



Dear Colleagues,

On behalf of the European Biotechnology Thematic Network Association (EBTNA), we are delighted to invite you to the European Biotechnology Congress 2025, a premier event that brings together biotechnology's multifaceted impacts and future potential.

This prestigious congress will be held in Tirana, Albania, from 11-13 September 2025, organized by EBTNA, the Academy of Sciences of Albania, and the University of Tirana. This year's congress provides a unique platform for scientists, academics, and industry leaders from diverse disciplines to redefine the boundaries of biotechnology and forge new collaborations.

Satellite events of different formats (Workshops hands-on, Training Schools, Round-Tables) supported by COST EU, International projects, and MAGI Balkans will enrich the congress program either preceding or during it.

At the heart of the Balkans and a crossroad of civilizations, Tirana is a testament to the coexistence of cultures, religions, and historical influences across the Mediterranean.

Tirana's welcoming atmosphere offers an unforgettable experience in addition to inspiring scientific sessions of the congress. We believe that your participation will significantly enhance the success of this event and foster knowledge sharing in the biotechnology field. Meanwhile, researchers and students will be offered an excellent opportunity to present and share their expertise and publish their abstracts and proceedings papers in a Special Edition of The EuroBiotech Journal

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A Bioinformatics Workflow for VUS Reclassification Using Multiple Tools

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Secretome dynamics of human Adipose-derived Mesenchymal Stem/Stromal Cells: The role of confluency and culture conditions

Zuzanna Fekner

Multivector Embedding and Bioinformatics Analysis of Genomic Data

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Transcriptomic biomarker development pipeline
– Monitoring off-label therapy in anaplastic thyroid cancer in extracellular vesicles

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Presented to

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in recognition of the outstanding development of the

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in the
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INVITED SPEAKER ABSTRACTS

IS1-Genomics in the diagnosis and treatment of rare diseases in Albania: Current status and upcoming challenges

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Background

Diagnosing rare genetic diseases remains challenging due to clinical complexity, limited access to advanced molecular testing, and the lack of effective treatments. As the only Medical Genetics Service in Albania, integrated within the University of Medicine and the University Hospital Center "Mother Teresa," our service acts as the national referral point for rare genetic diseases.

Results

Patients with confirmed molecular diagnoses are categorized by the affected organ systems. The most common disorders include neurodevelopmental, neuromuscular, and metabolic diseases, while connective tissue disorders, skeletal dysplasias, etc. are less frequent. We apply targeted molecular techniques such as SNaPshot and MLPA for rapid and cost-effective diagnosis of prevalent conditions like β -thalassemia, cystic fibrosis, Duchenne/Becker muscular dystrophy, and common genomic syndromes. FISH analysis is used in malignant hemopathies and currently we are in the process of implementing NGS panels. More complex analyses, including array CGH, WES, and WGS, are performed in international centers, significantly improving diagnostic yield and guiding clinical decisions. Barriers include limited access to NGS technologies and insufficient funding. Future priorities involve implementing disease-specific gene panels and integrating personalized medicine approaches.

Conclusion

Improving infrastructure and fostering international collaborations are essential to advancing care for patients with rare genetic diseases in Albania.

IS2-Unravelling the Evolutionary History of *Pinna nobilis*

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The endemic Mediterranean bivalve *Pinna nobilis* faced significant threats throughout its history that constantly imperilled its survival. This study represents the first effort to integrate historical and modern genetic data for this species spanning several centuries. We analyzed about 500 mitochondrial COI gene sequences from both historical (1700s-1990s) and modern (2000s) samples, also including those from populations that survived to the mass mortality that starting from 2016 led now *Pinna nobilis* on the brink of extinction. By standardizing a method of DNA extraction from ancient museum byssus gland fragments, we were able to reconstruct the evolutionary history of *Pinna nobilis* with unprecedented details. Phylogenetic and phylogeographic analyses revealed two primary sources for the modern genetic variability: (i) the fan mussel's early population originated in western Mediterranean about 2.5 million years ago, and (ii) the broader group of lineages involved in the first Mediterranean Pleistocene adaptive radiation. Our findings suggest the occurrence of genetic traits that evolved during *Pinna nobilis*' Pleistocene adaptive processes. These traits likely persisted to the present day and enabled the species to colonize the entire Mediterranean, conferring great resilience to the stressors.

IS3-Synthesis and characterization of a TiO₂-based hybrid nanocatalyst.

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Abstract

We synthesized and characterized a silver-doped TiO₂/graphite oxide (Ag-TiO₂/nGO) hybrid nano-photocatalyst with enhanced photocatalytic activity and potential antimicrobial applications. The catalyst was obtained via a single-step sol-gel method combined with microwave treatment, incorporating 1 wt% Ag:Ti on nano-graphite oxide sheets. X-ray diffraction confirmed the anatase TiO₂ phase and the presence of graphite oxide, while X-ray photoelectron spectroscopy confirmed the successful incorporation of silver. Fourier transform infrared spectra revealed Ti-O-Ti vibrations and carbon-related groups, and field-emission TEM analysis revealed a homogeneous nanoscale dispersion. The catalyst achieved 90% degradation of Rhodamine B under UV-Vis irradiation within 60 minutes. These findings highlight a cost-effective and efficient route for designing multifunctional TiO₂-based nanocatalysts.

Keywords: hybrid nanocatalyst; Ag-TiO₂; graphite oxide;

photocatalysis; XPS; XRD.

IS4-ER triage of infectious disease phyla using phagocytic luminescent imprints

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Emergency departments are a frontline gateway to inpatient medical care, are crowded, and contribute to close to half of all hospital admissions! Their patients, with different levels of severity, suffer a mismatch in their timeliness to care and the relative resource usage available. To supply effective and prioritized care to patients, triage upon arrival to the ER categorizes patients based on the severity of their illnesses. In the case of a suspected infectious disease, evaluation of occult bacteraemia, sepsis and septic shock are prioritized. Indeed, infectious diseases are a global lethal burden. The major obstacle in prescribing a timely and appropriate antimicrobial treatment (the ED plays an important part in the responsible use of antimicrobial agents) is not knowing whether the patient has an infection, where its focus is, and which are its etiological agents. So, the conventional approach is lacking, and this despite incremental improvement in sensitivity, specificity and multiplexing ability of ELISA, PCR standard tests, as the basic principle and procedures have remained the same. These methods require a dedicated facility, trained and skilled personnel, take a lot of time and require expensive equipment and consumables. LUMAI disrupts the ER/ICU diagnostics workflow by accelerating the time-to-treatment, by differentiating between microbial phyla, thus, lowering misdiagnosis and this, by using a single blood specimen. Our solution is a point-of-care diagnostic system, LUMAI, that will combine the ease of use of a self-contained proprietary cartridge, with a fluidic system to process the patient whole blood specimen and run the cell immune-assay, with that of a dedicated cloud-connected reader with attached AI analytics. This is a single platform that does not require multiple products to be developed, just to extend the same immune-cell-assay to a growing range of microbial phyla (first), and thereafter etiological agents (we already did COVID-19). Our test system will significantly improve turnaround times, analytical quality and usability which are the cornerstones of what is expected of a POCT. To-date we can differentiate viral infections from bacterial ones with a 91% accuracy in less than 30 minutes.

IS5-Multivector Embedding and Bioinformatics Analysis of Genomic Data

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Abstract

Introduction: The exponential growth of genomic data requires advanced computational strategies. A key shift involves converting raw genomic sequences into structured, high-dimensional vectors — a process called multivector embedding. This enables integration of biological features and application of machine learning techniques.

Materials and Methods: Genomic datasets, especially structural variants like indels and splicing-site-associated variants, underwent multivector embedding with domain-specific encodings. Feature selection prioritized biologically meaningful properties to preserve functional signals. Embedded data were processed using pipelines with supervised classifiers, deep neural networks, and dimensionality reduction. Vectorized outputs were formatted for secure blockchain storage with tokenization layers.

Results: Multivector embeddings improved bioinformatics task performance. Indel detection models showed significant gains in precision and recall. Splicing variant classifiers achieved strong discriminatory power and generalizability. Computational efficiency increased, enabling real-time diagnostics and large-scale screening.

Discussion: Vectorizing genomic data enables direct machine learning applications and compatibility with decentralized architectures. The multivector approach advances bioinformatics by enhancing analytical capability and structural adaptability.

Keywords: Multivector Embedding, Genomic Data, Machine Learning, Indel Classification, Splicing Variants, Tokenization, Blockchain Bioinformatics.

IS6-In Vivo Evaluation of Bioactive Compounds on Molecular Pathways in *Drosophila melanogaster*

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Abstract

Introduction: Natural bioactive compounds are a promising source of modulators for conserved molecular pathways in development and metabolism. *Drosophila melanogaster*, due to its genetic homology with humans and well-characterized signaling networks, is a key model for functional genomics and pharmacological screening.

Materials and Methods: A selection of bioactive compounds, including polyphenols and phytosterols, were tested in vivo on *D. melanogaster*. Doses were optimized to assess sub-cytotoxic effects. Metabolomics analysis using the NMR method and a targeted panel of metabolites, evaluated the modulation of pathways including oxidative stress and inflammation. Com-

prehensive pathway profiling revealed the biological impacts and their correlations with specific signaling networks.

Results: Several compounds significantly modulated the expression of the metabolites in conserved signaling cascades. Notably, some polyphenols activated antioxidant response elements (ARE) and downregulated inflammation pathways, suggesting potential applications in metabolic research. No cytotoxicity was observed at effective concentrations, confirming functional specificity.

Discussion: The findings support that natural molecules selectively influence molecular pathways in *D. melanogaster*, offering a robust platform for preclinical screening. The conservation of target pathways underscores the translational potential, especially for nutraceutical development and disease model validation.

Keywords: *Drosophila melanogaster*, Bioactive Molecules, Molecular Pathways, Antioxidant Response, Inflammation, In Vivo Screening.

IS7-Machine Learning-Based Polygenic Risk Score Analysis in Rare Diseases: A Case Study on Anorexia Nervosa, Lipedema, and Lymphedema

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Abstract:

Introduction: Polygenic risk scores (PRS) aid rare-disease genetics, yet tiny cohorts limit precision. We applied a machine-learning (ML) PRS built on 1 800 functionally annotated SNPs to restrictive anorexia nervosa, lipedema and lymphedema, benchmarking performance against the clumping-and-thresholding (C+T) pipeline.

Materials and Methods: After quality control, 730 variants plus 64 lymphedema-specific loci remained. Logistic ridge, lasso and elastic-net models learned SNP weights on 70 % of samples; PCA-guided support-vector machines purged ancestry outliers. Sex-stratified and C+T-derived PRS served as benchmarks.

Results: ML-PRS surpassed C+T, reaching AUC 0.70 for anorexia, 0.64 for lipedema and 0.78 for lymphedema, a 0.10–0.15 gain. Neurogenic variants dominated anorexia, whereas adipose-matrix and lymph-angiogenic signals characterised the vascular disorders.

Conclusion: Functionally guided ML modelling delivers robust, clinically informative PRS in small, sex-imbalanced cohorts and provides a transferable template for precision genomics in rare diseases.

Keywords: Polygenic Risk Score, Rare Diseases, Anorexia Nervosa, Lipedema, Lymphedema, Functional SNPs, Machine

Learning

IS8-Exosome-Associated Circulating Proteomic Biomarkers for HNSCC Diagnosis and Surgical Monitoring via High-Resolution LC-MS/MS Analysis

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Head and neck squamous cell carcinoma (HNSCC) ranks as the sixth most common cancer globally, with poor outcomes in recurrent or metastatic cases. Surgical resection is the primary treatment for oral cavity tumors, yet reliable preoperative biomarkers remain scarce. Liquid biopsy using exosomes presents a minimally invasive method for real-time tumor monitoring, as exosomes carry tumor-derived proteins and genetic material reflective of disease status.

This study evaluated the diagnostic potential of exosome-associated proteins in plasma from HNSCC patients (n=11), collected before (PP1, TV1) and one hour after (PP2, TV2) tumor resection. Exosomes were isolated using EXÖBead, galectin-coated magnetic beads, and analyzed by flow cytometry, nanoparticle tracking analysis, cryo-electron microscopy, and High-Resolution Liquid Chromatography Mass Spectrometry (HR-LC-MS/MS).

