don't have any other pathological findings. 3/5 patients who are in intermediate risc have increased CRP, 2/5 have WBC and FIB out of physiological range, and 4/5 have high D-DIMMER. The majority of the third group which is in high risc have approximately all the inflammatory factors significantly increased.

CONCLUSION

The measurement of SuPAR, as a non specific and prognostic biomarker, may be a risc stratification tool in order to improve the direct discrimination of the patients in emergency departments. However the usage of biomarker-based prognostic information for clinical decision is a concept that still needs additional research.

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Onset Of Full Body Rash In An Adolescent. A Diagnostic Challenge In The Emergency Department.

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INTRODUCTION
Rash infections are a common differential diagnostic problem in immigrant populations. Varicella(Chickenpox) is a viral infection caused by the Varicella-zoster virus (VZV), classified as a highly contagious, early childhood, rash infection, accompanied by fever and characteristic maculopapular rash. In infants, adolescents, adults and immunocompromised patients it may cause serious complications and has therefore been included in the Greek vaccination programme. Prior to the vaccination programme and according to ECDC reports, Varicella had a high incidence in children under 5 years of age. Specifically, 86.6% of children <15 years old were infected in Greece and internationally, 89-95.9%. New data emmerged after the last years moving immigrant population.
AIM
Describing a 16-year-old febrile patient with full-body maculopapular rash.
METHODS
A 16-year old female was referred to the Emergency Department(ED) of a tertiary care Greek hospital of Northern Greece, febrile with full body rash in July. Complete clinical and laboratory testing was performed.
RESULTS
The patient, residing in a refugee camp, was referred to the ED due to weakness, anorexia, headache, fever (37.8°C) and a full-body, pruritic, maculopapular rash. Laboratory testing: WBC: 5.7x10^3/μl, Ne: 39.9% (2.3x10^3/μl), Ly: 38.7% (2.2x10^3/μl), Mo: 20% (1.1x10^3/μl) Hb:12.5g/dl, Ht:37.4%, MCV:78.0 fl, RDW:13.8%, PLT: 230x10^3/μl, LDH:279U/L(<248U/L), ESR:12mm/hr, hsCRP:15.9mg/L. Peripheral blood smear: lymphoplasmacytoid lymphocytes with eccentric nucleus, protoplasm excessively basophilic, and perinuclear lucency. Viral tests: HbsAg, HCV, HIV: negative, HSV1 IgG, HSV2 IgG:negative, HSV1/2 IgM>3.5(positive) and VZV IgG:405.4mIU/ml, VZV IgM:>2.3 both positive. Most likely diagnosis, based on the morphology of the rash:-varicella. However, due to viral test results, RT-PCR with Elite InGenius® fully automated integrated system was performed to differentiate between HSV and VZV . HSV 1, 2 DNA was not detected. VZV DNA was detected, quantity equal to 2078 copies/ml.
CONCLUSIONS
Varicella (Chickenpox) shows seasonal outbreaks. The main outbreak season is spring and less often autumn, following new school-year beggining. Due to the vaccination programme the incidence in Greece has decreased significantly, although Varicella is an airborne infection. According to a Greek epidemiological study from 1982 to 2003, VZV infections requiring hospital admission occur in the summer, although lowest case counts are reported. An epidemiological study after 2020 on the impact of the VZV vaccination policy showed significant reduction in patients requiring hospital care. Nevertheless, there are insufficient epidemiological data regarding the emerging circumstances. Routine immunisation schedules and surveillance systems are not robust in refugees origin countries. This case is of-season according to international epidemiological data and no similar cases had been detected during the relevant time-period. Furthermore, patient's vaccination status was unknown. Regarding vulnerable social groups with unremarkable past medical and vaccination history there should be a high level of clinical suspicion of childhood rash diseases. Adolescent refugees are at high risk of VZV susceptibility due to lack of prior vaccination or infection at younger age in their countries of origin. This poses a significant public health concern due to VZV outbreak risk. Also, adolescents tend to develop severe disease and more extensive rash. Simultaneously, the main concern for adolescents with VZV is the increased risk of complications compared to younger children who experience mild disease. RT-PCR is an important tool at our disposal, with high sensitivity and specificity that leads to prompt and reliable diagnoses. Prompt diagnosis is of great importance due to the benefits of early antiviral treatment, which is most effective when administered within 24-48 hours and public health protection through outbreak prevention.

Development Of A Novel A CRF1 Receptor Non-Peptide Antagonist Against Congenital Adrenal Hyperplasia.

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Congenital adrenal hyperplasia (CAH) is a disease characterized by decreased glucocorticoid secretion from the adrenals and impaired glucocorticoid feedback inhibition of the hypothalamic-pituitary-adrenal (HPA) axis. This results in augmented secretion of the corticotropin releasing factor (CRF) and corticotropin (ACTH), leading to excessive production of adrenal androgens. Treatment of CAH aims to replace cortisol and reduce the excess of androgens. However, glucocorticoid replacement therapy often requires supraphysiological doses to suppress androgen excess, thus putting CAH patients at the risk of glucocorticoid overexposure. An approach to reduce the overproduction of adrenal androgens while administering glucocorticoids at physiological doses is to decrease the ACTH secretion by administrating CRF antagonists that selectively bind to the type 1 CRF receptor (CRF1R). The CRF1R mediates the effects of CRF on the HPA axis. Based on this concept two CRF1R non-peptide antagonists, tildacerfont and crinecerfont, have been developed and tested for the management of CAH. In an effort to develop novel CRF1R antagonists, we have designed, and pharmacologically evaluated a novel thiazolo[4,5-d] pyrimidine analog, M43. The M43 binds to CRF1R heterologously expressed in HEK 293 cells with high affinity (19.2 nM). The M43 is a potent CRF1R antagonist decreasing at the concentration of 1 μM the potency of the CRF analog-agonist, sauvagine, by more than six fold. In dose–response experiments the M43 displayed a half-maximal inhibitory concentration of 43 nM. Moreover 1 μM of the M43 markedly suppressed the sauvagine-induced proliferation of the RAW 264.7 macrophages, supporting the antagonistic properties on this analog. Computational modeling and molecular dynamics simulations rationalized the relationship between C43/CRF1R interactions, showing that the M43 engages a conserved allosteric pocket formed by transmembrane domains 3, 5, and 6, interacting with Asn283, Thr316 and other residues of the receptor. These interactions appear to lock CRF1R in an inactive conformation, preventing receptor rearrangements required for signaling and a biological effect. The M43 could serve as a lead compound for the development of non-peptide CRF1R antagonists against the CAH. Clin Pharmacol. 2025 Aug 29. doi: 10.1002/bcp.70254. Online ahead of print.PMID: 40883976

Development and Validation of a UPLC-MS/MS Method for Simultaneous Determination of Steroids in Blood Serum.

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Steroid hormones play a crucial role in regulating numerous physiological processes, including development, metabolism, and homeostasis. Acting as chemical messengers, they circulate in the bloodstream and influence distant organs. Altered steroid levels are associated with various pathological conditions, such as Cushing's syndrome, polycystic ovary syndrome (PCOS), congenital adrenal hyperplasia, osteoporosis, endometriosis, and neurodegenerative diseases like Alzheimer's. Therefore, accurate detection and quantification of steroids in biological fluids are critical for diagnosis and clinical monitoring. Traditional methods, such as immunoassays, often lack the specificity and sensitivity required for reliable steroid profiling. In contrast, liquid chromatography–tandem mass spectrometry (LC-MS/MS) has become the gold standard, offering high selectivity and the capability for simultaneous quantification of multiple steroids at very low concentrations. However, challenges remain due to the typically low serum concentrations of steroids (pg/mL to ng/mL), physiological variability, and the presence of both free and conjugated forms. These factors necessitate highly sensitive and robust analytical methods. In this study, we developed and validated an LC-MS/MS method for the simultaneous quantification of multiple steroids in human serum. Sample preparation included protein precipitation followed by liquid–liquid extraction to remove interferences and improve sensitivity. The method demonstrated excellent linearity (R^2 > 0.99 for most analytes), good repeatability (RSD% within acceptable limits), and high accuracy. Extraction recovery was consistent at both low and high concentration levels. Limits of detection and quantification ranged from parts-per-trillion (ppt) to parts-per-billion (ppb), confirming the method's high sensitivity. This validated LC-MS/MS approach offers a sensitive, accurate, and reliable tool for clinical diagnostics and bioanalytical research.

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Proteomic analysis in the investigation of myelodysplastic syndromes.

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ABSTRACT

Scope: This study aims to present the variety of methods of proteomic analysis for the investigation of the protein profile of patients with myelodysplastic syndromes (MDS), as well as unravel potential new biomarkers regarding this disease. MDS are among the least studied hematological diseases in protein level.

MATERIAL AND METHOD

An international literature search was conducted through Pubmed, ResearchGate, and Frontiers databases and keywords used were the following: myelodysplastic syndrome, proteomic analysis, proteomic profiling of patients with myelodysplastic syndrome, mass spectrometry as tool of proteomic analysis.

RESULTS

Mass spectrometry seems to be the reference method for protein identification and discovery of novel protein biomarkers. In the present study, different proteomic systems that require a very small amount of sample have been identified to be used, and include a variety of sample separation techniques, such as Nano-Liquid Chromatography, and different mass spectrometry systems, such as the quadrupole. These markers may be useful for better understanding the pathophysiology of MDS, but also a more effective treatment of MDS.

CONCLUSION

A variety of methods of proteomic analysis can contribute significantly to the investigation of the proteomic profile of patients with MDS, with the ultimate goal of finding novel biomarkers that will serve as tools of early diagnosis and treatment in clinical practice.

The applications of proteomics in diagnosis of glioblastoma: A systematic review of recent advances.

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ABSTRACT TOPIC: 28 Precision Medicine and omics technologies

Glioblastoma (GB) is the most aggressive primary brain tumor in adults, classified as a Grade IV astrocytoma by the WHO. It shows extensive heterogeneity, invasive behavior, and poor prognosis with median survival of only 12–18 months, making early diagnosis essential. A hopeful and rapidly evolving approach is proteomics, which through molecular profiling enables the discovery of reliable biomarkers in blood, cerebrospinal fluid, tumor tissue, urine, and extracellular vesicles (EVs).

For this reason, a systematic review was conducted across PubMed, Scopus, Cochrane, and ClinicalTrials.gov databases. Search strategies used controlled vocabulary and free-text terms related to glioblastoma (glioblastoma, glioblastoma multiforme, GBM, astrocytoma grade IV), proteomics (protein expression, protein profiling, mass spectrometry, LC-MS), and diagnostic applications (biomarkers and early detection). Synonyms and variations were applied across all databases. The search was limited to English-language human studies published between 2020 and 2025, and only articles on adults (≥18 years) exploring proteomic applications in glioblastoma diagnosis were included.

Following screening and eligibility assessment, the included studies highlighted a range of proteomic biomarkers with potential diagnostic value in glioblastoma. Among the most notable are Hsp70 (HSPA1A), Calcitonin Receptor Protein, Epidermal Growth Factor, and Lactate Dehydrogenase A (LDHA), all found elevated in extracellular vesicles of glioblastoma patients compared to healthy controls. In addition, proteins such as ALDH3B1, CSTB, and GNAI2 showed differential expression between pre-operative and post-operative samples. Other proteins, including SRPX identified in EVs, may indicate resistance to therapies such as temozolomide. Furthermore, proteins detected in cerebrospinal fluid, such as laminin subunit alpha-4 and osteopontin, have emerged as potential diagnostic markers. Importantly, large-scale proteomic data analyses, including integration with the Proteomic Atlas, were essential for identifying the broadest feasible set of candidate biomarkers.

In conclusion, proteomics shows strong potential as a diagnostic tool in glioblastoma. Nevertheless, despite these promising results, significant heterogeneity among studies and methodological limitations persist. Consequently, further large-scale, standardized, and clinically validated investigations are required before proteomics can be fully integrated into routine clinical practice for glioblastoma management.

Atypical symptoms leading to a life-threating diagnosis. A diagnostic challenge in the emergency department.

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INTRODUCTION
Thrombotic microangiopathy(TMA) is a diffuse obstruction of capillaries by platelet microthrombi, resulting in thrombocytopenia and ischemic dysfunction of many vital organs. Red blood cells(RBCs) pass through platelet microthrombi of small vessels and become fragmented. The patient develops anemia and a characteristic finding in the peripheral blood smear: schistocytes. Schistocytes are pathognomonic sign and indispensable for the diagnosis of TMA. The main representative of TMA is thrombotic thrombocytopenic purpura(TTP). Diagnostic criteria for TTP were established due to the difficulty in diagnosis: Microangiopathic hemolytic anemia(MAHA), Thrombocytopenia, Neurological manifestations, Renal failure, Fever. They had to be revised in 2006 because not all of them are present at the time of diagnosis: MAHA, Thrombocytopenia. Change in diagnostic criteria led to increased number of patients diagnosed with TTP.
AIM
Describing a 44-year-old female patient with headache and thrombocytopenia, 4 weeks postpartum.
METHODS
A 44-year old female was referred to the Emergency Department(ED) of a tertiary care Greek hospital of Northern Greece due to thrombocytopenia, 4 weeks postpartum. Complete clinical and laboratory testing was performed.
RESULTS
The patient was referred to the ED due to thrombocytopenia. The patient underwent a routine follow-up full blood count(FBC), 4 weeks postpartum. The patient reports a twin pregnancy. During pregnancy, she also exhibited thrombocytopenia, PLT:50.0x10^3/μL. She was diagnosed with benign pregnancy-associated thrombocytopenia and no theurapeutic intervention was done. Finally, she developed preeclampsia during labour. She also reported a first unremarkable pregnancy, 20 years ago. The patient had no other symptoms, apart from headache on admission. Her blood pressure was normal:120/80mmHg. Laboratory testing: WBC: 9.4x10^3/μl, Ne: 70.7% (6.7x10^3/μl), Ly: 20.1% (1.9x10^3/μl), Mo: 6.2% (0.6x10^3/μl) Hb:11.4g/dl, Ht:34.5%, MCV:86.7 fl, RDW:18.4%, PLT: 18x10^3/μl, LDH:743U/L(<248U/L), SGOT:20U/L, SGPT:13U/L, Creatinine:0,93mg/dl, Uric acid:7.2mg/dl, Total Bilirubin:1.4mg/dl, direct bilirubin: 0.4mg/dl, hsCRP:15.4mg/L. Peripheral blood smear(PBS) was performed due to thrombocytopenia, where PLT count was confirmed. PBC revealed spherocytes and schistocytes:2.4%. Based on these laboratory findings, TTP was suspected. Plasmic score was calculated: 7.The patient had high risk of TTP diagnosis. The patient underwent plasma exchange therapy(PEX) urgently in the middle of the night. Pripheral blood samples in order to determine ADAMTS-13 were collected before PEX. 2 days later the results of ADAMTS-13 confirmed the diagnosis of TTP. ADAMTS-13<1%. The test was performed using the ADAMTS-13 activity ELISA kit (Technozym).
CONCLUSIONS
TTP is a rare but life-threatening condition. Prompt diagnosis is of great importance due to the benefits of early treatment, which is most effective when administered within the first hours of the diagnosis. PEX is a life saving therapy for TTP. The clinician should have a strong clinical suspicion of TTP because without treatment TTP has a very high mortality rate, 90%. The diagnosis is mainly based on laboratory tests: FBC, PBS, LDH. Plasmic score is a clinical prediction score assisting in diagnosis before proceeding with specific diagnostic tests. ADAMTS-13, A Disintegrin-like And Metalloprotease with ThromboSpondin-1 repeats, has a central role in the pathophysiology of TTP. In ADAMTS-13 deficiency, large polymers of von Willebrand factor are formed, platelets adhere, accumulate, and white platelet clots form, blocking small vessels in vital organs, intravascular hemolysis occurs with fragmentation of RBCs as they pass through partially blocked capillaries. ADAMTS-13 determination confirmes TTP diagnosis. 2 months later the patient is under specific targeted treatment. She is asymptomatic and her monthly laboratory tests are within normal range.

Quantitative Profiling of Aromatic Amino Acids and Their Host–Microbial Co-metabolites in Human Urine via UPLC–MS/MS.

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ABSTRACT

The aromatic amino acids tryptophan, tyrosine and phenylalanine are involved in many biochemical pathways and their metabolism and co-metabolism by the human and the gut microbiota results in the production of a number of metabolites. Many of these are phenols which are excreted in the urine after either sulfation or glucuronidation by the host. These metabolic processes can be dysregulated due to factors such as inflammation, disease, dietary and/or pharmaceutical interventions. Validated, quantitative methods for the analysis of aromatic amino acids and their metabolites may therefore provide insights into host-gut microbiota symbiosis and its association with pathological conditions. As sulfation is often the favored form of conjugation for phenolic compounds, the development of analytical methods would benefit from access to the sulfate conjugates as reference standards, which unfortunately are scarce. To overcome this limitation nine sulfate conjugates were synthesized using standard chemical routes and were subsequently purified by preparative HPLC. Following structure confirmation (1H-NMR and MS/MS analysis) the standards were used along with 24 other analytes for the development and validation of a quantitative UHPLC-MS/MS-based assay. The method used a CSH Phenyl-Hexyl column to separate and analyze 33 aromatic amino acids and their metabolites in urine. The method was validated and subsequently applied to the analysis of urine obtained from 20 healthy individuals to obtain information on the relevant concentrations in human urine.

KEYWORDS

gut microbiota; sulfated metabolites; aromatic amino acids; chemical synthesis; method development; UHPLC-MS/MS

High resolution metabolomics by data-independent acquisition (DIA) reveals human serum metabolic alteration in patients with Alzheimer's disease, mild cognitive impairment, and healthy controls: A pilot study.

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INTRODUCTION

Alzheimer's disease (AD) is a complex neurodegenerative disease and it is the most prevalent form of dementia. AD is typically divided in three stages: preclinical, mild cognitive impairment (MCI), and dementia. The analysis of serum metabolome could support diagnosis providing a panel of non-invasive biomarkers that can used for the early identification and separation of patients with AD from healthy controls (HC), but also monitoring the conversion of MCI to AD.

METHODS

An ultra-performance liquid chromatography high resolution tandem mass spectrometry (UPLC-HR-MS/MS) metabolomics method was employed, in Data Independent Acquisition (DIA) mode, to investigate the metabolomic profile in serum from HC (n=22), MCI (n=53), and AD patients (n=84). Mzmine 4.5.0 software was used for data-preprocessing and metabolite identification, and MetFrag was used for confirmation of DIA MS/MS spectra. Both multivariate (MVA) and univariate statistical analysis were applied to identify potential biomarkers that differentiate the three groups. Significant metabolites were features with VIP>1 and $p<0.05$.

RESULTS

Eleven and four serum metabolites were identified to separate HC from AD, and MCI from AD, respectively. Amongst them, inosine, estriol, LysoPC(17:0), and two bile acids (Glycochenodeoxycholic acid, 3b-Hydroxy-5-cholenoic acid) differentiated HC from AD. ROC model showed satisfactory predictive accuracy to separate HC from AD patients (AUC: 0.713).

CONCLUSIONS

Herein, we demonstrated that the metabolomics profile in human serum from HC, MCI, and AD patients is significantly altered. Two bile acids were identified as potential biomarkers (HC vs AD, MCI vs AD) which corroborates recent reports. These findings need to be validated in larger human cohorts to elucidate the underlying mechanisms to AD pathophysiology.

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TOPIC

Analytical technologies and applications

Blood Microsampling Technologies in Disease Biomarker Discovery and Health Monitoring.