Proteomic analysis identified 14 EV proteins, with platelet-derived growth factor subunit B (PDGFB) and tissue inhibitor of metalloproteinases 3 (TIMP3) significantly elevated in preoperative samples. These proteins are associated with tumor progression pathways and induced proliferation in HNSCC cell lines.

Our findings suggest that exosome-derived PDGFB and TIMP3 are promising diagnostic biomarkers for assessing tumor presence and surgical efficacy, with potential application in real-time, perioperative cancer monitoring.

IS9-Integrating Machine Learning into ACMG-Based Variant Classification Pipelines for Improved Clinical Interpretation

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Introduction: We developed a classification algorithm designed to differentiate genetic variants into two categories—'simple' and 'complex'—based on annotations from the American College of Medical Genetics and Genomics (ACMG) criteria. Variants initially labeled through an in-house automated pipeline were tracked for subsequent review and modification by clin-

ical geneticists. A 'simple' variant retained its original annotation without alterations, while a 'complex' variant underwent manual revision due to discrepancies or inaccuracies in the ACMG criteria assignment.

Methods: We explored various supervised machine learning approaches, to effectively predict whether a genetic variant would require further geneticist intervention. Recognizing clinical priorities, the primary evaluation metric focused on reducing False Negatives (FNs)—complex variants misclassified as simple—as such errors could overlook significant clinical insights. Consequently, the algorithm favored higher sensitivity, accepting a slight increase in False Positives (FPs)—simple variants misclassified as complex—to minimize clinical risks. The pipeline was integrated into a bioinformatics workflow for filtering and prioritizing variants from whole exome and genome sequencing data.

Results: Our optimal model employed a Gradient Boosting algorithm, with the lowest FN rate. While the increase in FPs slightly elevated manual review workload, the critical reduction in FNs enhanced overall clinical safety and variant interpretation reliability.

Conclusion: This approach streamlines genetic variant assessment workflows, effectively prioritizing complex cases for geneticist attention, thus promoting both efficiency and accuracy in clinical genomics interpretation.

Keywords: ACMG Guidelines, Variant Classification, Machine Learning, Genetic Diagnostics, Bioinformatics Pipeline

IS10-Multi-Layer Data Integration Model for Omics Analysis

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Abstract

Introduction: The integration of genomic, proteomic, and metabolomic data is a key approach for prioritising genetic variants. Proteomic and metabolomic profiles provide complementary information on protein function and metabolic activity, offering insights beyond sequence data. This multi-omics integration enables the reconstruction of interaction networks, supports the identification of biomarkers and therapeutic targets, and improves understanding of disease mechanisms. The complexity of biological systems demands integrative strategies that trace how genomic variation triggers phenotypic change across molecular layers. Multi-omics fusion is essential, yet a central bottleneck is following the ripple of a single variant through protein networks and metabolic pathways.

Materials and Methods: We created a three-layer framework integrating genomic, proteomic, and metabolomic datasets as interconnected planes. The platform links molecular la-

yers using (i) canonical correlation analysis, (ii) network-level coupling, and (iii) pathway-based maps combining curated routes with high-throughput data. Saliva was collected for genomic analysis and plasma for proteomic and metabolomic profiling. Sample preparation protocols were identified and optimised. Genomic variants were classified using the MA-GI-ACMG algorithm. Proteomic and metabolomic analyses were performed on matched samples to identify imbalances in disease-relevant pathways.

Results: Applied to inherited retinal dystrophies (IRDs), the pipeline prioritised pathogenic variants by integrating genomic data with proteomic and metabolomic profiles obtained through high-resolution mass spectrometry. By correlating IRD-associated genes with plasma metabolite changes, we identified variants, particularly in metabolic-enzyme genes, whose loss of function leads to substrate accumulation or product depletion in key pathways. These molecular alterations provide mechanistic support for the interpretation of each prioritised allele.

Discussion: The multi-layer approach refines variant interpretation in rare diseases and enables system-level prioritisation grounded in convergent functional and metabolic evidence. In IRDs, it revealed variants affecting key pathways, supporting their pathogenicity. This strategy enhances diagnostic accuracy and supports the identification of biomarkers and therapeutic targets.

Keywords: Multi-Omics Integration, Genomics, Proteomics, Metabolomics, Variant Prioritization, Retinal Dystrophies, Systems Biology, Network Analysis.

IS11-Fluorescence correlation spectroscopy in the study of the bioactivity of natural products: a case study of aurein1.2

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Fluorescence correlation spectroscopy is a powerful method to study the diffusion characteristics of molecules and molecular assemblies, allowing not only size determination but also the detection of aggregation, mixing and sequestration. Here membrane interactions of the antimicrobial peptide aurein 1.2 are used to showcase the capabilities of the method. Using a combination of a planar system (imaging total internal reflection fluorescence correlation spectroscopy ITIR-FCS) and confocal FCS dye leakage experiments, we examined the mechanisms of membrane binding and disruption. Our findings reveal that phenylalanine residues serve as critical membrane anchors that determine peptide-membrane interactions through hydrophobic forces rather than electrostatic interactions. These results challenge conventional models of antimicrobial peptide function and provide direction for developing more effective antimicrobial agents based on specific amino acid interactions rather than general physicochemical properties.

IS24-Electrochemical sensor for 5-hydroxymethylfurfural

determination based on Molecularly Imprinted Polymers

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The determination of the concentration of 5-hydroxymethylfurfural (HMF) in honey is an indicative parameter for monitoring the quality of honey. An electrochemical sensor for the determination of HMF has been developed on carbon electrodes modified with graphene carboxylate-nickel and molecularly imprinted polymer (MIP). Through the experimental design, the optimal conditions for the preparation of the polymer with methacrylic acid as monomer, divinylbenzene as crosslinker and AIBN as polymerization initiator have been investigated, based on the voltammetric response of the sensor. A sensor for the determination of HMF has also been developed based on the electropolymerization of beta cyclodextrin on carbon electrodes as MIP. Both methods of MIP preparation of the sensor have advantages and disadvantages in their use in different sample matrices. Methods used in preparation of the sensor response site have given satisfactory results in the determination of HMF using electroanalytical techniques.

Key words: 5-hydroxymethylfurfural; HMF; MIP, Honey

IS12-Length-weight relationship and condition factors of the stocks of *Alburnus scoranza* and *Squalius cephalus* from Albanian part of Ohrid Lake

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Abstract

Common chub and Scoranza bleak as well as 19 other species and subspecies are components of the native ichthyofauna present in Ohrid Lake. Based on the analyzes of the samples taken from the catches of these two fishes, in the years 2023 and 2024, we had estimated the values of the coefficients a and b in LWRs as well as the values for three types (K , K' and K_n) of condition factors. The values of the coefficients in the LWRs for the common chub's stock, were: a) For all the 11-month period of the study $W = 0.0077TL^{3.1587}$ $r = 0.968$; b) in the active grazing period $W = 0.0045TL^{3.2709}$ $r = 0.921$ and, c) after the breeding season $W = 0.0135TL^{2.8266}$ $r = 0.925$. The respective values in the Scoranza bleak's stock, were: a) $W = 0.0132TL^{2.728}$ $r = 0.968$; b) $W = 0.0094TL^{2.901}$ $r = 0.934$ and, c) $W = 0.0173TL^{2.6486}$ $r = 0.907$. As for the condition factors, the highest average value was calculated for $K=2.079\pm0.029$, in the common chub's stock during the active grazing period. The lowest average value was calculated again for $K=0.685\pm0.032$, in the Scoranza bleak's stock, immediately after the breeding season.

Key words: Ohrid Lake, Scoranza bleak, common chub, condition factor, breeding.

IS13-From sequence to significance: functional insights into rare genetic disorders

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Abstract:

Rare genetic disorders affect fewer than 1 in 2,000 individuals and often present significant diagnostic challenges, with an average diagnostic odyssey of 4–5 years. Next-generation sequencing (NGS) technologies such as whole-exome sequencing (WES) have improved the detection of pathogenic variants, yet many cases remain unresolved due to variants of uncertain significance (VUS) and noncoding alterations. Moving beyond routine testing, functional approaches are essential to validate genotype–phenotype relationships and clarify disease mechanisms. A multi-layered strategy integrating genomics, transcriptomics, metabolomics, and metagenomics with *in vitro* and *in vivo* functional assays enables deeper insights. RNA sequencing identifies splicing anomalies and expression dysregulation, while metabolomic profiling uncovers disrupted biochemical pathways in unexplained metabolic disorders. Model systems—including patient-derived fibroblasts, *Xenopus*, and *Drosophila* models—provide mechanistic validation of candidate variants. This comprehensive approach facilitates biomarker discovery, enhances diagnostic accuracy for VUS, and informs personalized therapeutic strategies. Functional genomics serves as a critical bridge between sequence data and clinical significance, ultimately advancing precision medicine for patients with rare genetic diseases.

IS14-Industrial waste valorization: next-generation bioenergy for a greener future in albania

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Abstract

The increasing environmental impact of industrial waste and the urgent need for sustainable energy solutions have driven significant interest in the valorization of industrial by-products for bioenergy production. This paper reviews the latest advancements in transforming various types of industrial waste into next-generation bioenergy, emphasizing innovative biological, chemical, and thermochemical conversion technologies. Key focus areas include the integration of waste valorization processes with circular economy principles, enhancement of bioenergy yield and quality, and reduction of greenhouse gas

emissions.

Case studies highlight successful applications in sectors such as agro-industrial, chemical manufacturing, and municipal waste management. In Albanian sectors such as agro-industrial, there are successful case studies highlighting the valorization of industrial waste for bioenergy production. One notable example is the biomass energy project supporting the olive oil industry, where organic waste from olive oil and other related industries is converted into bioenergy. Furthermore, broader integration of agro-industrial waste into circular economy models in Albania is gaining attention, with specific emphasis on sustainable biorefinery processes that turn agro-waste into renewable energy products like bioethanol, biogas, and biofertilizers. These approaches not only help mitigate environmental pollution but also contribute to economic development by converting waste into valuable energy resources.

The findings demonstrate the potential of industrial waste valorization not only to mitigate environmental pollution but also to serve as a cost-effective, renewable energy source, contributing to a greener and more sustainable future. Challenges and future research directions are discussed to facilitate the transition from laboratory-scale innovations to industrial-scale implementations.

Keywords: industrial waste, bioenergy, biotechnology issue, actual solutions, perspective

IS15-Mining Probiotic Solutions as Alternatives to Antibiotics: From Bench to Market

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Abstract

Increasing restrictions on antimicrobial use in livestock production have intensified the search for sustainable, science-based alternatives to prevent disease and maintain productivity. Our research focused on developing an intravaginal probiotic formulation for dairy cows to improve reproductive health and reduce reliance on antibiotics. Candidate lactic acid bacterial strains with immunomodulatory and antimicrobial potential were identified and tested in controlled transition cow trials. In a series of peer-reviewed studies, intravaginal administration of selected lactic acid bacteria during the periparturient period modulated local and systemic immune responses, reducing postpartum uterine infection rates (Deng et al., 2015a). Probiotic treatment expedited uterine involution and favorably altered plasma hormonal profiles (Deng et al., 2015b), improved metabolic status, and increased milk yield and composition (Deng et al., 2016). Furthermore, it reduced the incidence of purulent vaginal discharge and lowered systemic inflammatory markers such as plasma haptoglobin concentrations (Ametaj et al., 2014). Collectively, these effects enhanced fertility at first insemination and supported overall herd productivity. Following proof-of-concept, formulation optimization addressed viability, stability, and farm-level prac-

ticality. In collaboration with Healthy Cow Corp., the product was scaled up, branded as *ProPreg*, and commercialized for use in the United States and globally. Adoption by dairy producers has demonstrated measurable improvements in reproductive outcomes, reduced therapeutic antibiotic use, and contributed to on-farm sustainability. The development of *ProPreg* exemplifies successful translation of applied microbiome science from bench to market, providing a replicable framework for advancing functional microbial technologies in livestock production. This innovation offers an effective, non-antibiotic strategy for improving dairy cow reproductive health, aligning with regulatory and consumer demands for reduced antimicrobial use while enhancing animal welfare, farm profitability, and environmental stewardship.

IS16-Remote sensing of buried landmines by microbial bioreporters: modulating the risks of GMMs release

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Landmines and explosive remnants of war pose a global humanitarian problem which claims numerous casualties long after the conflict has ended. Current approaches for the location of landmines, such as metal detection, which require physical presence at the minefield, involve high risk to personnel; these methods are also costly, time consuming, and have a high rate of false positive results. No currently viable technology allows the remote detection of buried explosive devices. A possible solution may be provided by the use of genetically engineered microorganisms, molecularly “tailored” to emit an optical signal in the presence of trace explosives escaping for the landmine and accumulating in the soil above it. This optical signal can serve to generate a physical map of the mine location. We have previously described the remote detection of buried explosives using bioluminescent microbial (*Escherichia coli*) bioreporters, which were subjected to several synthetic biology approaches in order to significantly enhance their major performance parameters. The improved sensor strains displayed signal intensities over 10,000-fold higher and 2,4-dinitrotoluene (DNT) detection thresholds over 100-fold lower than the parental construct. The pathways towards these achievements will be described, as well as additional research efforts towards the prevention of environmental proliferation of the genetically engineered microorganisms following their environmental release. These included the deletion of antibiotics resistance markers, integrating a dependency on specific nutritional ingredients, and the introduction of a “self-destruct” mechanism that enters into effect several hours following the field release.

IS17-Microscopic Algae and Their Biotechnological Potency

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Biotechnological and ecological significance of microscopic algae lies in their abundance, and extreme biodiversity. Their simple development allows them to adapt to prevailing environmental conditions. The term microscopic algae (microalgae) covers an informal assemblage of unrelated groups of predominantly aquatic microorganisms that carry out oxygen-evolving photosynthesis but lack specialized water- and food-conducting tissues. They are mostly unicellular microorganisms (pro- or eukaryotic) but some are forming filaments or colonies. The enormous biodiversity of microalgae offer a great potential for exploitation in biotechnological, environmental, biomedical, pharmaceutical, food and agricultural industries as well as for biofuels. They are nonfood based feedstock resources using otherwise non-productive, non-arable land utilizing wide variety of water sources. Microscopic algae represent the 'best of both worlds', combining the high growth rate and ease of cultivation of microorganisms. Considerable progress has been made in recent years in regards to the development of strategies to improve them. Our favorite phototrophic eukaryotic microorganism the flagellate *Euglena gracilis* with its wide latitude of growth conditions has been shown to be a suitable source for production of several compounds used for the production of biomedicaments, cosmeceuticals, nutraceuticals, biomaterials, biofuels as well as diverse applications in environmental biotechnology including ecotoxicological risk assessment and bioremediation.

Keywords: phototrophic microorganisms, microalgae, plant and environmental biotechnology, *Euglena gracilis*

IS18-What does wastewater say about us?

(Wastewater based epidemiology and surveillance for population health monitoring)

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Wastewater-based epidemiology (WBE), a rapidly evolving field where biomarkers indicative of human behavior, exposure, and activity, assessed through wastewater analysis, may provide a viable option to evaluate changes in public health. Community wastewater has long been known to contain a mixture of toxic chemicals, pathogens, pollutants, drugs, hormones etc. Therefore, wastewater treatment facilities provide

important venues for epidemiological investigations of emerging diseases. Indeed, WBE can monitor large populations and has the potential to provide an early-warning platform for spread of diseases and/or of contaminants. WBE has become a key tool in SARS-CoV-2 surveillance and epidemiology. In previous work with the Bedouin community in Southern Israel we explored the applicability of wastewater surveillance on fully, partially and fully off-grid Bedouin communities. Our findings suggest that sewage surveillance can be a critical aspect of disease outbreak surveillance and control in areas with insufficient human testing in particularly in off-grid communities. Today we continue to monitor off-grid Bedouin communities wastewater for viruses, e.g., SARS-CoV-2, consumption of artificial sweeteners, smoking and more. Indeed, as stress has been found to contribute to various health risks and behavioral changes during an individual lifespan, targeting biomarkers indicative of stress related behaviors of a population can also help to address public health issues. Using this tool, is therefore important, as physiological stress affects an individual's sense of well-being, and overall health, with chronic stress linked to the top six leading causes of death. As to date there are no national scale social surveys, that assess stress within a specific community, using measurable health and behavioral stress markers in wastewater may provide an important tool. Monitoring levels of endogenous stress hormones, nicotine, cotinine, caffeine and anti-depression/anxiety drugs in wastewater will provide information regarding stress level in a population.

IS19-Bridging Science and Society: Biotechnology Innovation and Accessibility in Kosovo

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Abstract

Biotechnology in Kosovo holds transformative potential for healthcare, agriculture, and environmental sustainability, yet remains largely underutilized. While institutions such as the University of Prishtina are involved in research on diagnostics, microbiology, and animal/crop improvement, their efforts are limited in scale, fragmented, and not closely connected to commercial or public applications. Structural challenges—such as outdated labs, lack of modern equipment, inadequate maintenance, poor funding, and the lack of high skilled professionals—severely hinder the sector's growth. Moreover, the legal framework for biosafety and intellectual property is outdated, discouraging investment and innovation. Public understanding of biotechnology is low, often shaped by misconceptions, particularly around GMOs. A significant disconnect exists between scientific output and real societal needs, with minimal engagement from end-users like farmers and patients. Despite this, Kosovo's large youth population, growing scientific interest, and access to EU programs like Horizon Europe offer substantial opportunity. Biotechnology

also aligns with Kosovo's green economy goals and benefits from potential contributions of the diaspora. A success story—the use of PCR and genotyping to help conserve the Balusha sheep breed—illustrates the practical, community-level value of biotechnology. To realize this potential, Kosovo must integrate biotechnology into national development strategies, upgrade biosafety laws, improve funding, and prioritize science communication. Collaboration across government, academia, industry, civil society, and diaspora is essential. Bridging the gap between science and society is not optional—it is a necessity for a locally grounded, inclusive, and sustainable biotechnology future in Kosovo.

Keywords: biotechnology, Kosovo, science-society gap, innovation policy, biotech education.

IS20-Liposomal topical delivery systems incorporating natural functional bioactives: advances and perspectives

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Liposomes as carrier systems of active substances, composed of phospholipid layers, offer numerous advantages in the delivery of these substances, such as improving their stability, prolonging their release time, and increasing bioavailability at the targeted site of action.

This review aims to analyse the latest innovations in liposomal formulation technology intended for application through the skin.

This scientific study also addresses the complete classification of liposomes based on their structure and size, the different types of liposomes, describes their components, as well as traditional and modern methods of preparation. A special focus has been given to technological innovations, such as the development of deformable or elastic liposomes (transferosomes, ethosomes, etc.) and structural modifications (addition of ligands, pH-sensitive or temperature-sensitive liposomes, etc.). Through the analysis of the latest scientific literature, the benefits these formulations offer in dermatological therapy and in the cosmetic industry have been examined, including applications in skin diseases such as psoriasis, skin cancer, acne, and skin aging.

The results show that liposomes represent a very promising alternative for future transdermal formulations, with potential for more targeted, safer therapies and fewer side effects.

IS21-Microbial polymer of poly-γ-glutamic acid: biosynthesis, various applications, and future perspectives

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Microbial polymers are biodegradable materials produced by a diverse group of microorganisms. They have enormous potential because they can be produced from renewable resources under controlled conditions. They can also play a significant role in mitigating negative environmental impacts, and can encourage sustainability across various industries.

Poly-γ-glutamic acid (γ-PGA) is a biodegradable and water-soluble polymer produced by bacteria, especially *Bacillus* species. This natural biopolymer is made of glutamic acid monomers connected by amide linkages between γ-carboxylic acid groups, which differs significantly from other proteins. Numerous microorganisms can produce this anionic homopolyamide outside their cells. Cultivation of different microbes can lead to the production of γ-PGA with different properties such as molar mass, crystallinity as well as different stereochemical compositions, which contribute greatly to a diversity of applications. This talk will give detailed insights into microbial synthesis of γ-PGA and its physicochemical properties. Additionally, it will provide an updated overview relevant to sustainable and cost-effective production of this biopolymer, along with examples of applications in medicine, pharmacy, cosmetics, food products and agriculture.

Keywords: γ-PGA, wastes, sustainability, biomaterials, *Bacillus*

IS22-Emerging green and blue biotechnologies & Services prospects at University of Tirana, Albania

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The Department of Biotechnology of the Faculty of Natural Sciences of the University of Tirana, Albania, established in 2008, is a leader among higher education institutions in the field of biotechnology in the country. This unit carries out its activities in teaching, scientific research and services to the third party, evidenced by the BSc, MSc and PhD programs in Biotechnology, participation in 9 research projects, publication of 35 articles during the year 2025 alone, and several services to the third parties. Important innovations in the department's activities include the ability to provide services such as standardized assessment of water pollution by pathogenic bacteria, determination of cytotoxicity in water based on cellular biosensors, measurement of microbial load on industrial surfaces using cellular sensors, and assessment of phytoplankton biomass using fluorescence microscopy.

The research directions of the biotechnology department have evolved over the years, contributing to the directions of agrobiotechnology-"green biotech" (early molecular detection of vi-

ruses and phytoplasmas of fruit trees, assessment of the genetic diversity of grapevine, olive, aromatic-medicinal plant populations, molecular, physiological, biochemical assessment of the tolerance of local grains to abiotic and biotic factors and eugenic memory, stabilization of new methods of conservation and in vitro micropropagation of plants of economic interest, use of induced mutagenesis for the genetic improvement of agricultural crops, etc.). Also, a number of projects of the department address issues of environmental biotechnology (Aquaculture-related; Assessment of water quality under the pressure of industrial pollution, tourism, agricultural pollution, urban pollution, climate change, etc.; Assessment of cytotoxicity in waters using cellular biosensors; Monitoring of the level of trophic biomass, composition and diversity of phytoplankton under the pressure of pollutants, etc.).

An important aspect of the activity of the Department of Biotechnology is the internationalization of the activity, which culminated in the cooperation in the organization of the EBTNA Congress 2025 in Tirana, Albania.

IS23-Biotechnology for sustainable development in Albania and Kosova livestock and aquaculture sector

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Abstract

Biotechnology plays a vital role in transforming livestock and aquaculture systems in Albania and Kosova, two countries where rural livelihoods and food security depend heavily on animal production. Despite long-standing challenges, such as low productivity, fragmented disease-control programs, and pressure on indigenous genetic resources, recent advances indicate significant potential for modernization and growth. In livestock production, both countries have strengthened their use of reproductive biotechnologies, particularly artificial insemination (AI), supported by locally produced and imported high-merit semen. Kosova's GENKOS center and Albania's AI networks have accelerated genetic improvement in cattle and small ruminants. The successful implementation of embryo transfer technologies, demonstrated through collaborative projects such as the first embryo-derived calf in Kosova, highlights the feasibility of advanced assisted reproductive technologies in the region. Enhanced diagnostic capabilities, including PCR, ELISA, and molecular assays, have improved responses to endemic and emerging diseases, while molecular tools such as microsatellites, SNPs, AFLP markers, and mtDNA analyses support the preservation and characterization of important indigenous breeds, including Busha cattle, Balusha and Bardhoka sheep, and other native ruminants. Aquaculture biotechnology has progressed through improved hatchery

practices, broodstock management, and conservation-oriented restocking programs. Albania's diverse aquaculture, spanning seabass, seabream, trout, and mussels, benefits from innovations in fry production, hormonal induction in cyprinids, and the restoration of native species such as the Ohrid trout (*Salmo letnica*) and Prespa carp. Kosova, although landlocked, has advanced its freshwater aquaculture through selective breeding in trout hatcheries and adoption of Recirculating Aquaculture Systems (RAS). Both countries adhere to EU-aligned restrictions on genetically modified fish while focusing on sustainable, climate-resilient aquaculture models. A forward-looking biotechnology roadmap emphasizes genomic selection, regional gene banks, ISO-accredited laboratories, digital traceability, and cross-border collaboration. By integrating innovation with biodiversity preservation and institutional cooperation, Albania and Kosova are positioned to become regional leaders in sustainable biotechnology and rural economic development.