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Blood microsampling/microsamples (BμS) presents a "patient centric" collection technique with significant advantages over conventional (liquid blood, plasma, and serum) matrices ranging from ease and convenience, improved storage and transportation logistics, enhanced longitudinal research among others. The aim of our study is to investigate the current efforts involved in bridging and implementing blood microsampling (BμS) in routine targeted and untargeted biomarker analysis for global patient health.
In our recently published manuscript, we evaluated original research articles ranging from January 2021 to January 2025 covering studies bridging dried and liquid BμS against conventional matrices. From these, 18 manuscripts were on targeted biomarker analysis and eight on untargeted metabolomics.
Our review showed that BμS devices can provide accurate and precise quantitative results in comparison to conventional matrices. Regarding untargeted metabolomics, BμS devices can provide equal or even more information on metabolic profiles in comparison.
Despite the promising results, certain research inadequacies and challenges for BμS implementation in the clinical lab remain: 1) need for larger diverse study groups covering wide concentration ranges 2) use of recommended capillary blood as opposed to venipuncture blood 3) their integration in multiomics studies (genomics, proteomics, and metabolomics) for more confidence 4) execution of full validation experiments.

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Reference intervals for serum concentrations of osteocalcin for Greek adult men an women.

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BACKGROUND-OBJECTIVE
Bone turnover markers (BTMs) reflect the metabolic activity of bone tissue and can be used to monitor osteoporosis therapy. Osteocalcin (OCN), a bone protein produced by osteoblasts, plays a crucial role in bone health by regulating bone mineralization and quality. It also acts as an endocrine hormone, with its undercarboxylated form influencing whole-body energy metabolism. To adequately interpret BTMs, method-specific and population specific reference intervals are needed. We aimed to determine reference intervals for serum concentrations of OCN for the Greek adult population.
METHODS
We collected samples from 431 apparently healthy Greeks (142 men as well as 149 pre- and 140 post-menopausal women), who volunteered to participate in our study. Data on socio-demographic characteristics, medical histories and medications were collected and subjects with conditions or receiving medications that affecting bone metabolism were excluded. Dual-energy x-ray absorptiometry (DXA) used to measure bone mineral density (BMD) in all participants. All blood collections were performed in the morning after overnight fast. Serum OCN concentrations were measured by an automated immunoassay on the ISYS analyzer (Immunodiagnostic Systems,Boldon,UK). The RI was defined as the central 95% range. We determined RI according to CLSI guide C28-A3 and using the MedCalc Software.
RESULTS
The median age of men, pre- and post-menopausal women were 49, 42 and 57 years respectively. DEXA results revealed that 342 participants had normal BMD, 79 were osteopenic and 10 had osteoporosis which excluded from analysis. Since our data were not normally distributed (Shapiro-Wilk test) in any group and after testing for outliers (Tukey test), we used the non-parametric method suggested by the CLSI guide in order to determine the RI. Multiple regression analysis revealed that age, sex, menopausal status and BMD were fectors significantly affecting OCN levels. Subjects with osteopenia exhibited significantly higher values for OCN compared to those with normal BMD [median (percentiles)] 16.80 ng/mL(13.50-20.72) vs 20.00ng/mL(15.03-27.03). Post-menopausal women exhibited significantly higher values 18.50ng/mL(14.95-27.05) compared to pre-menopausal women 16.50ng/mL (12.50-20.43) and men 17.25ng/mL (12.50-20.43).
Separate reference intervals were calculated and suggested for subjects with normal BMD (8.65-36.25ng/mL), with osteopenia (10.33-48.98ng/mL) as well as for men (9.80-39.60ng/mL), pre-menopausal (7.55-35.30ng/mL) and postmenopausal women(10.67-50.20).
CONCLUSION
We provide reference intervals for Osteocalcin concentrations in serum for the Greek adult population using an automated immunoassay. Our data may aid to interpret bone turnover in the Greek adult population

Performance Evaluation HBSAG and ANTI-HBS Immunoassays Chemilunescence Between Maglumi X Series, Snibe Diagnostics and Another Commercial Brand.

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Hepatitis B virus (HBV) infection continues to pose a significant global public health challenge, with the potential to progress to chronic liver disease, cirrhosis, and hepatocellular carcinoma. This study aimed to evaluate the analytical performance of the Snibe Diagnostics MAGLUMI® HBsAg and Anti-HBs chemiluminescent immunoassays, through comparison with an established commercial method. The evaluation included assessments of precision and method correlation using routine clinical serum samples and quality control materials.

Precision testing was performed using serum pools to determine intra- and inter-assay variability, while correlation studies compared assay results with those obtained from established clinical methods and a commercial comparator assay (Brand A). A total of 100 frozen serum specimens were selected and subsequently analyzed with MAGLUMI® HBsAg assay. Results were then compared with those obtained from the currently implemented instruments in the laboratory. In addition, 85 frozen serum samples were analyzed to evaluate the correlation between the MAGLUMI® Anti-HBs assay and a comparator assay (Brand A).

For precision testing of the MAGLUMI® HBsAg and Anti-HBs kits, two levels of serum pools, negative and positive derived from freshly frozen specimens were aliquoted. Each aliquot was measured five times daily over five consecutive days. The mean and standard deviation (SD) were calculated, and both intra- and inter-assay imprecision were expressed as coefficients of variation (%CV).

The results for HBsAg total precision (%CV) ranged from 18.30% for negative pool to 31.0% for positive pool, reflecting higher analytical variability, particularly at lower concentrations. In contrast, the Anti-HBs assay demonstrated improved precision, with total %CV consistently at 22.4% across both concentration levels, indicating better analytical reproducibility. Moreover, the results demonstrated strong correlation with the comparator method (HBsAg: $r = 0.9209$, Anti-HBs: $r = 0.9291$, $p < 0.0001$).

These findings confirm the reliability and robustness of the Snibe Diagnostics MAGLUMI® assays and support their suitability for routine use in clinical laboratories for the serological assessment of HBV infection.

Circulating miRNome in multiple myeloma: The evaluation of a circulating miR-risk signature ameliorates patients' prognostication.

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The monitoring of multiple myeloma (MM) requires lifelong surveillance involving invasive procedures, primarily bone marrow biopsies, affecting patients' quality-of-life. In the era of liquid biopsy, the identification of non-invasive MM-specific molecular markers could improve risk-stratification and accurately identify high-risk patients towards personalized prognosis and therapy. Circulating miRNAs (miRs) have emerged as novel minimally invasive liquid biopsy tools due to their remarkably stability in body fluids, including plasma, allowing early diagnosis, prognosis and treatment resistance monitoring. Herein, total RNA was extracted from plasma samples of 162 patients, 6 with monoclonal gammopathy of undetermined significance (MGUS), 6 with smoldering MM (sMM) and 150 with MM, and total circulating miR levels were quantified using Qubit microRNA assay kit. Then, circulating miR-seq was performed in 15 MM and 12 MGUS/sMM patients, to dive into circulating miRNome in MM progression. Quantification of circulating miRs was assessed by in-house RT-qPCR and extended statistical and survival analysis using patients' mortality and progression (death and/or relapse) were performed. Intriguingly, elevated levels of total circulating miRs were significantly associated with aggressive disease phenotype, including R-ISS staging ($p=0.001$), LDH ($p<0.001$) and B2M ($p=0.002$) levels, and was strongly correlated with poor OS ($p=0.034$) and patients' short-term progression ($p=0.045$). Subsequently, circulating miR-seq revealed a statistically significant upregulation of miR-29a-3p, miR-193b-3p and miR-148a-3p in MM vs MGUS/sMM patients ($FC>2$ & $p<0.05$). In this context, survival analysis demonstrated that elevated circulation levels of miR-29a, miR-193b and miR-148a are associated with significantly reduced patient survival, in terms of both OS and PFS. Prompted by the abovementioned miRs clinical impact, a circulating miRNA-based risk score signature was developed, utilizing exponentiated regression coefficients derived from univariate Cox regression analysis, and used for the stratification of the patients into "high-risk" and "low-risk" groups. Notably, the survival analysis of our screening cohort highlighted that high-risk patients were correlated with short-term progression (HR=3.063; bootstrap $p=0.001$) and poor survival (HR=4.176; bootstrap $p=0.001$). Additionally, multivariate Cox regression analysis illustrated the circulating miR high-risk signature as a potent predictor of worse survival (HR=3.054; bootstrap $p=0.005$) and higher risk for post-treatment progression (HR=2.380; bootstrap $p=0.004$) of MM patients, independently of R-ISS stage, high-risk cytogenetics [t(4;14), t(14;16), del(17p13), gain/amp(1q21)], LDH, B2M, creatinine levels, patients' gender and age. Finally, the integration of miR-risk signature with established disease markers including R-ISS stage, high-risk cytogenetics and response to 1st-line therapy (IMWG guidelines), unveiled a powerful risk-stratification strategy for MM treatment outcome. Ultimately, our study developed and identified a circulating miR-based risk signature as a robust predictor of unfavorable treatment outcome and post-treatment progression, contributing to non-invasive MM prognostication and personalized treatment decisions.

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Uncovering Novel Prognostic Biomarkers in End-Stage Renal Disease via Proteomic Analysis.

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ABSTRACT TOPIC
"Precision Medicine and omics technologies"
PURPOSE
The prognosis of End-Stage Renal Disease (ESRD) is crucial for optimizing treatment strategies. The identification of novel biomarkers is key to early diagnosis and timely intervention. Advances in proteomics have facilitated the discovery of reliable biomarkers associated with chronic kidney disease (CKD), cardiovascular conditions and related comorbidities.
MATERIALS AND METHODS
For the purposes of this study, a literature search was conducted using the databases PubMed and Google Scholar. The search terms used were "Proteomic analysis" and "End-Stage Renal Disease". 20 out of 139 articles were the most relevant to the topic. Studies examining acute kidney injury, animal models, pediatric patients, and diabetic nephropathy were excluded.
RESULTS
Recent proteomic analyses performed in CKD and ESRD patients highlighted elevated inflammatory mediators (IL-6, IL-1β, IL-8) as strongly associated with cardiovascular mortality, while BNP and NT-proBNP remain established markers for heart failure prognosis. In ESRD, biomarkers, such as TNFR1, FGF23, KIM-1 and suPAR are strongly associated with disease progression and adverse outcomes. Notably, KLOTHO and FGF23 contribute to increased cardiovascular risk, even in early CKD. Among the strongest predictors of kidney failure and mortality are KIM-1, suPAR, sTNFR1, hs-cTnT, NT-proBNP, and GDF-15.
CONCLUSION
Proteomic biomarkers provide valuable insights into the mechanisms, progression, and cardiovascular risks of CKD and ESRD. Markers, such as TNFR1, FGF23, KIM-1, suPAR and BNP/NT-proBNP demonstrate strong prognostic potential. However, variability in study design and evidence, population heterogeneity, lack of standardization, unproven cost-effectiveness and added benefit over existing diagnostic tools currently limit their clinical application. Large-scale, longitudinal, and clinically integrated validation studies are essential to translate discovery into improved CKD/ESRD patient outcomes.

Reference intervals for saliva cortisol concentrations in Greek adults using an automated immunoassay.

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BACKGROUND-OBJECTIVE
Saliva cortisol is a valuable, non-invasive tool for testing hypothalamic-pituitary-adrenal axis function, diagnosing adrenal disorders like Cushing's syndrome and adrenal insufficiency, monitoring the circadian rhythm, and evaluating mental health conditions such as depression. It is also used is used as a biomarker of the human stress response. Its ease of collection and ability to measure free cortisol make it a practical alternative to blood tests, especially in research and in children, allowing for multiple samples to be taken in a natural setting. In this study we aimed to determine reference intervals for saliva concentrations of cortisol for the Greek adult population
METHODS
Saliva samples were collected in the morning (between 7 and 8 am) and in the night (between 10 and 11 pm) healthy adult greek volunteers. Subjects with hypertension, diabetes, with diseases that were known to affect hypothalamic-pituitary-adrenal axis function and under treatment that affect cortisol levels were excluded. Collections were performed using the Salivette collection system. Samples were centrifuged at 1000g for 2 min and the harvested saliva was stored at -30oC until testing. Saliva cortisol was measured with a fully automated chemiluminescent immunoassay on the ISYS analyser (Immunodiagnostic Systems, Boldon, UK). The reference interval was defined as the central 95% range. We determined reference intervals according to CLSI guide C28-A3 and using the MedCalc Software.
RESULTS
We collected morning and evening saliva samples from 139 healthy donors (55 men and 84 women). The median age of men and women were 33years (range 18-65) and 40 (range 18-70) respectively. Median BMI of men and women was 25.66 (range 20.29-43,25) and 23.32 (range 18,25-32.98) respectively. In men donors 50.9% were overweight and 11.3% obese whereas in women only 28.5 were overweight and only 7.1% were obese. Women exhibited marginally higher values of saliva cortisol in both morning and evening collections. We calculated common reference intervals for men and women using the non-parametric method suggested by CLSI C28-A3 guide. The results are shown in the following table

	Morning collections (7-8 am)	Evening collections (10-11 pm)
No of subjects	139	139
Mean (μg/dL)	0.383	0.067
SD (μg/dL)	0.214	0.061
Median (μg/dL)	0.330	0.040
Reference Interval (μg/dL)	0.090 -1.040	0.020 – 0.340

CONCLUSIONS
We provide RI for saliva Cortisol concentration for the Greek adult population using an automated chemiluminescent immunoassay. Our data may aid to interpret saliva Cortisol levels in the Greek adult population

The effect of 60-day head-down tilt bed rest with and without high intensity jump training on biochemical markers: The cologne rsl study.

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Prolonged exposure to microgravity increases systemic oxidative stress and decreases antioxidant capacity. The 6° head-down tilt (HDT) bed rest position is the most frequently used experimental model to simulate microgravity space environment in humans [1]. The study investigated the effect of 6° HDT bed rest with and without jump exercise on certain biochemical markers. This study included 23 healthy, non-smoking male adults aged between 23 and 45 years, with a body mass index (BMI) between 20 and 26 kg/m2, who were recruited and randomly assigned to one of two groups: a control group (n=11) and an exercise group performing jump training (n=12). The study consisted of 60 days of the 6° HDT bed rest position, preceded by baseline data collection (BDC) and followed by a 7-day recovery period at the ENVIHAB Medical Research Facility of the Aerospace Centre in Cologne, Germany. Biochemical analyses revealed similar trends in both study groups for total antioxidant capacity (TAC), adenosine deaminase (ADA), adenosine deaminase 2 (ADA2), glucose (GLU), phosphorus (PHOS), calcium (CA), cholesterol (CHOL), triglycerides (TRIG), high-density lipoproteins (HDL) and low-density lipoproteins (LDL). These parameters showed an upward trend at initial HDT phase and followed by distinct changes during early recovery phase, and returned to baseline by the seventh day of recovery, remaining within normal ranges throughout. In the control group, creatine phosphokinase (CPK) levels increased above the normal range at initial HDT phase and initial recovery phase, whereas in the exercise group CPK levels remained within normal values (Table 1). In conclusion, jump exercise appears to modulate CPK levels in the exercise group, suggesting a protective role against microgravity and muscle strains. These findings provide insight into physiological adaptation to simulated microgravity and highlight the importance of exercise countermeasures in spaceflight analogues.

1. Dolopikou CF, Kourtzidis IA, Tsiftsis AN, Margaritelis N V., Theodorou AA, Paschalis V, et al. Systemic redox biomarkers suggest non-redox mediated processes in the prevention of bed rest-induced muscle atrophy after exercise training: The Cologne RSL study. Acta Astronaut 2020;168:116–22. https://doi.org/10.1016/J.ACTAASTRO.2019.12.002.

Table1. Mean values and SD of biochemical marker at different timepoints in the studygroups

BIOCHEMICAL MARKERS	NORMAL RANGE	GROUPS	MEAN VALUES ± STANDARD DEVIATION VALUES								
			BDC1	HDT2	HDT14	HDT30	HDT40	HDT50	HDT60	R1	R7
TAC	1,20- 2,40 mmol/L	CONTROL	1,29 ± 0,15	1,44 ± 0,19	1,38 ± 0,15	1,42 ± 0,25	1,40 ± 0,20	1,36 ± 0,11	1,36 ± 0,14	1,36 ± 0,15	2,05 ± 2,42
		EXERCISE	1,26 ± 0,16	1,38 ± 0,19	1,35 ± 0,18	1,35 ± 0,17	1,33 ± 0,18	1,29 ± 0,12	1,27 ± 0,12	1,27 ± 0,19	1,27 ± 0,14
ADA	<40 U/L	CONTROL	9,34 ± 1,46	9,47 ± 1,64	10,29 ± 1,88	10,17 ± 2,38	11,38 ± 4,10	10,69 ± 3,06	9,82 ± 3,03	9,01 ± 2,26	9,02 ± 1,81
		EXERCISE	8,86 ± 1,26	8,88 ± 1,30	9,24 ± 1,70	8,91 ± 1,64	9,02 ± 1,18	8,72 ± 1,16	8,31 ± 1,01	7,83 ± 1,14	8,93 ± 1,51
ADA2	<20 U/L	CONTROL	6,55 ± 1,45	6,69 ± 1,75	7,52 ± 1,99	7,41 ± 2,38	8,40 ± 3,92	7,92 ± 2,88	13,47 ± 20,94	6,17 ± 2,21	6,22 ± 1,77
		EXERCISE	6,04 ± 0,77	5,85 ± 0,93	6,43 ± 1,37	6,23 ± 1,27	6,20 ± 0,90	6,06 ± 0,87	5,64 ± 0,83	5,22 ± 0,68	5,87 ± 1,30
GLU	70- 100 mg/dL	CONTROL	87,82 ± 3,60	93,91 ± 30,52	87,45 ± 4,03	88,55 ± 6,33	88,64 ± 4,59	88,55 ± 5,65	86,27 ± 4,71	89,18 ± 6,59	88,18 ± 5,84
		EXERCISE	90,09 ± 3,48	87,83 ± 5,02	89,67 ± 4,10	89,50 ± 4,66	92,92 ± 4,25	91,25 ± 4,43	90,92 ± 6,61	91,58 ± 4,81	90,42 ± 4,40
PHOS	2,5- 4,5 mg/dL	CONTROL	3,85 ± 0,47	4,33 ± 0,45	4,41 ± 0,28	4,38 ± 0,25	4,37 ± 0,29	4,46 ± 0,33	4,44 ± 0,37	3,87 ± 0,32	4,17 ± 0,46
		EXERCISE	3,67 ± 0,29	4,32 ± 0,32	4,18 ± 0,34	4,14 ± 0,33	3,99 ± 0,33	4,28 ± 0,34	4,14 ± 0,26	4,03 ± 0,42	3,98 ± 0,33
CA	8,6- 10,3 mg/dL	CONTROL	9,41 ± 0,26	9,50 ± 0,37	9,57 ± 0,28	9,52 ± 0,33	9,53 ± 0,30	9,58 ± 0,28	9,45 ± 0,30	9,29 ± 0,36	9,13 ± 0,30
		EXERCISE	9,46 ± 0,20	9,45 ± 0,26	9,60 ± 0,26	9,43 ± 0,26	9,49 ± 0,22	9,43 ± 0,24	9,48 ± 0,24	9,08 ± 0,58	9,35 ± 0,39
CHOL	<200 mg/ dL	CONTROL	168,55 ± 28,88	188,18 ± 34,44	171,36 ± 26,82	171,27 ± 27,76	162,09 ± 27,45	169,73 ± 31,93	166,27 ± 33,74	149,91 ± 30,48	159,36 ± 24,90
		EXERCISE	166,27 ± 23,44	182,83 ± 24,84	166,42 ± 21,80	161,67 ± 24,87	157,33 ± 20,93	159,17 ± 16,39	158,25 ± 20,57	142,17 ± 15,77	157,17 ± 20,47
TRIG	<150 mg/ dL	CONTROL	74,82 ± 15,73	98,91 ± 23,56	83,45 ± 16,90	95,64 ± 28,34	95,64 ± 21,58	96,09 ± 29,82	86,82 ± 22,82	72,55 ± 23,85	80,55 ± 14,24
		EXERCISE	95,73 ± 39,29	118,00 ± 41,54	95,00 ± 25,27	100,58 ± 29,31	106,92 ± 29,42	104,50 ± 32,08	99,50 ± 29,47	89,58 ± 28,85	104,50 ± 30,32
HDL	>45 mg/dL	CONTROL	59,64 ± 10,74	61,00 ± 10,76	53,27 ± 9,54	51,55 ± 8,68	48,82 ± 8,83	48,64 ± 9,21	48,82 ± 7,74	48,64 ± 7,66	52,18 ± 8,94
		EXERCISE	55,45 ± 9,28	55,75 ± 9,21	49,83 ± 7,06	48,58 ± 5,74	47,92 ± 5,84	46,75 ± 5,80	47,58 ± 4,80	45,58 ± 4,40	49,58 ± 6,02
LDL	<110 mg/ dL	CONTROL	94,00 ± 24,41	107,55 ± 28,94	101,45 ± 23,53	100,64 ± 23,02	94,09 ± 23,24	101,73 ± 27,04	100,18 ± 27,83	86,64 ± 25,66	91,09 ± 19,77
		EXERCISE	91,64 ± 17,20	103,42 ± 19,88	97,50 ± 16,40	92,83 ± 20,54	87,92 ± 16,52	91,67 ± 13,77	90,75 ± 15,74	78,83 ± 14,27	86,67 ± 16,63
CPK	40- 320 U/L	CONTROL	84,40 ± 34,98	262,36 ± 461,94	58,45 ± 25,87	64,09 ± 25,87	77,73 ± 20,27	64,55 ± 31,73	80,27 ± 41,56	1264,36 ± 1071,49	166,18 ± 177,43
		EXERCISE	83,55 ± 71,27	122,08 ± 68,87	76,00 ± 30,11	62,42 ± 15,38	51,17 ± 19,68	64,92 ± 26,01	66,25 ± 12,00	177,33 ± 73,82	97,17 ± 40,99