Key words: Biotechnology; Livestock; Aquaculture; Genetic Resources; Assisted Reproductive Technologies; Indigenous Breeds; Genomic Tools; Hatchery Innovation; Sustainability;

IS24-Clinical and Economic Valuation of Medical Innovation: application to (POC4Trage)

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Medical innovation pricing is constrained by the incremental cost-effectiveness ratio, a central factor in value-based pricing. In the Netherlands, for example, the willingness-to-pay threshold is €80,000 per QALY. To counter perceptions of excessive pricing, we developed the Integrated Valuation Model—a tool that supports both early-phase valuation and late-stage pricing of medical innovations.

This model represents a paradigm shift in reimbursement policy by integrating economic valuation principles, including expected free cash flows and the cost of capital, to support pricing decisions. It justifies drug prices that exceed conventional ICER thresholds by demonstrating financial viability, particularly for treatments with high development costs and small patient populations.

The model enables scenario analysis and collaborative parameter adjustments with governments, maintaining conservative assumptions to ensure credibility. It has been applied successfully in the Netherlands and Belgium, aiding bio- and device companies in market access, price negotiations, and strategic development.

Additionally, the model supports stakeholders such as medical professionals and patient advocacy groups in ensuring timely access to innovative therapies. Transparent government involvement further enhances the model's legitimacy, promoting fair pricing and sustainable reimbursement for orphan drugs. We will illustrate the concept for digital health and medical innovation for urgent care in five conditions in prehospital setting (POC4Trage).

IS25-Parallel-plate Micro(bio)Reactors

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Abstract

Parallel-plate micro(bio)reactors provide powerful platforms for sustainable process intensification by enabling enhanced transport, precise process control, and safe microscale operation with straightforward linear scale-up. Recent advances illustrate their broad applicability across biocatalysis, separation, and energy processes. Time-scale analysis (TSA) has proven essential for identifying transport limitations in enzymatic systems, such as uric acid reduction in biomedical microdevices (Asgharpour et al., 2024). Functional hydrogels, including Cu-alginate for click chemistry and redox-responsive gels for pollutant degradation, highlight their potential in green catalysis and environmental remediation (Ramšak et al., 2024; Ambrožič et al., 2024). Model-based design has further enabled continuous biotransformations with immobilized yeast in hydrogel films (Menegatti et al., 2024). Beyond biocatalysis, integration of 3D printing and predictive modeling yielded a microfluidic pervaporation device achieving >97% VOC removal (Potočnik et al., 2025). In parallel, plasma-assisted chemical-looping dry reforming demonstrated room-temperature methane and CO₂ conversion into separate, high-purity H₂ and CO streams, providing a carbon-negative hydrogen route (Chen et al., 2025). Together, these advances establish parallel-plate micro(bio)reactors as scalable, multifunctional platforms for intensified and sustainable chemical and biochemical production.

IS26-Immobilized Enzyme Microreactors for Sustainable Valorization of Biobased Materials

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Biocatalytic processes offer transition to more sustainable manufacturing of pharmaceuticals, especially when starting from the bio-based resources. Reactor miniaturization, continuous operation, and integration with in situ product removal, process analytics, and cascade reactions that reduce the number of process steps enable process intensification. Examples of efficient biocatalytic processes development comprising enzyme and substrate screening, medium engineering, and biocatalyst immobilization to intensify biocatalytic processes will be presented.

Keywords: microbioreactor, biocatalyst immobilization, microreactors

ORAL PRESENTATION ABSTRACTS

OP1-Rapid Detection of *Pseudomonas aeruginosa* via Quorum Sensing-Responsive Bioluminescent Biosensor

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Abstract

Pseudomonas aeruginosa, an opportunistic gram-negative pathogen, poses significant clinical and environmental risks, particularly because of its robust quorum sensing (QS) system, which regulates virulence and biofilm formation. Quorum-sensing molecules (QSMs), such as N-butyl-L-homoserine lactone (C4-HSL) and N-(3-oxododecanoyl)-L-homoserine lactone (3-oxo-C12-HSL), serve as reliable biomarkers for the early detection of *P. aeruginosa*. In this study, we developed a fiber-optic whole-cell biosensor platform based on alginate-encapsulated bioluminescent *P. aeruginosa* bioreporters that are responsive to QSMs. The encapsulation matrix was reinforced with a poly-L-lysine (PLL) coating that preserved cell viability and structural integrity, while allowing the diffusion of small signaling molecules. The biosensor system demonstrated robust stability in the presence of cation scavengers and maintained functional responsiveness following long-term storage at 4 °C and – 80 °C, enabling immediate deployment without the need for reactivation. Upon exposure to synthetic QSMs or cell-free supernatant of wild-type *P. aeruginosa* (PAO1), the bioreporter microbeads exhibited a concentration-dependent bioluminescent response. The RhlR-based reporter system exhibited a dynamic range of 10 µM to 0.1 nM, with a detection limit of 50 pM for C4-HSL. Similarly, the LasR-based system showed a detection range of 5 µM to 0.2 nM and a sensitivity threshold of 0.1 nM for 3-oxo-C12-HSL. Additionally, the biosensor reliably detected the quorum sensing inhibitor (QSI) furanone C-30 in a dose-dependent manner, highlighting its utility for screening anti-virulence compounds. This proof-of-concept study establishes a portable, stable, and sensitive optical biosensing platform for the detection of QS activity with potential applications in clinical diagnostics, environmental bio-surveillance, and anti-virulence drug discovery.

Keywords: alginate hydrogels; microbeads; optical biosensors; bioencapsulation; autoinducers; *Pseudomonas aeruginosa*; quorum sensing; C4-HSL; 3-oxo-C12-HSL; Furanone C-30; QS inhibitor; whole-cell biosensors.

OP2-Genetic Investigation of the Albanian Population

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Albanian Academy of Sciences

The Albanian Academy of Sciences has undertaken the first comprehensive, large-scale genetic study of the Albanian population, aiming to explore its genetic structure, diversity, and historical origins. This multidisciplinary project integrates analyses of Y-chromosome STR markers, autosomal STRs, and mitochondrial DNA (HVR1+HVR2) sequences from a representative sample across all 12 districts and major subdialects of the country. Covering approximately 500 individuals, the study provides a detailed insight into geographic and dialectal genetic variation, north–south differentiation, and potential admixture patterns. The results contribute to understanding the unique genetic heritage of Albanians within the broader European and Mediterranean context, laying the groundwork for future genome-wide SNP studies and ancient DNA comparisons.

OP3-Impact of sustainable aquaculture practices on environmental microbiomes: structural and functional insights through high-throughput techniques

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Sustainable aquaculture is increasingly adopting advanced technologies such as Recirculating Aquaculture Systems (RAS) and Integrated Multi-Trophic Aquaculture (IMTA) to minimize environmental impacts and improve resource efficiency. Despite their growing implementation, the effects of RAS and IMTA on the environmental microbial communities, key drivers of nutrient cycling and ecosystem functioning, remain largely disregarded. A deeper understanding of how

these systems influence the aquatic microbial diversity is essential to optimize their long-term sustainability. This study explored the structural and functional shifts of microbial communities in waters and sediments collected at full-scale RAS and IMTA systems using high-throughput methods (flow cytometry, 16S rRNA gene sequencing, Biolog assays). In RAS, heterotrophy and nitrate reduction increased in water, while sediments showed enrichment of sulfur-reducing bacteria (e.g., *Desulfocapsaceae*, *Desulfosarcinaceae*). In IMTA, primary species farming (finfish and mussels) was associated with decreased alpha-diversity and increased sulfur metabolism, whereas the occurrence of extractive species (sea cucumbers) did not show significant effects. Our results highlighted the effects of aquaculture practices on microbial ecosystem services, supporting microbiome-based strategies for monitoring and managing aquaculture sustainability.

OP4-Germline *SDHx* Variants in Paraganglioma: Experience from a Single-Center Cohort

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Paragangliomas are rare neuroendocrine tumors, and a considerable proportion is associated with germline variants, particularly in *SDHx* genes. We analyzed 13 patients with a clinical diagnosis of paraganglioma who underwent targeted next-generation sequencing including known susceptibility genes. Pathogenic or likely pathogenic variants were identified in 2 patients (15.4%). One patient carried a missense variant in *SDHB* (rs138996609, NM_003000.2, c.688C>T, p.Arg230Cys, exon 7), while another harbored a nonsense variant in *SDHC* (rs201286421, NM_001035511.1, c.43C>T, p.Arg15*, exon 2). No disease-associated variants were detected in the remaining 11 patients. Our findings confirm the contribution of *SDHB* and *SDHC* variants to the pathogenesis of paraganglioma and highlight the importance of NGS-based genetic screening. Interestingly, the variant detection rate in our series (15.4%) was lower than the 30–40% commonly reported in the literature. This discrepancy may be attributed to the limited sample size, the clinical characteristics of our cohort, or variants not captured by the applied sequencing panel. Population-specific differences may also contribute. These observations emphasize the need for further studies to explore additional genetic or environmental contributors to paraganglioma.

Keywords: Paraganglioma, *SDHB*, *SDHC*, germline variants, next-generation sequencing

OP5-Expanding the Phenotypic Spectrum of *OTX2* Mutations: A Case Report

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The orthodenticle homeobox 2 (*OTX2*) gene encodes a transcription factor essential for craniofacial, pituitary, and ocular development. Heterozygous mutations in *OTX2* are associated with microphthalmia/anophthalmia, retinal dystrophy, pituitary abnormalities and brain malformations. We report a 10-year-old female who was referred to our clinic by the pediatric endocrinology department with unilateral anophthalmia, short stature, and spina bifida occulta. Physical examination additionally revealed microcephaly, posteriorly rotated low-set ears, and a Darwin tubercle on the left auricular helix, bilateral pes planus, and sandal gap deformities of the feet. Cranial MRI revealed a small, deformed sella turcica, ectopic neurohypophysis, and absence of the right ocular globe. Whole-exome sequencing identified a heterozygous nonsense variant in the *OTX2* gene (NM_021728.4: c.337C>T; p.Gln113Ter). The variant was confirmed by Sanger sequencing, and segregation analysis revealed that the mutation was not detected in the parental blood and buccal samples.

This case expands the phenotypic spectrum associated with *OTX2* mutations. To our knowledge, it represents the first report from Türkiye of *OTX2*-related anophthalmia/microphthalmia. This study highlights the phenotypic variability of *OTX2* mutations, demonstrating that identical variants may lead to distinct clinical manifestations. We believe these findings provide novel insights by further delineating the clinical heterogeneity of *OTX2*-related disorders.

Keywords: *OTX2* mutation, anophthalmia, microphthalmia, whole-exome sequencing

OP6-Breaking the Limits of Exome: A Deep Intronic *PHEX* Variant Caught by Whole Exome Sequencing

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Abstract:

Hypophosphatemic rickets (HR) is typically caused by pathogenic variants in the *PHEX* gene. We present a 4-year-old male with bowed legs and growth delay. Laboratory tests showed hypophosphatemia and elevated alkaline phosphatase. Targeted panel testing including *PHEX*, *FGF23*, and *DMP1* was negative. Due to persistent clinical suspicion, Whole Exome Sequencing (WES) was performed. WES analysis involved **reassessment** of HR-related genes (*ENPP1*, *FAM20C*, *SLC34A3*, *PHEX*). Manual inspection revealed a deep intronic *PHEX* variant, c.1768+173A>G (SpliceAI **delta: 0.95**), suggesting a high probability of splice disruption. This variant has been previously reported via Whole Genome Sequencing (WGS), but is commonly missed by **conventional panels** due to limited intronic coverage. Our case represents the **first WES-based identification** of this functionally rele-

vant variant.