Abbreviations: ADA: adenosine deaminase, ADA 2:, adenosine deaminase 2, BDC 1: baseline data collection, CA: calcium, CHOL: cholesterol, CPK: creatine phosphokinase, HDL: high-density lipoproteins, HDT 2,14,30,40,50,60: head-down tilt, GLU: glucose, LDL: low-density lipoproteins, PHOS: phosphorus, R 1,2: recovery period, TAC: total antioxidant capacity, TRIG: triglycerides.

Διερεύνηση της αναιμίας σε αιμοκαθαιρόμενους ασθενείς

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ΕΙΣΑΓΩΓΗ
Η αναιμία είναι συχνή επιπλοκή της Χρόνιας Νεφρικής Νόσου και σχετίζεται με αυξημένη νοσηρότητα, αυξημένη θνητότητα και υποβάθμιση της ποιότητας ζωής των ασθενών. Η παθογένειά της είναι πολύπλοκη και οφείλεται σε ανεπάρκεια σιδήρου και μη επαρκή παραγωγή ερυθροποιητίνης. Σκοπός της εργασίας μας είναι η διερεύνηση της αναιμίας σε αιμοκαθαιρόμενους ασθενείς.
ΥΛΙΚΟ ΚΑΙ ΜΕΘΟΔΟΙ
Στη μελέτη έχουν συμπεριληφθεί 121 αιμοκαθαιρόμενοι ασθενείς, 88 άνδρες (72.7 %) και 33 γυναίκες (27.3 %), ηλικίας 24 ως 75 ετών, στους οποίους έγινε μέτρηση για σίδηρο ορού, φερριτίνη, βιταμίνη Β12 και φυλλικό οξύ. Οι μετρήσεις έγιναν στον αυτόματο βιοχημικό αναλυτή Abbott Architect C8000 και στον αυτόματο ανοσολογικό αναλυτή Cobas 6000 Roche. Η στατιστική επεξεργασία των αποτελεσμάτων έγινε με το MINITAB 19.
ΑΠΟΤΕΛΕΣΜΑΤΑ
Οι μέσες τιμές των υπό διερεύνηση παραμέτρων ήταν: Β12 άνδρες 658.0 και γυναίκες 575.5 pg/mL, σίδηρος ορού άνδρες 62.9 και γυναίκες 56.9 μg/dL, φερριτίνη άνδρες 609.0 και γυναίκες 402.7 ng/mL και φυλλικό οξύ άνδρες 5.92 και γυναίκες 6.54 ng/mL. Δεν παρατηρείται στατιστικά σημαντική διαφορά στη μέση τιμή μεταξύ ανδρών και γυναικών για καμία από τις τέσσερις παραμέτρους. Τα αποτελέσματα συνοψίζονται στον παρακάτω πίνακα

		ΑΝΔΡΕΣ		ΓΥΝΑΙΚΕΣ	
		n	%	n	%
ΣΙΔΗΡΟΣ Τ.Α. ΑΝΔΡΕΣ 60-160 μg/dL Τ.Α. ΓΥΝΑΙΚΕΣ 40-150 μg/dL	ΑΝΕΠΑΡΚΕΙΑ	48	39.7	12	9.9
	ΦΥΣΙΟΛΟΓΙΚΑ ΕΠΙΠΕΔΑ	37	30.6	20	16.5
	ΥΨΗΛΟΤΕΡΑ ΕΠΙΠΕΔΑ	3	2.5	1	0.8
ΦΕΡΡΙΤΙΝΗ Τ.Α. ΑΝΔΡΕΣ 20-240 ng/mL Τ.Α. ΓΥΝΑΙΚΕΣ 10-120 ng/mL	ΑΝΕΠΑΡΚΕΙΑ	1	0.8	0	0.0
	ΦΥΣΙΟΛΟΓΙΚΑ ΕΠΙΠΕΔΑ	34	28.1	9	7.4
	ΥΨΗΛΟΤΕΡΑ ΕΠΙΠΕΔΑ	53	43.8	24	19.8
ΒΙΤΑΜΙΝΗ Β12 Τ.Α.200-960 ng/mL	ΑΝΕΠΑΡΚΕΙΑ	1	0.8	0	0.0
	ΦΥΣΙΟΛΟΓΙΚΑ ΕΠΙΠΕΔΑ	79	65.3	30	24.8
	ΥΨΗΛΟΤΕΡΑ ΕΠΙΠΕΔΑ	8	6.6	3	2.5
ΦΥΛΛΙΚΟ ΟΞΥ Τ.Α.3.98-26.8 ng/mL	ΑΝΕΠΑΡΚΕΙΑ	19	15.7	7	5.8
	ΦΥΣΙΟΛΟΓΙΚΑ ΕΠΙΠΕΔΑ	69	57.0	26	21.5
	ΥΨΗΛΟΤΕΡΑ ΕΠΙΠΕΔΑ	0	0.0	0	0.0

ΣΥΜΠΕΡΑΣΜΑΤΑ
Συνολικά 60 (49.6 %) ασθενείς, 48 άνδρες και 12 γυναίκες, παρουσίαζαν ανεπάρκεια σιδήρου, 1 άνδρας ανεπάρκεια Β12 και 26 ασθενείς (21.5 %), 19 άνδρες και 7 γυναίκες, ανεπάρκεια φυλλικού οξέος. Επιπρόσθετα 4 ασθενείς (3 άνδρες και 1 γυναίκα), είχαν επίπεδα σιδήρου υψηλότερα από το ανώτατο όριο του διαστήματος αναφοράς και 11 ασθενείς (8 άνδρες και 3 γυναίκες) είχαν επίπεδα βιταμίνης Β12 υψηλότερα από το ανώτατο όριο του διαστήματος αναφοράς. Το παρατηρούμενο ποσοστό σιδηροπενίας είναι υψηλό στον υπό μελέτη πληθυσμό. Συνολικά 77 ασθενείς (63.6 %) είχαν επίπεδα φερριτίνης υψηλότερα από το ανώτατο όριο του διαστήματος αναφοράς, τα οποία σχετίζονται με τη χρόνια φλεγμονή της νεφρικής νόσου.

Συσχέτιση αντισωμάτων έναντι της καρδιολιπίνης με κλινικές οντότητες.

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ΕΙΣΑΓΩΓΗ

Τα αντιφωσφολιπιδικά αντισώματα συνιστούν μια ετερογενή ομάδα αυτοαντισωμάτων, τα οποία στρέφονται είτε έναντι των πρωτεϊνών δέσμευσης φωσφολιπιδίων, είτε έναντι του συμπλόκου πρωτεϊνών και φωσφολιπιδίων. Σε αυτή την ομάδα περιλαμβάνονται αντισώματα έναντι της β2-γλυκοπρωτεΐνης IgG και IgM, αντισώματα έναντι καρδιολιπίνης IgG και IgM καθώς και το αντιπηκτικό του λύκου. Σκοπός της εργασίας μας είναι η διερεύνηση των αντισωμάτων έναντι της καρδιολιπίνης στους ασθενείς του Ναυτικού Νοσοκομείου Αθηνών και η συσχέτιση τους με κλινικές οντότητες.

Υλικά και μέθοδοι. Στη μελέτη έχουν συμπεριληφθεί τα αποτελέσματα από 1498 ασθενείς που ελέγχθηκαν κατά το χρονικό διάστημα 2018-2024. Οι 667 ήταν άνδρες (44.5 %) και 831 γυναίκες (55.5 %). Οι μετρήσεις έχουν γίνει με τα αντιδραστήρια Anti-Cardiolipin IgG και IgM της εταιρείας Dia Metra, Perugia, Italy. Οι μετρήσεις διενεργήθηκαν στον αναλυτή Brio 2 Dialab. Επιπρόσθετα, στους ασθενείς έγιναν μετρήσεις για συμπλήρωμα ορού (C3 και C4), τροπονίνη υψηλής ευαισθησίας, D-Dimer, APTT και έλεγχος αυτοαντισωμάτων. Περαιτέρω πληροφορίες για το ιατρικό τους ιστορικό αντλήθηκαν από το LIS.