Conclusion:

Deep intronic variants can cause disease through aberrant splicing, pseudoexon inclusion, and cryptic splice site activation. This case underscores their diagnostic relevance and supports expanding gene panels and diagnostic workflows to include **intronic regions uncovered by WGS or functional studies**. Early detection is crucial for timely diagnosis and targeted therapy such as burosumab.

Keywords: Hypophosphatemic rickets, *PHEX*, Deep intronic variant, Whole Exome Sequencing (WES), Splicing defect

OP7-Microbiological stability analyses of brewers spent grains and proposals of various treatment techniques in order to extend their shelf life for different uses

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Abstract

Brewers' Spent Grains (BSG), a by-product of the brewing industry, are highly perishable due to their high moisture content and rich nutritional composition, making them susceptible to microbiological spoilage. As a result, effective stabilization methods are critical to extend their shelf life and enable their safe and sustainable reuse in animal feed, food products, or bioenergy. This research aims to evaluate the safety and shelf life of BSG intended for both human and animal consumption, by assessing the influence of physicochemical factors – namely temperature, pH, and water activity on spoilage, and exploring stabilization strategies such as acidification and alginate encapsulation, in order to establish microbiological stability parameters. We predicted microbial degradation by applying a mathematical model based on bioengineering principles, combining a degradation rate model with an exponential decay function to estimate shelf life across different environmental conditions. For the experimental purposes of this study, we used Fresh BSG samples collected at the Stefani & Co Brewery in Tirana, Albania. The microbiological analyses were conducted Plate Count Agar through pour plate and Wort Agar through spread plate techniques. Acidification using food-grade acids effectively lowered the pH of BSG to a range of 3.2 – 4.5, significantly inhibiting microbial activity while also affecting soluble protein and sugar content. A novel stabilization approach employing sodium alginate (1.5 – 2 %) cross-linked with CaCl₂ reduced surface water activity from approximately 0.96 to 0.90 – 0.92. This method alone extended the shelf life by up to two weeks. When combined with acidification, the synergistic effect further enhanced microbiological stability. The findings demonstrate that simultaneously controlling multiple intrinsic factors

temperature, pH, and water activity, is significantly more effective than altering a single parameter. Acidification and alginate coating resulted not only practical, but also cost – effective in extending BSG shelf life and aflatoxin prevention. These approaches support the safe and sustainable reuse of BSG in both the food and feed industries by enhancing storage stability and reducing spoilage risks.

Keywords: Brewery Spent Grain, mathematical modeling, pretreatment, microbiological stabilization, shelf life, alginate treatment.

OP8-Control strategies against infectious disease in aquaculture: preliminary data

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Aquaculture, i.e. the breeding of aquatic organisms from early stages of development to commercial scale, is currently an industry that produces animal proteins for human consumption worth millions of dollars per year.

Despite increasing technological advances, many infectious agents that cause disease outbreaks and mortality lead to significant economic losses. In aquaculture, the most damaging diseases are caused by viruses and bacteria. Several control strategies, including vaccination, have been developed, but to date, there are not many effective vaccines available against most infectious diseases that affect fish farms worldwide. Therefore, research into the development of vaccines and other new strategies against existing and emerging infectious diseases is urgently needed. One of the possible strategies to prevent the emergence of the most common diseases is represented by genetic improvement for disease resistance. In this study, the Lysozyme gene (LYZII) encoding an anti microbial peptide, characteristic of the acute phase of the infection, was studied. RT-PCR test was developed and the discovery of new polymorphisms (SNPs) in the target gene were associated with a resistant/susceptible phenotype.

OP9-Blockchain-Based Management of Genetic Data

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Abstract

Introduction: The growing volume of genomic data from diagnostic laboratories demands secure, efficient, and priva-

cy-compliant data infrastructures. To address this, we developed a blockchain-based platform enabling decentralized genetic data sharing while ensuring traceability and confidentiality. **Materials and Methods:** Each laboratory stores full genomic sequences locally and retains control over raw data. A proprietary multivector embedding tool extracts and vectorizes selected features, producing tokenized, non-identifiable representations. Only these tokens are shared on the blockchain. Strict data governance policies allow analysis only on aggregated data, preventing individual-level reconstruction.

Results: The platform supports real-time collaborative analysis without exposing sensitive information. It enables efficient sequence similarity searches, supports shared workflows, and guarantees immutable data logging. The architecture is scalable and cost-effective; labs use the service freely, incurring minimal blockchain transaction costs.

Discussion: This approach ensures secure, privacy-preserving genetic data management across a federated network. Integrating multivector embedding with blockchain enables seamless, ethical data sharing and high-throughput analytics while protecting patient confidentiality and institutional autonomy.

Keywords: Blockchain, Genetic Data, Multivector Embedding, Tokenization, Federated Genomics, Privacy-Preserving Analytics, Genomic Data Security, Distributed Bioinformatics.

OP10-Multifunctional Zein-Agarose@Au Composite Hydrogel for Targeted Silibinin Delivery in Colon Cancer Therapy

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In this study, biodegradable hydrogel films based on natural proteins and polysaccharides were synthesized to improve controlled drug release, cytocompatibility and antibacterial properties. Biosynthesized AuNPs were incorporated in situ into cancer drug-loaded hydrogels to enhance their antibacterial, biocompatible, and cytotoxic characteristics. Then, to investigate the association of Silibinin drug used in cancer treatment with AuNPs, drug release profile was evaluated under different environmental conditions and release kinetics were analyzed. In addition, antibacterial effects were determined by testing Gram-negative and Gram-positive bacteria by Disk Diffusion method. As a result, the cytocompatibility of Silibinin drug

and AuNPs in hydrogel networks and their effects on cancer cells were determined by MTT assay using human dermal fibroblasts (CCD1079KSk) and colon cancer (HT-29) cell lines. Thus, AuNPs created a synergistic effect in cancer treatment and strengthened the effect of Silibinin on tumor cells. In addition, it was determined that it exhibited a biocompatible structure by showing minimal toxicity to healthy human skin cells. This innovative drug delivery system has the potential to offer a biomaterial-based alternative in both cancer treatment and wound dressing material with its controlled release feature.

Acknowledgement: This study was supported by Çanakkale Onsekiz Mart University Scientific Research Coordination Unit (COMU BAP), Project number: FBA-2024-4968

OP11-Metabolic Response to Ultraviolet Radiation of Some Agroindustrial Plant Species – a Biotechnological Approach

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The experiments were focused on the response of some plant species of agroindustrial interest following vegetal embryos exposure to ultraviolet radiation. We evidenced metabolic changes in young plantlets exposed to UV-C radiation during early ontogenetic stages. Total soluble protein content was found linearly increased with ultraviolet radiation dose. Antioxidant enzymes were found differently changed, with a progressive decreasing trend of superoxidedismutase activity but with non-linear response of catalase. The lipid peroxidation indirect marker, the malondialdehyde content changed differently for relatively low radiation exposure levels compared to the higher ones quite similar to catalase activity variation which suggested complex processes of plant cells ability to deal with oxidative stress. Box-plot approach was applied to describe the comparative statistical distributions of plant roots and stems that revealed stimulatory bioeffects on plant growth in the case of relatively low energy impact, the photoassimilatory pigments being found changed accordingly. Genetic impact expressed as chromosomal modifications were evidenced in the vegetal embryos metaphase sustaining the use of biotechnological tool based on ultraviolet C radiation exposure.

OP12-Non-linear Dynamics Investigation in Gait in Neurological Patients Using a Custom-Built STM32 Sensor System

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Why is quantitative gait analysis so important in patients with nervous system disorders such as hemiplegia? Current clinical

tools often fail to detect subtle impairments early, so this task still depends on experienced professionals or new methods. To address this, we built a wearable sensor system with an STM32 microcontroller and six three-axis accelerometers placed at the hips, knees, and ankles. Impulse response tests were conducted on a group of hemiparetic patients to identify differences. Acceleration signals were processed using detrended fluctuation analysis (DFA) to calculate the Hurst exponent (H), a fractal measure that reflects the complexity and timing of gait patterns. Our results showed that healthy individuals had H values generally between 0.65 and 0.92, representing the variability and adaptability of typical gait. Patients with hemiparesis had higher H values, mostly 1.02–1.28, especially on the affected side, suggesting less variation and a more rigid, compensatory gait. These findings highlight the potential of custom sensor technology combined with nonlinear dynamics for objective gait analysis. This could help refine clinical evaluation criteria and support personalized rehabilitation strategies for patients with neurological impairments.

OP13-Investigating the oncogenic potential of alcohol-related microbial alterations through *in silico* analysis

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Abstract

Chronic alcohol consumption causes dysbiosis and disrupts microbial functions. However, the potential role of alcohol-related dysbiosis in cancer development remains largely unexplored. Here, the possible contributions of alcohol-related microbiota alterations to carcinogenesis were investigated by *in silico* analysis. Microbial taxa associated with alcoholism were extracted from the Disbiome database, and taxon set enrichment analysis was performed to identify the gene sets related to these taxa. Host-intrinsic factors were determined using MicrobiomeAnalyst. The identified genes were then compared with the DisGeNET database to assess their functional relevance in alcohol-related comorbidities. Additionally, the cancer-related functions of the genes were evaluated using GEPIA, which utilizes public data from the Cancer Genome Atlas. Thirteen genes (*FBXO34*, *PCDHA2*, *PIWIL4*, *CPA2*, *CDH20*, *SLC45A4*, *NTNG2*, *CHRNA2*, *DAPL1*, *TELO2*, *MANBA*, *PLXNC1*, *KCNIP4*) were determined to be associated with alcoholism-related microbial taxa. Metabolic syndrome was the most significantly associated disease related to a total of 20 taxa. *CPA2*, *NTNG2*, *DAPL1* and *PLXNC1* were differentially expressed in at least one cancer dataset; *DAPL1* was most commonly altered across cancer types. Our findings provide *in silico* evidence linking

alcoholism-related dysbiosis to alcohol-induced diseases, particularly cancer, and shed light on the importance of microbiome-based strategies for risk assessment and alcohol cessation interventions.

Keywords: alcoholism, microbiome, dysbiosis, functional enrichment analysis, bioinformatics.

OP14-Photoprotective and Antioxidant Potential of Mycosporine-like Amino Acids (MAAs) Derived from *Coccomyxa subellipsoidea* ASYA6

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Extremophilic microalgae that thrive in Antarctica have evolved robust biochemical mechanisms to withstand severe environmental conditions, including high UV radiation and oxidative stress. Among these mechanisms, the production of mycosporine-like amino acids (MAAs) plays a critical protective role. In this study, we investigated *Coccomyxa subellipsoidea* ASYA6, an Antarctic psychrotolerant green microalga, as a novel source of photostable and mycosporine-like Amino Acids.

MAAs were extracted from freeze-dried biomass using methanol and subsequently purified via semi-preparative HPLC. Structural identification and purity assessment were performed using LC-MS/MS and ¹H NMR spectroscopy. UV-Vis absorption analysis revealed a broad-spectrum UV protection capacity, with absorption maxima ranging from 310 to 360 nm. Additionally, thermal and pH stability assays demonstrated that these compounds retained their structural integrity under stress conditions relevant to formulation and storage.

The antioxidant potential of MAA-rich fractions was evaluated using the DPPH radical scavenging assay. Results showed high antioxidant capacity, comparable to that of ascorbic acid, highlighting the potential of these compounds to mitigate oxidative stress in damaged or UV-exposed skin tissues. Given their natural origin, photostability, broad-spectrum protection, and biocompatibility, these compounds offer a sustainable alternative to synthetic UV filters, which often raise environmental and health concerns.

Overall, this study introduces a previously unreported source of MAAs and demonstrates its potential in the development of eco-friendly, multifunctional biomaterials for use in dermatology and regenerative medicine.

Keywords: *Coccomyxa subellipsoidea* ASYA6, mycosporine-like

amino acids, UV protection

Research Area: Bioactive and Natural Biomaterials

OP15-Decoding Cystic Fibrosis in Turkish Patients: Multi-Omics Insights into Genotype-Phenotype Correlation

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Abstract

Cystic Fibrosis (CF) is an autosomal recessive disorder caused by mutations in the *CFTR* gene, which encodes a chloride channel essential for epithelial ion transport. Over 2,000 *CFTR* variants have been identified, resulting in significant genotypic and phenotypic heterogeneity. Although *CFTR* modulators such as **Trikafta**[®], **Symdeko**[®], and **Kalydeco**[®] have improved patient outcomes, these therapies target only a subset of mutations, leaving individuals with rare variants without effective treatment options. This study aims to bridge this gap by generating integrative multi-omics data from Turkish CF patients, a population characterized by high genetic diversity and limited existing data on the *CFTR* mutation spectrum.

Samples from 43 CF patients (15 homozygous and 28 compound heterozygous) included blood, saliva, urine, and stool for whole genome sequencing (WGS), whole transcriptome sequencing (WTS), metabolomics, lipidomics, and metagenomics analyses. Preliminary transcriptomic analysis revealed upregulated mitochondrial genes (*MT-CO1* (100%), *MT-ND1* (32.6%), *MT-ATP6* (13.9%)) associated with energy metabolism; immune response genes (*HLA-A* (53.5%), *S100A8* (65.1%)) linked to chronic inflammation; and cytoskeletal genes (*ACTB* (97.7%)) implicated in *CFTR* trafficking. Conversely, several non-coding RNAs, including *misc_RNA*, *Y_RNA* (37.2%), and lncRNAs such as *ENSG00000253215* (11.6%), *ENSG00000253168* (*Lnc-PDGFR1-1*) (11.6%), and *ENSG00000254054* (*Lnc-PCM1-1*) (11.6%), as well as protein-coding genes like *FGL1* (11.6%) and *RNA5SP256* (5S ribo-

somal pseudogene) (11.6%), were significantly downregulated. Metagenomic profiling demonstrated increased *Actinobacteria*, *Firmicutes*, *Fusobacteria*, *Euryarchaeota*, and *Synergistetes*, along with decreased *Proteobacteria* and *Bacteroidetes*, indicating dysbiosis associated with disease severity.

By integrating multi-omics data, this study aims to improve understanding of genotype-phenotype relationships, enhance prognostic accuracy, and support precision medicine approaches in CF. Ultimately, combining genomic, transcriptomic, metabolomic, and microbiome profiles is expected to facilitate the development of personalized therapies for patients with rare *CFTR* mutations, improving clinical management and long-term outcomes.

Keywords: Cystic Fibrosis, *CFTR*, multi-omics, precision medicine, rare mutations.

OP16-Treatment process of waste to produce clean non-polluting fuels

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Abstract

The present study aims to create a clean biomass fuel for energy production by processing waste and biomass residues have been done. Solid residues including washed grape pomace and olive mill underwent elemental and proximate analyses to determine their suitability. These materials were then dried, using a specially designed thermal screw dryer, with temperature monitoring conducting during the process. The goal was to reduce the moisture content using hot gas from a boiler exhaust. The main purpose of the drying process is to reduce moisture content of a certain product or residue. This thermal process is based on heat and mass transfer between a drying fluid and biomass residue (Al-Kassir, et. al, 2005), (Kassir Al-Karany, 2013).

Thankfulness: The authors of this paper would like to express their gratefulness to Junta de Extremadura of Spain for its economic aid granted to the research groups (GR24) and (GR24001). for the development of this study.

OP17-Exploring genetic diversification among *Salmo letnica* morphotypes in Lake Ohrid

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The Ohrid trout (*Salmo letnica*), endemic to Lake Ohrid (Albania-North Macedonia), is traditionally divided into four morphotypes based on morphology and spawning behaviour. Genetic tools can help identify the possible population structure among these morphotypes. This preliminary study analysed mitochondrial Control Region sequences from 127 individuals sampled along the Albanian shore of Lake Ohrid and compared them with other *Salmo* species. Phylogenetic and clustering analyses revealed low mitochondrial differentiation among the four morphotypes, suggesting ecological divergence not yet reflected at mitochondrial level. In contrast, a clear genetic distinction from the sympatric *S. ohridanus* was confirmed. Moreover, the findings supported the hypothesis that *S. letnica* is an endemic species evolved from ancestral *S. farioides* landlocked populations within Lake Ohrid. To further investigate the genetic structuring among morphotypes, ongoing analyses using microsatellite loci are underway.

OP18-Evaluation of groundwater pollution in Shkodër and Malësia e Madhe using the Compact Dry EC method

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This study aimed to assess the bacteriological quality and physico-chemical parameters of groundwater collected from wells and boreholes in the city of Shkodër and the Malësia e Madhe region. Special attention was given to the presence of fecal contamination indicator bacteria such as *Escherichia coli* and intestinal enterococci, as well as opportunistic bacteria including *Klebsiella oxytoca* and *Pseudomonas aeruginosa*. During the period January – April 2024, a total of 25 water samples were analyzed, of which 15 were from boreholes and 10 from wells. Bacteriological analyses were performed using the Compact Dry EC test and the membrane filtration method with nitrocellulose membranes. Physico-chemical parameters, specifically pH and electrical conductivity, were measured in situ using AQUALYTIC system devices, while turbidity was measured using the Turb 430 IR/T device. Microbiological analysis showed that 52% of the samples were positive for *Pseudomonas aeruginosa*, 40% for *Klebsiella oxytoca*, 36% for intestinal enterococci, and 24% for *Escherichia coli*. The average values of the physico-chemical parameters were: pH = 7.86, conductivity = 428.75 µS/cm, and turbidity = 2.89 NTU/FNU.

This study was conducted at the Wolfdieter Sixl Microbiological Diagnostic Center, Faculty of Natural Sciences, University of Shkodër "Luigi Gurakuqi".

Keywords: *Escherichia coli*, *Enterococcus intestinalis*, *Klebsiella oxytoca*, *Pseudomonas aeruginosa*, pH, conductivity, turbidity.

OP19-Metabolic Reprogramming in Cancer: The Central Role of the Warburg Effect

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#Equal work

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Cancer remains a leading cause of global mortality, with over 20 million new cases and 10 million deaths annually (WHO). Beyond genetic alterations, tumor development involves profound dysregulation of cellular signaling and metabolic pathways. One **hallmark of cancer** metabolism is the **Warburg effect**, characterized by the preferential use of aerobic glycolysis over oxidative phosphorylation, even in oxygen-rich conditions. Although energetically less efficient, this shift enables rapid ATP production, facilitates biosynthesis of nucleotides, amino acids, and lipids, and supports the high proliferation rate of cancer cells.

Furthermore, lactate accumulation resulting from enhanced glycolysis acidifies the tumor microenvironment, promoting immune evasion, angiogenesis, invasion, and metastatic potential. These adaptations not only sustain tumor growth under hypoxic and nutrient-limited conditions but also offer selective advantages over normal cells.

This study aims to summarize key metabolic alterations associated with oncogenesis, focusing on the Warburg effect as a central mechanism that underpins cancer cell survival and progression. Emphasis is placed on the therapeutic implications of targeting cancer metabolism, an emerging strategy in precision oncology. A deeper understanding of these metabolic vulnerabilities may support the development of novel anticancer interventions and improve patient outcomes.

OP20-Preparation of Cationic Based Super Macroporous Cryogel Composites by Green Synthesis Method and Investigation of Biomedical Application

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In this study, to develop a multifunctional carrier system for

biomedical applications, super macroporous cryogels in semi-IPN structure were synthesized using cationic APTMACl, HEMA and sodium alginate. Cryogels were synthesized by a free radical polymerization method with MBA crosslinker at -24 °C. The obtained cryogels were first loaded with Ag⁺ ions and then AgNPs were formed by *in situ* green synthesis method using *Cornus mas* plant extract. Then, characterization studies were carried out by FTIR, XRD, SEM, TGA and TEM analysis; As a result of TEM images, the average size of AgNPs was determined to be 7.85 nm. Semi-IPN@Ag Model drugs Cefazolin and Sodium diclofenac were loaded, and *in vitro* release studies were carried out in pH 7.4 PBS medium at 37 °C. Drug release kinetics were calculated and the appropriate model for controlled drug release of the system was determined. As a result of antimicrobial tests, Semi-IPN@Ag was effective against both Gram-positive and Gram-negative bacteria. In addition, it was determined that the system after green synthesis showed a high level of antioxidant activity based on TEAC and total phenolic content. These results revealed that the developed system is a strong candidate for applications such as drug delivery, infection control and reduction of oxidative stress.

Acknowledgement: This study was supported by Çanakkale Onsekiz Mart University Scientific Research Coordination Unit (COMU BAP), Project number: FBA-2025-5094

OP21-Therapeutic potential of trained autologous t cell therapy in the treatment of mast cell tumors

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Background

Mast cell tumors (MCTs) are neoplastic diseases commonly observed in dogs and rarely but aggressively in humans. However, standard treatment options remain limited, and comprehensive studies investigating the role of immunotherapies—particularly T cell-based approaches—in the treatment MCTs are lacking. This study aims to elucidate the effects of co-culturing trained T cells with mast cell tumor (MCT) cells by evaluating their impact on cell viability and cytotoxicity.

Materials and Methods

HMC-1 cells were co-cultured with human T cells for 3 days, after which T cells were isolated and re-exposed to fresh HMC-1 cells. Four experiment groups were set up to assess the impact of T cell count and prior HMC-1 lysate exposure on HMC-1 viability after 7 days, using a triplicate viability assay.

Results

Our results showed significant main effects of co-culture ($p < 0.01$) and T cell count ($p = 0.001$) on MCT cell viability. A significant interaction between co-culture and T cell count was also observed ($p = 0.0032$) indicating co-culture effects on viability increased with higher cell densities.

Conclusion

Our findings demonstrate that the co-culture of trained autologous T cells with MCT cells significantly reduces tumor cell

viability, highlighting its potential as an innovative immunotherapeutic option for treatment-refractory MCTs. Future studies will be essential to further validate its efficacy.

OP22-Novel therapeutic approach based on trains of electrical impulses for the stimulation of the vagus nerve – a practical educational application

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Recent advancements in neuromodulation highlighted the potential of non-invasive vagus nerve stimulation (VNS) in improving the acute and chronic pain syndromes, certain heart activity parameters like heart rate variability and arrhythmia, anxiety and disorders of consciousness as well as the average brain focus. In this paper it is presented the original system assembled for the demonstrative study of vagus nerve auricular stimulation aiming to increase the subject attention and concentration. The stimulation sessions included both continuous single impulse mode and trains of impulses (1-30 Hz) application. The results were visualized on a computer via a remote encephalograph and specialized software that displays a global attention indicator and the brain waves amplitudes. About 30 second stimulation has successfully proved the didactic purpose by demonstrating the improvement of the short term memory and of the brain relaxation evidenced by doubling the attention indicator and reducing the meditative tendency. Further large-scale studies are planned to establish optimal stimulation parameters and long-term efficacy of this non-invasive system as a promising therapeutic approach.

OP23-HOMA Index and Insulin Resistance: A Preventive Indicator of Diabetes Risk in the Albanian Population

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Abstract:

Insulin resistance (IR) is a central metabolic disorder in the pathogenesis of type 2 diabetes mellitus (T2DM) and related conditions such as cardiovascular disease and non-alcoholic fatty liver disease (NAFLD). The Homeostatic Model Assessment of Insulin Resistance (HOMA-IR) index is a simple, cost-effective method widely used for early IR detection; however, its application in the Albanian population remains under-explored.

In this cross-sectional study, we analyzed data from 2,670 individuals aged over 20, randomly selected from patients undergoing routine check-ups at Intermedica Medical Laboratory during 2024–2025. IR was assessed using the HOMA-IR index with a diagnostic threshold of 3.16, achieving a sensitivity of 75% and specificity of 61%. Biochemical parameters (glucose,

insulin, HbA1c, lipid profile) were measured, and anthropometric and lifestyle data were collected through structured questionnaires. Participants were stratified into normoglycemic, prediabetic, and diabetic groups based on HbA1c values. We found a high prevalence of IR: 58.3% in the normoglycemic group and 100% in both prediabetic and diabetic groups. Among diagnostic markers, HOMA-IR demonstrated the highest performance (AUC = 0.814), significantly outperforming glucose (AUC = 0.766) and insulin (AUC = 0.746) ($p < 0.0001$). The strongest predictors of IR were a sedentary lifestyle and a positive family history of diabetes.