Αποτελέσματα: Από το σύνολο των ασθενών 12 είχαν αντισώματα IgG θετικά (6 άνδρες και 6 γυναίκες) και 21 IgM θετικά (8 άνδρες και 13 γυναίκες). Τα αποτελέσματα των ασθενών συνοψίζονται στον παρακάτω πίνακα.

ΦΥΛΟ	IgG	IgM	ΗΛΙΚΙΑ	C3	C4	D DIMER	APTT	ΤΡΟΠΟ-ΝΙΝΗ
ΑΝΔΡΕΣ	1.0	15.5	24	116.0	22.5	0.32	20.3	3.0
	0.3	13.7	38	111.0	21.3	0.44	59.9	4.0
	0.8	14.2	43	106.0	20.5	0.25	27.8	9.9
	0.5	22.0	52	104.7	9.9	0.15	38.7	3.0
	0.5	70.0	62	124.0	27.3	0.65	37.2	3.1
	0.5	44.9	68	127.4	24.0	1.98	34.5	97.3
	0.5	70.0	73	99.0	17.3	0.22	47.9	41.8
	0.5	49.2	77	121.7	30.3	3.07	48.5	374.0
ΓΥΝΑΙΚΕΣ	1.3	14.6	20	84.8	22.8	0.18	40.9	3.0
	1.0	75.0	21	86.7	8.9	0.56	40.3	4.6
	0.5	14.9	25	103.0	17.2	2.86	29.1	4.7
	0.5	15.0	28	100.0	35.0	0.17	36.6	3.0
	5.1	19.5	36	77.7	21.5	0.26	32.9	3.0
	25.2	17.7	36	54.8	10.9	2.07	42.7	5.3
	1.0	17.3	51	87.3	15.5	0.25	26.7	5.8
	0.5	14.0	52	156.0	30.9	0.58	28.2	3.0
	0.5	60.8	54	99.0	32.0	0.44	29.2	7.2
	0.5	15.0	56	97.0	47.8	0.65	28.2	22.2
	0.5	25.0	66	111.2	13.5	2.21	24.3	39.4
	1.0	75.0	73	129.0	39.5	1.31	27.8	275.0
	0.5	61.3	79	106.8	11.7	1.36	35.6	9.0

Παρατηρούμε παθολογικά αποτελέσματα στις εξετάσεις της πήξης για τους 15 από τους 21 ασθενείς, καθώς και παθολογικά αποτελέσματα του συμπληρώματος ορού και της τροπονίνης για τους 6 από τους 21 ασθενείς. Όσον αφορά στις κλινικές οντότητες 2 ασθενείς ήταν θετικοί για COVID-19, 6 για αυτοάνοσα νοσήματα (θυρεοειδίτιδα, ΣΕΛ και πολυμυοσίτιδα), 3 είχαν κακοήθεια, 5 είχαν άλλες λοιμώξεις (ουρεόπλασμα, κολπίτδα από αιμόφιλο, CMV, EBV και β-αιμολυτικός στρεπτόκοκκος), 1 έπασχε από σακχαρώδη διαβήτη τύπου 2, 3 είχαν καριδακή ανεπάρκεια και 1 υπέστη αναφυλακτικό σοκ.
Συζήτηση: τα αντισώματα έναντι της καρδιολιπίνης είναι η πιο κοινή μορφή αντιφωσφολιπιδικών αντισωμάτων και διαδραματίζουν σημαντικό ρόλο στη διαδικασία πήξης του αίματος, Η παρουσία τους υποδηλώνει ότι ο ασθενής έχει αυξημένο κίνδυνο εμφάνισης υποτροπιάζουσας θρόμβωσης και στις γυναίκες κίνδυνο νοσηρότητας κατά την εγκυμοσύνη. Τα αντισώματα καρδιολιπίνης συναντώνται συχνά σε αυτοάνοσα νοσήματα. Επιπρόσθετα, ανευρίσκονται παροδικά σε ασθενείς με οξείες λοιμώξεις και ορισμένες μορφές κακοήθειας. Οι παρατηρηθείσες κλινικές οντότητες συνάδουν με τα βιβλιογραφικά δεδομένα. Όσον αφορά στον ασθενή με το αναφυλακτικό σοκ, έχει βρεθεί ότι διάφορες λιποπρωτεΐνες που περιέχονται σε σπόρους και καρπούς, καθώς και στους ξηρούς καρπούς, μπορεί να προκαλέσουν σοβαρή τροφιμογενή αναφυλαξία και η κατανάλωση τους συνδέεται με την παρουσία αντιφωσφολιπιδικού συνδρόμου και την σχετιζόμενη με αυτό εμφάνιση θρόμβωσης.

Σύνδρομο CREST - εργαστηριακά ευρήματα.

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ΕΙΣΑΓΩΓΗ
Το σύνδρομο CREST (Calcinosis, Raynaud's phenomena, Esophageal dysmobility, Sclerodaktyly και Telangiectasias) ή ακροσκλήρυνση, είναι ένα αυτοάνοσο νόσημα με σημαντική θνητότητα και 10ετή επιβίωση περίπου 75%. Συνιστά ιδιαίτερη μορφή της συστηματικής σκληροδερμίας. Το σύνδρομο CREST είναι συ¬χνότερο στις γυναίκες, ενώ στα παιδιά, είναι σπάνιο. Σκοπός της εργασίας μας είναι η παρουσίαση των εργαστηριακών ευρημάτων σε ασθενείς με σύνδρομο CREST.
Υλικά και Μέθοδοι: πρόκειται για αναδρομική μελέτη των ασθενών που εξετάστηκαν για αυτοάνοσα νοσήματα κατά το χρονικό διάστημα 2020-2025. Ελέχθηκαν συνολικά 5369 ασθενείς ηλικίας 18 ως 70 ετών.
Αποτελέσματα: Συνολικά 8 ασθενείς, όλες γυναίκες έπασχαν από σύνδρομο CREST. Τα εργαστηριακά ευρήματα συνοψίζονται ως εξής:

- Γενική αίματος: σε όλες τις ασθενείς παρατηρήθηκε αναιμία και αυξημένη ΤΚΕ, σε 4 ηωσινοφιλία και σε 3 λευκοκυττάρωση.
- Γενική ούρων: σε 2 ασθενείς παρατηρήθηκε αιματουρία, σε 2 λευκωματουρία σε και 1 ανιχνεύθηκε ουροχολινογόνο
- Βιοχημικές εξετάσεις: 4 ασθενείς είχαν αυξημένα ένζυμα ηπατικής βιοχημείας και 2 αυξημένα επίπεδα ουρίας και κρεατινίνης. Σε όλες παρατηρήθηκαν αυξημένες τιμές CRP
- Έλεγχος αυτοαντισωμάτων: Σε όλες τις ασθενείς ανιχνεύθηκαν αντικεντρομεριδιακά αντισώματα, συνδεόμενα με τα αντιγόνα CENP-B Ο τίτλος ήταν 1/640 σε 2 ασθενείς και 1/1280 σε 6 ασθενείς. Σε 1 ασθενή παρατηρήθηκαν θετικά AMA (αντιμιτοχονδριακά αντισώματα) σε τίτλο 1/80.

ΣΥΜΠΕΡΑΣΜΑΤΑ
Τα αντικεντρομεριδιακά αντισώματα ανιχνεύονται στο 50-96% των ασθενών και επιτρέπουν την ορολογική διάκριση του συνδρόμου CREST από άλλες ποικιλίες της συστηματικής σκληροδερμίας, άλλα αυτοάνοσα νοσήματα και πρωτοπαθή φαινόμενα Raynaud. Οι τίτλοι τους δεν μεταβάλλονται με την πάροδο του χρόνου ή την πορεία της νόσου, ούτε σχετίζονται με την έκταση της προσβολής των οργάνων του σώματος. Η παρατηρούμενη λευκοκυττάρωση σχετίζεται με προχωρημένη προσβολή των σπλάγχνων και των μυών, ενώ η περιφερική ηωσινοφιλία παρατηρείται στο 15% περίπου των ασθενών και σχετίζεται με τη γενικευένη φλεγμονή των ιστών και του δέρματος. Τα ευρήματα από τη γενική ούρων υποδεικνύουν ότι είναι πιθανό να εκδηλωθεί νεφρική ανεπάρκεια στο μέλλον. Η αναιμία παρατηρείται στο 25% περίπου των ασθενών και οφείλεται στην αναιμία της χρόνιας φλεγμονής και λιγότερο συχνά, σε άλλα αίτια, όπως η ανεπάρκεια βιταμίνης Β12 ή φυλλικού οξέος. Επιπρόσθετα σε ποσοστό 51.2 % των περιπτώσεων του συνδρόμου μπορεί να υπάρχει αλληλοεπικάλυψη με πρωτοπαθή χολική κίρρωση, όπως παρατηρήθηκε στην ασθενή με θετικά AMA.

Προσδιορισμός του χρόνου επίδοσης αποτελέσματος για τα δείγματα του τμήματος επειγόντων περιστατικών.

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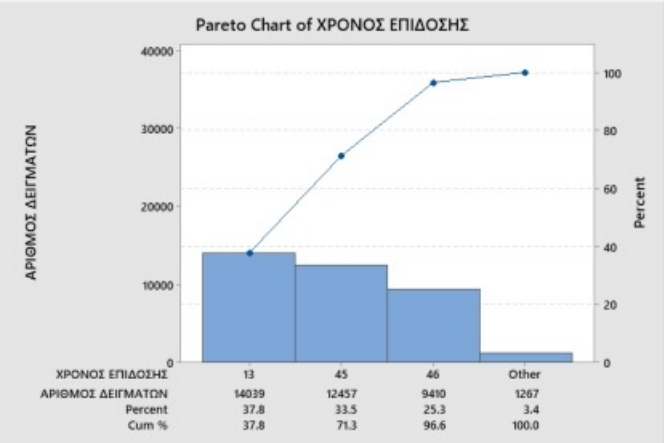
Ο χρόνος επίδοσης του αποτελέσματος (TAT-Turn Around Time) είναι κρίσιμος παράγοντας για την έγκαιρη διάγνωση και επιλογή θεραπείας του ασθενή. Σαν TAT ορίζεται, ο χρόνος από την παραλαβή του δείγματος στο Εργαστήριο μέχρι την επίδοση του αποτελέσματος. Ο TAT έχει ευρεία εφαρμογή ως δείκτης ποιότητας στα κλινικά εργαστήρια. Σκοπός της εργασίας ήταν η εκτίμηση του TAT για τα επείγοντα δείγματα από τα ΤΕΠ.
Για την εκπόνηση της μελέτης καταγράφηκαν όλα τα δείγματα από τα ΤΕΠ του έτους 2024. Από το LIS έγινε καταγραφή του χρόνου παραλαβής και του χρόνου επικύρωσης/έγκρισης των αποτελεσμάτων. Κατόπιν υπολογίστηκε ο χρόνος επίδοσης αποτελεσμάτων για κάθε δείγμα, από τη διαφορά των χρόνων. Ακολούθησε στατιστική επεξεργασία των αποτελεσμάτων με το MINITAB 19.