Conclusion: Insulin resistance is highly prevalent in the Albanian population, even prior to diabetes onset. HOMA-IR is a reliable, effective tool for early IR identification and holds strong potential for integration into national diabetes prevention programs.

Keywords: HOMA-IR; Insulin Resistance; Type 2 Diabetes; Early Detection; Albania

OP24-Exploring Mumio's influence: From standard culture to tissue-like structures

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Objective

Mumio is a natural substance that has been used for hundreds of years due to its healing properties. The aim of the study was to assess the effect of the pharmaceutical form of Mumio on the growth of normal (SV-HUC-1) and bladder cancer cell lines (T24, HTB-9) in 2D and 3D culture.

Methods

In 2D culture, the MTT assay, real-time cell growth analysis, fluorescence and light microscopy, and flow cytometry were used. In 3D culture, spheroids were obtained using ultra-low attachment 96-well plates. Cell viability and caspase activity were assessed using luminescence assays. HE and Ki-67 staining, as well as molecular analysis, were also performed.

Results

In 2D culture, Mumio affected the viability of tested cells in a time and concentration-dependent manner. We observed a selectivity of Mumio against cancer cells. In 3D culture, Mumio cytotoxic effects was less pronounced compared to 2D culture. Performed analysis showed the influence of the tested substance on inhibiting the cell cycle in the G1 phase and reducing cell viability by maintaining DNA synthesis.

Conclusions

Mumio has promising properties for the supportive treatment of urinary bladder cancer. Further investigations should be

performed to confirm this hypothesis.

OP25-Cryobiotechnologies for preservation of plant germplasm in Kazakhstan

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Conservation of plant biodiversity is a critical component of sustainable development, particularly in the context of climate change, ecosystem degradation, and increasing anthropogenic pressure.

The Institute of Plant Biology and Biotechnology has developed advanced protocols for micropropagation and cryopreservation of numerous fruit, berry, nut, and forest plant species. These biotechnological methods address several critical challenges:

- Conservation of rare and endangered plant species of Kazakhstan's flora through *in vitro* culture and cryogenic storage
- Preservation of germplasm from economically valuable agricultural crops, including both local and introduced varieties and hybrids
- Elimination of plant viruses and production of virus-free material for clonally propagated crops
- Restoration of degraded ecosystems and support for natural population recovery

Micropropagation and cryopreservation protocols have been successfully developed for a wide range of valuable crops, including apple, pear, apricot, raspberry, blackcurrant, barberry, honeysuckle, cherry, potato, hazelnut, and walnut.

Cryotherapy protocols, combined with chemotherapy and thermotherapy, have been optimized for the eradication of viruses in *in vitro* plants of apple, raspberry, and potato. A national cryogenic germplasm bank has been established in Kazakhstan, operating at -196°C, and currently holds 1,240 accessions representing wild forms and varieties of *Malus*, *Pyrus*, *Rubus*, *Ribes*, *Lonicera*, and *Berberis*.

This research was supported by the Science Committee of the Ministry of Science and Higher Education of the Republic of Kazakhstan, Program No. BR28712539.

OP26-A Bioinformatics Workflow for VUS Reclassification Using Multiple Tools

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Introduction:

Variants of uncertain significance (VUS) pose a challenge in

the interpretation of medical genetics. In silico tools—computational methods—help predict whether a variant could be disease-causing. This approach does not require laboratory experiments and is particularly helpful in rare diseases where studies are limited. By combining different bioinformatics tools, we can gain a deeper understanding of how a variant affects a gene or protein and make more accurate clinical predictions.

Methods and Results:

We used a bioinformatics workflow to analyze 76 VUS found in a gene. As a rare disease example, we demonstrated how in silico tools can support variant classification. After filtering with REVEL and AlphaMissense, we selected 28 variants for further analysis. We utilized tools such as PolyPhen-2 and SIFT for functional effect prediction, ConSurf for conservation analysis, and gnomAD for population frequency data. We also applied SpliceAI for splicing prediction, DynaMut2 and HOPE for protein stability, and COACH-D to investigate binding sites. This provided us a clearer idea of the possible effects of each variant.

Conclusion:

Our study demonstrates that combining multiple in silico tools is effective for classifying VUS. This method supports better clinical decisions and shows the power of bioinformatics in modern genetics.

Keywords: Pathogenicity prediction, protein dynamics, precision medicine, variant classification

OP27-Zingiber officinale Roscoe Attenuates Metabolic Dysregulation in Streptozotocin-Induced Type 2 Diabetic Mice: An Integrated Biochemical and In Vivo Analysis

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Abstract

Type 2 diabetes mellitus (T2DM) is a multifactorial metabolic disorder characterized by chronic hyperglycemia, insulin resistance, and β -cell dysfunction. This study evaluated the antidiabetic efficacy of *Zingiber officinale* Roscoe in a high-fat diet and streptozotocin (STZ)-induced T2DM mouse model. Diabetic BALB/c mice received oral administration of aqueous *Z. officinale* extract (250 mg/kg and 500 mg/kg) for four weeks. Phytochemical profiling confirmed the presence of diverse bioactive constituents, while in vitro assays demonstrated significant pharmacological activity relative to standard antidiabetic agents. Weekly assessments of fasting blood glucose and body weight, along with intraperitoneal glucose tolerance testing, revealed that *Z. officinale* extract markedly improved glycemic control and metabolic homeostasis, highlighting its potential as a complementary therapeutic agent for T2DM.

OP28-Study of Some Bioeffects of Silver Nanoparticles on Beneficial Fungi in the Environment

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Given the large annual production of silver nanoparticles for a wide range of uses in cosmetics, textiles, disinfection, hygiene, advanced medicine, the fate of nanoparticles released into water and air after use has raised increasing concern. The effects of silver nanoparticles synthesized in the laboratory by reduction with gallic acid on a species of cellulolytic fungi from the environment, with an important role in the degradation of cellulose waste in the biosphere, were studied. The research was focused on some antioxidant enzymes like, catalase and superoxide dismutase. Catalase activity increased as evidence of the activation of defense mechanisms against hydrogen peroxide, i.e. the intensification of enzymatic biosynthesis. This process suggested by the 7 day results seems to be much attenuated up to 14 days. Superoxide dismutase activity varies insignificantly both at 7 days and at 14 days, with a slight tendency to decrease with increasing silver nanoparticle concentration. The concentration of malondialdehyde, an indicator of membrane lipid peroxidation, shows a tendency to increase with the concentration of silver nanoparticles, while the content of soluble proteins shows a tendency to decrease after 14 days of fungal culture. Further extension of the present nanotoxicity study is planned on young seedlings from spontaneous vegetation.

OP29-Uncovering genetic factors in miscarriages: A Biotech perspective from Albania's clinical experience

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Abstract

Recurrent pregnancy loss remains a significant reproductive health challenge, often with unexplained causes. Emerging biotechnological advances have enabled deeper exploration into the genetic basis of miscarriages. This study presents a comprehensive overview of the genetic factors associated with miscarriages, drawing on clinical data and case studies from Albanian healthcare institutions. Using molecular diagnostics such as QF-PCR, MLPA and chromosomal microarray analysis (CMA), we investigated chromosomal abnormalities, gene mutations, and polymorphisms implicated in pregnancy loss. Our findings highlight a frequency of 51.7% of uncontaminated early pregnancy loss (≤ 12 weeks) with chromosomal aneuploidies and mutations in genes related to coagulation,

immune regulation, and embryonic development. Stratified in ages under 30 years 43.4% overall abnormality and respectively Trisomies 48.7%, Triploidy 26.1%, Monosomy 16.5% ; ages 31-35 years abnormalities in 53.9% with Trisomies more frequent; Age ≥ 36 abnormality rate increased to 71.4%, with respectively Trisomies 79.7%, Triploidy 6.4% and Monosomy 6.4%; other specific chromosomal categories found Trisomy 16 in 32.8% and Trisomy 22 in 6.9% ; structural chromosomal rearrangements are found in about 3.6% of recurrent miscarriage of the specimens. This study reveals the importance of integrating genomics test and genetic counseling into routine reproductive care in Albania. Furthermore, it demonstrates how biotechnology can enhance diagnostic accuracy, inform therapeutic decisions, and improve outcomes for affected couples.

Keywords: miscarriages, karyotype, chromosome analysis, CMA, QF-PCR.

OP30-Uncovering the Role of Cuproptosis Genes in HNSCC: Insights into Immune Modulation and Cell Death Crosstalk

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Cuproptosis is a recently characterized, copper-induced form of non-apoptotic cell death, with its role in cancer biology still largely unexplored. This study investigates the genomic and transcriptomic landscape of cuproptosis-associated genes (CAGs) in head and neck squamous cell carcinoma (HNSCC), with emphasis on their clinical and immunological relevance. A total of 523 HNSCC cases from TCGA were analyzed using multiple bioinformatics tools, including cBioPortal, TIMER, GEPIA2, DAVID, and UALCAN. Over 70% of patients exhibited alterations in at least one CAG, with CDKN2A, DLAT, and GLS being most frequently affected. These alterations were linked to advanced tumor stage and HPV-negative status. Somatic copy number variations in CAGs significantly influenced immune cell infiltration, particularly affecting CD8⁺ T cells and dendritic cells. Co-expression analysis revealed strong associations between CAGs and immunoregulatory genes (e.g., IL-6R, TGFBR1), as well as DNA repair genes, suggesting roles in immune modulation and genomic maintenance.

These findings underscore the potential of cuproptosis-related genes as contributors to immune evasion and tumor progression in HNSCC. MRPS5 and SOD1 emerged as promising biomarkers for metastasis and immune suppression, warranting further experimental validation.

OP31-Microbial quality of surface waters in some areas in Albania- situation and future prospects

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Abstract

Surface waters are all natural bodies of fresh, marine or estuarine water used for recreational purposes. They include lakes, rivers that have untreated natural waters. These waters are used for irrigation, bathing, fishing and even domestic use. Therefore, the assessment of pathogens in surface waters is necessary, since their microbial quality is linked to the incidence of diseases transmitted by the use of contaminated, untreated surface waters. It is vital that with different methods of identification and assessment of bacterial indicators such as *fecal coliforms*, *fecal streptococci* and *E. coli*, the reasons that influence the spread of waterborne pathogens with an impact on public health are identified. Water quality in our country, as and in developing countries, has deteriorated due to demographic shifts of the population to urban areas, industrialization, water pollution from untreated domestic wastewater, municipal waste, agricultural practices, etc. As a result of microbial pollution of water sources, the risks to public health are considerable. From several studies of waters in several areas in Albania such as the Adriatic Sea Durres, the Erzen River etc. it has resulted that a considerable number of the stations analyzed, microbial pollution has been above the permitted norms. In this article, in addition to reviewing the existing microbial quality from microbial assessment in several years and assessing the health risk, we conclude on some of the main gaps today in surface water management and reflect on possible future directions for research in this field.

Keywords: Surface waters, public health, *Fecal coliforms*, *Fecal streptococci* and *E. coli*

OP32-Agro-industrial plant proteins in cultivated meat production

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Plant proteins are emerging as promising alternatives to animal-derived components in cell culture media for cultivated meat production. Traditionally, animal blood serum has been used for its rich content of growth factors and nutrients, but it is costly, unethical, and compositionally inconsistent. To address these issues, researchers are exploring plant proteins (and their hydrolyzed derivatives) isolated from crops like soy, wheat, and rice, or agro-industrial byproducts such as oil-cakes made of de-oiled rapeseed. The protein provides nutrients that promote muscle and fat cell growth in serum-free or serum-reduced conditions and may also contain bioactive compounds beneficial for cell metabolism. While variability in composition and batch-to-batch consistency remain challenges, ongoing

research is working to standardize plant proteins and their hydrolysates for cell culture applications. Replacing animal-derived components with plant-based alternatives is a critical step toward fully defined, animal-free media suitable for scalable and ethical meat cultivation. As this field evolves, plant proteins are expected to play an increasingly central role in the formulation of next-generation culture media. In this context, we report on improved performance of myoblasts and adipocytes grown in low-serum media supplemented with flaxseed protein isolates. The cells demonstrated enhanced differentiation compared to those cultured in conventional media.