Τα αποτελέσματα συνοψίζονται στον παρακάτω πίνακα.

	ΧΡΟΝΟΣ ΕΠΙΔΟΣΗΣ	ΑΡΙΘΜΟΣ ΔΕΙΓΜΑΤΩΝ
ΓΕΝΙΚΗ ΑΙΜΑΤΟΣ	13	14039
ΕΞΕΤΑΣΕΙΣ ΠΗΞΗΣ	46	2339
ΤΕΣΤ ΚΥΗΣΕΩΣ	11	660
ΤΡΟΠΟΝΙΝΗ	46	7071
ΒΙΟΧΗΜΙΚΕΣ ΕΞΕΤΑΣΕΙΣ	45	12457
ΓΕΝΙΚΗ ΟΥΡΩΝ	40	607

Η κατανομή συχνοτήτων και τα αντίστοιχα ποσοστά παρουσιάζονται στο παρακάτω διάγραμμα Pareto. Σύμφωνα με αυτό στο 90% των TAT βρίσκεται στο διάστημα (0:11, 0:46 min). Σε όλες τις παριπτώσεις ο TAT δεν υπερβαίνει τα 60 min, όπως προβλέπεται από τις διεθνεις κατευθυντήριες οδηγίες. Παρατηρήθηκαν 30 ακραίες τιμές επί συνόλου 37173 δειγμάτων (ποσοστό 0.08%), με χρόνο TAT μεγαλύτερο από 46 min, οι οποίες οφείλονται στην ποιότητα των δειγμάτων, όπως αιμολυμένα και θρομβούμενα δείγματα, για το οποία έγινε αίτημα για αποστολή νέου δείγματος.



Διερεύνηση παρεμβολής στη μέτρηση του ρευματοειδούς παράγοντα.

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Σκοπός της εργασίας είναι η διερεύνηση παρεμβολής στη μέτρηση του ρευματοειδούς παράγοντα, σε ασθενή με πυρετό αγνώστου αιτιολογίας.

Υλικά και μέθοδοι: άνδρας ασθενής 56 ετών προσήλθε στα ΤΕΠ με εμπύρετο από τετραημέρου. Στον ασθενή διενεργήθηκε πλήρης εργαστηριακός έλεγχος με γενική εξέταση ούρων, γενική εξέταση αίματος, βιοχημικές εξετάσεις, έλεγχος αντισωμάτων για ηπατίτιδα Α, Β, C, HIV, EBV, CMV, Toxoplasma και Brucella, καθώς και πλήρης έλεγχος αυτοαντισωμάτων.

Αποτελέσματα: Τα αποτελέσματα του ελέγχου για ιοπυς και βακτήρια ήταν όλα αρνητικά. Από τον εργαστηριακό έλεγχο παρατηρήθηκαν οι παρακάτω παθολογικές τιμές. ΤΚΕ=36, CRP=72.4 mg/L και RF=3270.0 IU/mL Παρατηρήθηκε πολύ υψηλή τιμή για τον RF οπότε ζητήθηκε και νέο δείγμα την επόμενη μέρα. Οι επαναλήψεις που διενεργήθηκαν στα δυο δείγματα του ασθενούς παρουσιάζονται στον παρακάτω πίνακα. Αφορούν σε μετρήσεις σε διαφορετικούς αναλυτές, αντιδραστήρια διαφορετικών κατασκευαστικών οίκων καθώς και σε διαφορετικούς εργαστηριακούς χώρους. Όλες οι μετρήσεις έχουν προκύψει μετά από αραίωση του δείγματος 1:100. Οι αραιώσεις 1:2. 1:4, 1:10 και 1:20 έδιναν αποτέλεσμα μεγαλύτερο από το ανώτερο όριο γραμμικότητας της αναλυτικής μεθόδου (>98.6).

ΕΡΓΑΣΤΗΡΙΟ	ΑΝΑΛΥΤΗΣ	ΔΕΙΓΜΑ	ΑΝΤΙΔΡΑΣΤΗΡΙΟ	ΑΠΟΤΕΛΕΣΜΑ
ΕΡΓΑΣΤΗΡΙΟ Α	ΑΝΑΛΥΤΗΣ Α_1	1	ΕΤΑΙΡΕΙΑ_Α	3270,0
ΕΡΓΑΣΤΗΡΙΟ Α	ΑΝΑΛΥΤΗΣ Α_2	1	ΕΤΑΙΡΕΙΑ_Α	3278,0
ΕΡΓΑΣΤΗΡΙΟ Α	ΑΝΑΛΥΤΗΣ Α_1	2	ΕΤΑΙΡΕΙΑ_Α	3383,0
ΕΡΓΑΣΤΗΡΙΟ Α	ΑΝΑΛΥΤΗΣ Α_2	2	ΕΤΑΙΡΕΙΑ_Α	3401,0
ΕΡΓΑΣΤΗΡΙΟ Β	ΑΝΑΛΥΤΗΣ Α	1	ΕΤΑΙΡΕΙΑ_Α	3530,9
ΕΡΓΑΣΤΗΡΙΟ Β	ΑΝΑΛΥΤΗΣ Β	2	ΕΤΑΙΡΕΙΑ_Α	3370,6
ΕΡΓΑΣΤΗΡΙΟ Β	ΑΝΑΛΥΤΗΣ Α	1	ΕΤΑΙΡΕΙΑ _Β	3420,0
ΕΡΓΑΣΤΗΡΙΟ Β	ΑΝΑΛΥΤΗΣ Β	2	ΕΤΑΙΡΕΙΑ _Β	3386,0
ΕΡΓΑΣΤΗΡΙΟ Γ	ΑΝΑΛΥΤΗΣ Γ	1	ΕΤΑΙΡΕΙΑ _Γ	3655,0
ΕΡΓΑΣΤΗΡΙΟ Γ	ΑΝΑΛΥΤΗΣ Γ	2	ΕΤΑΙΡΕΙΑ _Γ	3411,3
ΕΡΓΑΣΤΗΡΙΟ Γ	ΑΝΑΛΥΤΗΣ Δ	1	ΕΤΑΙΡΕΙΑ_Δ	3558,0
ΕΡΓΑΣΤΗΡΙΟ Γ	ΑΝΑΛΥΤΗΣ Δ	2	ΕΤΑΙΡΕΙΑ_Δ	3477,9

ΣΥΖΗΤΗΣΗ

μετά από λεπτομερή διερεύνηση πιθανών παρεμβολών στη μέτρηση και σύμφωνα με το ιατρικό ιστορικό και τη φαρμακευτική αγωγή που ακολουθεί ο ασθενής, η υψηλή τιμή του RF αποδίδεται σε παρεμβολή από τη χορήγηση μεθυλοντόπα (αντιϋπερτασικό φάρμακο). Σύμφωνα με τη βιβλιογραφία η μεθυλντόπα μπορεί να ευθύνεται για μέτρηση ψευδώς αυξημένων επιπεδων ανοσοσφαιρίνης IgG, διαφόρων αντισωμάτων και ρευματοειδούς παράγοντα. Η αλληλεπίδραση φαρμάκων και εργαστηριακών αναλύσεων αποτελεί παράγοντα που θα πρέπει να λαμβάνεται σοβαρά υπόψη κατά τη συνταγογράφηση του εργαστηριακού ελέγχου του ασθενούς. Πολλά φάρμακα μπορούν να επηρεάσουν την εγκυρότητα των αποτελεσμάτων κατά τρόπο που μπορεί να παραπλανήσει τον κλινικό ιατρό και να οδηγήσει το εργαστήριο σε άσκοπες επαναλήψεις και σπατάλη πόρων.

Διερεύνηση περιστατικού τρανσαμινασαιμίας απο HCV λοίμωξη.

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ΕΙΣΑΓΩΓΗ: η χρόνια HCV-λοίμωξη αυξάνει 27 φορές τον επιπολασμό ανάπτυξης ΗΚΚ. Ο ΗΚΚ θεωρείται ως η βασική αιτία θανάτου σε κιρρωτικούς ασθενείς.
ΣΚΟΠΟΣ: της παρούσας μελέτης ήταν η περαιτέρω διερεύνηση της τρανσαμινασαιμίας.
ΑΤΟΜΙΚΟ ΑΝΑΜΝΗΣΤΙΚΟ:ασθενής 57 ετών, ημιδαπός χωρίς διεγνωσμένα υποκείμενα νοσήματα,αναφέρει το τελευταίο 12μηνο,κόπωση, αρθραλγίες, μυαλγίες.Απέδιδε την κατάστασή του στην ενασχόλησή του ως λιμενεργάτης,και ελάμβανε συνταγογραφημένα αντιφλεγμονώδη φάρμακα για τις αρθραλγίες.Κατά τον πρώτο έλεγχο εντοπίστηκαν ευρήματα, όπως η υπεργλυκαιμία, η υπερουριχαιμία, η τρανσαμινασαιμία, και συνεστήθη περαιτέρω έλεγχος, συμπεριλαμβανομένου των ιογενών ηπατιτίδων.Ο ασθενής επέστρεψε έναν χρόνο μετά,ωχρός,με αναφερόμενη απώλεια βάρους(>25),με δυσπεπτικά ενοχλήματα, καταβολή,μυοσκελετικούς πόνους,πετέχειες στον κορμό/κοιλιακή χώρα,καθώς δεν προέβη στον συνιστώμενο έλεγχο,διακόπτοντας την χρήση της αντιφλεγμονώδους αγωγής για τις αρθραλγίες.
ΥΛΙΚΟ ΚΑΙ ΜΕΘΟΔΟΙ
Υλικό→γενική αίματος,βιοχημικός έλεγχος,έλεγχος αιμόστασης
Αιματολογικός έλεγχος→αναλυτής CelltacG/NIHON-KOHDEN
Βιοχημικός→KONELAB60
Έλεγχος αιμόστασης→ACL-ELITE
ΑΠΟΤΕΛΕΣΜΑΤΑ:

ΕΡΓΑΣΤΗΡΙΑΚΟΣ ΕΛΕΓΧΟΣ	ΜΑΡΤΙΟΣ 2023	ΜΑΡΤΙΟΣ 2024
ALP	N 121 u/l	↑ ↑ ↑ 1440 u/l
γ-GT	↑ 82 u/l	↑ ↑ ↑ 452 u/l
ALT	↑ 76 u/l	↑ ↑ 131 u/l
AST	↑ 45 u/l	↑ ↑ ↑ 282 u/l
ολική χολερυθρίνη	↑1.30 mg/dl	↑ ↑ ↑ 2,6 mg/dl
αριθμός αιμοπεταλίων	N 227 x 103 /μL	↓ ↓ 89 x 103 /μL
τιμή INR	N 1,0	↑ ↑ 2,8

N : ΦΥΣΙΟΛΟΓΙΚΈΣ ΤΙΜΕΣ ↑ : ΑΥΞΗΜΕΝΗ ΤΙΜΗ ↓ : ΜΕΙΩΜΕΝΗ ΤΙΜΗ

Ο ασθενής παραπέμφθηκε για ενδελεχή κλινικοεργαστηριακό(συμπεριλαμβανομένου και του ιολογικού ελέγχου για τις A,B,C ηπατίτιδες)έλεγχο όπου διεγνώσθη με πρωτοπαθή ηπατοκυτταρικό καρκίνο επί εδάφους χρόνιας HCV λοίμωξης.
ΣΥΜΠΕΡΑΣΜΑΤΑ:για την πρόληψη των προαναφερθέντων επιπλοκών,η έγκυρη και έγκαιρη διάγνωση των ιογενών ηπατιτίδων,κυρίως της HCV,HBV λοιμώξεων,είναι σημαντική για την αύξηση του προσδόκιμου επιβίωσης των ασθενών και την προάσπιση της δημόσιας υγείας γενικότερα.

Συγκριτική ανάλυση εφαρμογής μέτρων βιοασφάλειας σε κλινικά εργαστήρια Κέντρων Υγείας και Νοσοκομείων στην Ελλάδα.

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ΕΙΣΑΓΩΓΗ
Η βιοασφάλεια στα κλινικά εργαστήρια αποτελεί θεμελιώδη προϋπόθεση για την προστασία του προσωπικού, των ασθενών και της ευρύτερης κοινότητας. Παρά τη σημασία της, τα διαθέσιμα δεδομένα για το επίπεδο εφαρμογής μέτρων βιοασφάλειας στα εργαστήρια Κέντρων Υγείας και Νοσοκομείων στην Ελλάδα, καθώς και για τη συγκριτική τους αποτίμηση, παραμένουν περιορισμένα.
ΜΕΘΟΔΟΛΟΓΙΑ
Διεξήχθη μελέτη μικτής μεθοδολογίας με χρήση δομημένων ερωτηματολογίων που συμπληρώθηκαν από εργαστηριακό προσωπικό (n = 158 στα Κέντρα Υγείας· n = 415 στα Νοσοκομεία) και τυποποιημένων λιστών ελέγχου που καταγράφηκαν από πιστοποιημένο σύμβουλο διαχείρισης βιολογικών κινδύνων (n = 35 και n = 36, αντίστοιχα). Η ανάλυση επικεντρώθηκε σε τέσσερις τομείς: (Α) Εγκαταστάσεις και Τεχνικά Μέτρα, (Β) Διοικητικά Μέτρα, (Γ) Μέσα Ατομικής Προστασίας (ΜΑΠ), (Δ) Ετοιμότητα σε Έκτακτες Ανάγκες. Υπολογίστηκαν διαφορές ποσοστών (Δpp), διαστήματα εμπιστοσύνης 95% (CI) και επίπεδα σημαντικότητας ($p < 0.05$).
ΑΠΟΤΕΛΕΣΜΑΤΑ
Τα Νοσοκομεία κατέγραψαν σταθερά υψηλότερα ποσοστά συμμόρφωσης σε σχέση με τα Κέντρα Υγείας σε όλους τους τομείς. Οι μεγαλύτερες αποκλίσεις εντοπίστηκαν στις υποδομές και τα τεχνικά μέτρα, όπου τα Κέντρα Υγείας παρουσίασαν σοβαρότερες ελλείψεις (π.χ. περιορισμός πρόσβασης, αυτόκαυστα, θάλαμοι βιοασφάλειας). Στα διοικητικά μέτρα, αναδείχθηκαν ουσιαστικά κενά και στις δύο κατηγορίες, κυρίως στην εκτίμηση κινδύνου, την ύπαρξη SOPs, εγχειριδίων βιοασφάλειας και θεσμοθετημένου υπευθύνου βιοασφάλειας, με τα Κέντρα Υγείας να εμφανίζουν τη μεγαλύτερη υστέρηση. Η διαθεσιμότητα ΜΑΠ ήταν γενικά υψηλή, με τα Νοσοκομεία να υπερτερούν λόγω καλύτερης θεσμικής οργάνωσης (γραπτές πολιτικές, ιατρός εργασίας), αν και και στα δύο περιβάλλοντα καταγράφηκε η απουσία θεσμοθετημένων πολιτικών για την εφαρμογή και αφαίρεσή τους. Στον τομέα της ετοιμότητας σε έκτακτες ανάγκες, τα Νοσοκομεία διέθεταν πιο οργανωμένα σχέδια και συστήματα αναφοράς, ενώ στα Κέντρα Υγείας καταγράφηκαν σημαντικά κενά.
ΣΥΜΠΕΡΑΣΜΑΤΑ
Τα εργαστήρια των Νοσοκομείων στην Ελλάδα εμφανίζουν πιο ανεπτυγμένο και οργανωμένο σύστημα βιοασφάλειας σε σύγκριση με τα Κέντρα Υγείας· ωστόσο, και στα δύο εργαστηριακά περιβάλλοντα εντοπίστηκαν ουσιαστικές ελλείψεις σε υποδομές, διοικητικές διαδικασίες και ετοιμότητα. Τα ευρήματα αυτά υπογραμμίζουν την ανάγκη για συνολική ενίσχυση των συστημάτων βιοασφάλειας, με ιδιαίτερη έμφαση στα Κέντρα Υγείας, ώστε να επιτευχθεί πλήρης ευθυγράμμιση με τα εθνικά και διεθνή πρότυπα και να ενισχυθεί η προστασία του προσωπικού, της κοινότητας και του περιβάλλοντος.
ΛΕΞΕΙΣ-ΚΛΕΙΔΙΑ
Βιοασφάλεια, Διαχείριση Βιολογικών κινδύνων, Κλινικά εργαστήρια, Κέντρα Υγείας, Νοσοκομεία

Θα χρηματοδοτηθεί από το ΕΛΚΕ ΠΑΔΑ

Metabolic Syndrome Index: A novel stratification marker based on the metabolic profile.

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Metabolic Syndrome (MetS) is a cluster of metabolic abnormalities, including central obesity, insulin resistance, hypertension and dyslipidemia that increase the risk of type 2 diabetes mellitus and cardiovascular disease, linked to chronic low-grade inflammation, which promote atherogenesis and accelerate cardiovascular morbidity (Fahed et al.,2022).
The aim of the present study is to investigate the metabolic profile of 153 participants at risk of MetS and to compare this profile between two groups –individuals with MetS and those without– classified according to the five fundamental criteria of the IDF MetS definition (Zimmet at al., 2005), in the framework of an EU-funded research project "Combating Diet Related Non-Communicable Disease Through Enhanced Surveillance".
For this purpose, anthropometric parameters (such as body weight, height, body mass index, waist circumference, waist-to-hip ratio, height-to-waist ratio), that provide an overview of body composition and adipose tissue distribution, with particular emphasis on central obesity were analyzed. Additionally, dietary habits were recorded, and Healthy Eating Index (HEI), MEDAS Score, Dietary Inflammatory Index (DII) were calculated as well. In parallel, in the collected samples, biochemical markers –such as fasting blood glucose levels and glycated hemoglobin (HbA1c), lipid profile (total cholesterol, LDL-C, HDL-C, triglycerides), inflammatory mediators (CRP), and specific saccharides and amino acids– were analyzed, with the metabolite panel to be based on a UPHLC MS/MS analytical method. The data were analyzed using multivariate statistical methods and visualization modes.
Results indicated that, out of 52 anthropometric parameters only a small number demonstrate the ability to distinguish between the two groups. None of the dietary scores and indices showed statistically significant correlations with MetS factors. Out of 33 biochemical parameters tested and 11 (or 13) hematological indices, 8 were well related with a p-value less than 0.01, among them TyG_Index and SGPT – both power indicators of insulin resistance and elevated cardiometabolic risk. It is noteworthy that 9 of the 12 measured metabolites exhibited significant correlations with the Metabolic Syndrome. The integration and multivariate analysis of the above various parameters lead to a novel marker, Metabolic Syndrome Index, which facilitates the stratification of individuals according to metabolic risk. This approach provides a rigorous framework for both early preventive strategies and the design of targeted therapeutic interventions.

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GREEK

A

B

C

D

E

L

M

N

O

P

Q

R

S

T

V

W

Z

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