Keywords: plant proteins, cell culture media formulation, animal component-free, sustainability, cultivated meat

OP33-Essential Oils as Alternative Therapy in Bovine Mastitis

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Bovine mastitis remains one of the most prevalent and economically detrimental diseases in the dairy sector, affecting milk production, composition, and animal welfare. It manifests in clinical and subclinical forms and is caused by a broad range of pathogenic agents. While antibiotic therapy remains the mainstay of treatment, the increasing prevalence of antimicrobial resistance and the presence of drug residues in milk have raised serious concerns regarding food safety, therapeutic efficacy, and public health. In response, alternative therapeutic strategies are increasingly explored. Essential oils (EOs) derived from medicinal plants have raised attention due to their antimicrobial, anti-inflammatory, antioxidant, and immunomodulatory activities.

Studies summarizing *in vivo* evidence regarding the efficacy of EOs extracted from *Origanum vulgare*, *Thymus vulgaris*, *Zataria multiflora*, *Lavandula angustifolia*, and *Minthostachys verticillata* in managing bovine mastitis are available. These plant-derived compounds can reduce intramammary bacterial load and somatic cell counts while contributing to the improvement of clinical symptoms associated with mastitis. Their intramammary or topical application has shown no significant adverse effects on animal health, udder integrity, or milk quality. Despite encouraging results, current evidence remains primarily confined to experimental models. Further well-designed, large-scale clinical trials are required to validate therapeutic efficacy, assess long-term safety, and support standardization for effective implementation in evidence-based mastitis control programs.

OP34-Momordica charantia: A Biotechnological Approach in Medicine

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Abstract

Momordica charantia, or bitter melon, has become an important medicinal plant because of its richness in secondary metabolites that may have effects in different therapeutic approaches.

Its alkaloids, flavonoids, glycosides, and saponins are thought to be responsible for its antibacterial, anti-inflammatory, anti-diabetic, and anti-cancer activities. Recent developments in biotechnology have produced innovative protocols and methods which can improve the bioactive components of this medicinal plant for use in drug development and clinical applications. The studies have demonstrated that bitter melon can be used to create medical agents with fewer adverse effects than traditional treatments, such as cancer-fighting medications and tablets that can control diabetes. With an emphasis on *in vitro* culture, extraction methods, molecular mechanisms of action, and the potential applications of this medicinal plant in modern medicine, this review aims to investigate the biotechnological approaches, improving the therapeutic qualities of bitter melon. As interest in sustainable biotechnology and natural medicines develops and grows worldwide, *Momordica charantia* shows potential as a valuable resource in the battle against infections and chronic diseases.

Keywords: Biotechnology, Medicine, Secondary metabolites, *Momordica charantia*

OP35-Cryopreservation optimization for shoot tips of rare endangered Rosaceae species *Prunus ulmifolia* and *Spiraeanthus schrenckianus*

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The *Rosaceae* family includes numerous species of significant economic and ecological value, some of which are currently threatened with extinction. *Prunus ulmifolia* and *Spiraeanthus schrenckianus* are rare representatives of this family, with restricted distributions that are highly vulnerable to anthropogenic impacts and climate change. In the context of escalating environmental threats, one of the promising strategies for their conservation is cryopreservation at -196°C .

For the cryopreservation of shoot tips of *P. ulmifolia* and *S. schrenckianus*, the PVS2 vitrification method was employed. To adapt *in vitro* shoots, cold acclimation (CA) was applied under the following conditions: 22°C with light intensity of

10 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ for 8 h, and 16 h at -1 °C in darkness. The duration of CA ranged from 0 to 7 weeks. Exposure to the cryoprotectant (PVS2) was tested for 40, 50, 80, and 100 min.

The highest survival rates were achieved after 6 weeks of CA and 100 min of PVS2 exposure – 83.3% for *P. ulmifolia* and 60.0% for *S. schrenckianus*. In the absence of CA, no viable shoot tips were recovered after cryopreservation.

Keywords: *Rosaceae* family, *Prunus ulmifolia*, *Spiraeanthus schrenckianus*, cryopreservation, shoot tips.

Funding: This research was funded by the Ministry of Science and Higher Education of RK (BR28713087).

OP36-Lipid Composition Of Olive Pomace

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Olive pomace is a puree formed by fragments of stone, sections of peel and residues of olive pulp, which remains after pressing the olives to obtain Extra Virgin Olive Oil and Virgin Olive Oil. The fruit of *Olea europaea* L. is a plant matrix containing high levels of fatty acids (98-99% of the total weight of EVOO) and low amounts (1-2%) of phenols, phytosterols, tocopherols and squalene, molecules with beneficial activity for human health [1,2]. From the olive pomace is possible to extract measured quantities of oil ranging from 3 to 6% by weight by pressing or centrifugation [3]. The oil obtained is called crude olive pomace oil and is not edible. The composition of pomace oil is similar to that of olive oil and what distinguishes it is the richness of linoleic acid (9.5 -15.5%) with the addition of elaidinic acid (0.2%), a trans isomer of oleic acid. Although rich in residual lipids, vitamins and bioactive phenolic compounds, opomace oil is mainly composed of insoluble dietary fibres, with a high lignin content, which makes it difficult to use directly in foods [3]. The aim of the study was to use the pomace as a waste material to extract a product beneficial to human health. Therefore, the olive pomace was extracted using innovative techniques that allowed the final product to maintain an excellent lipid profile. The pomace oil we analyzed was found to be rich in neutral and polar lipids, such as phospholipids, and showed higher quantities than soybean oil. This composition would allow the pomace extract to be used for nutritional purposes.

OP37-The role of S100A8 in adipose-bone axis mediated immuno-metabolic crosstalk in Breast Cancer Metastasis

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Abstract:

Bone metastasis in advanced primary breast cancer patients is a global health concern. Bone marrow adipose tissue (BMAT) provides a cultivating ground for tumour spread, however the underlying molecular mechanisms are not yet fully understood. Present study employed an insilico approach to identify bone lesion (BL) associated differentially expressed genes (DEGs) in breast cancer (BC) by employing the GEO2R tool on GEO database sourced microarray expression data. To this BL DEGs list, DEGs associated with BMAT were applied. Common DEGs were obtained and subjected to protein-protein interaction (PPI) and functional enrichment analysis using STRING 12.0. Subsequently, the immuno-metabolism associated genes' list derived from GeneCards was mapped. Immune filtration was estimated using TIMER 2.0. A total of 16 BL in BC associated genes were found to be commonly dysregulated for BMAT. These were mainly enriched for immune associated terms including immune system and neutrophil degranulation. Amongst these genes, *S100 calcium binding protein A8* (*S100A8*) was found to be immuno-metabolic in nature. It associated negatively with M0 and M1 macrophages but positively with M2 highlighting pro-tumorigenic potential in BC. Hence, targeting *S100A8* may provide a therapeutic window into the BMAT mediated immuno-metabolic crosstalk to address bone metastasis in BC.

OP38-African Swine Fever Virus circulation in areas of wild boars feeding area

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African swine fever (ASF) is a contagious disease of pigs, causing significant economic effects; the wild boars are considered of major epidemiological importance due to their ability to spread the virus. The aim of study was to evaluate the risk of ASFV transmission by feed in area where wild boars are circulating. Forty samples of corn grains were collected from a feeding area. The samples underwent DNA viral extraction using QIAamp DNA kit and the identification of the ASFV was performed by real time PCR using the protocol recommended by OIE Terrestrial Manual 2019.

Following the real-time PCR assay, all the corn grain samples analyzed resulted to be negative. The validation of the test was assessed by using positive and negative controls.

This negative result may suggest that feed may have a lower po-

tential to transmit the ASFV, although other studies have confirmed this role. However, this study has a limitation, given the low number of the tested samples and possibly the low quantity of viral DNA in samples.

Funding: Program of the Ministry of Agriculture and Rural Development of Romania, project ADER 10.1.1. 2023-2026.

OP39-Resilient Native Flora on Mine Lands: Linking Phytoremediation Strategies to Bioeconomic Opportunities

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Abstract

This study explores the phytoremediation potential of native tree species naturally colonizing abandoned mine lands in Portugal. Species such as *Pinus*, *Eucalyptus*, and *Quercus* have demonstrated resilience to metal-contaminated, nutrient-poor soils, enabling their use in soil stabilization and pollution attenuation. Through field observations and metal accumulation analysis, we found that while these trees show moderate metal uptake compared to herbaceous species, their high biomass and adaptability make them suitable for phytostabilization and selective phytoextraction in peripheral contamination zones. Importantly, harvested biomass presents bioeconomic opportunities when metal content is managed within safe thresholds. Options include bioenergy generation (incineration, biofuels), phytomining, biochar production, and application as adsorbents in wastewater treatment. This work underscores the dual benefit of ecological restoration and resource recovery, advocating for an integrated approach that balances environmental remediation with sustainable economic use. Proper risk assessment is essential to ensure environmental and health safety in biomass utilization strategies.

Keywords: Bioenergy, Biomass offtake, Economic revenue, Environmental remediation, Phytoremediation.

OP40-Advanced Delivery Systems in Oral Iron Formulation: Comparative Analysis of Iron Bisglycinate, Liposomal Iron, and Ferrous Sulfate in Clinical Practice

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Abstract

Purpose

To evaluate and compare the clinical effectiveness and tolerability of three oral iron formulations—iron bisglycinate, liposomal iron, and ferrous sulfate—in treating iron deficiency anemia, with a focus on their biotechnological formulation advancements and patient outcomes.

Methodology

A real-world observational pilot study was conducted involving three general practitioners who each monitored 10 patients diagnosed with iron deficiency anemia (total n=30). The patients were assigned to receive one of the three iron formulations. Baseline and post-treatment hematologic parameters—hemoglobin, serum ferritin, and sideremia—were measured using Roche diagnostic equipment. Patients were followed under the same dietary guidelines and treatment durations.

Results

Liposomal iron showed the highest tolerability and significant improvement in serum ferritin levels. Iron bisglycinate demonstrated moderate efficacy with fewer gastrointestinal side effects, whereas ferrous sulfate, although effective in increasing hemoglobin, was associated with a higher rate of gastrointestinal discomfort and treatment discontinuation in some patients.

Conclusion

Biotechnologically enhanced formulations like liposomal iron and iron bisglycinate offer promising alternatives to conventional ferrous salts, improving patient compliance and minimizing side effects. Further randomized studies are needed to confirm these findings.

OP41-Mechanisms of phagocytic response of neutrophil granulocytes to the induction of antibiotic-resistant bacteria

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Background: The aim of the study was to determine the specific phagocytic activity of neutrophilic granulocytes when exposed to antibiotic-resistant and antibiotic-sensitive bacterial strains *Staphylococcus aureus* and *Klebsiella pneumoniae*

Objective: neutrophilic granulocytes of blood isolated from healthy people (n=21) and bacterial strains MRSA, MSSA and *K. Pneumoniae* resistant and sensitive to antibiotics.

Methods: The double disc method was used to detect antibiotic resistance. Neutrophil granulocytes were analyzed on an FC-500 flow cytofluorimeter (Beckman Coulter, USA) in whole peripheral blood induced by FITC-labeled bacteria. The phagocytic index (PhI) and phagocytic number (PhN) were determined. Statistical analysis was evaluated by Statistica 10.0. **Results:** When studying the phagocytic activity of neutrophils in response to MRSA, compared with MSSA, PhI and PhN of actively phagocytic cells were 6.2 and 7.6 times higher ($P<0.001$), respectively. At the same time, the PhI of weakly phagocytic cells decreases by 1.7 times ($P<0.001$). In response to resistant strains of *K. Pneumoniae*, PhI and PhN of actively phagocytic neutrophil granulocytes were 1.1 times ($P<0.05$) and 1.6 times ($P<0.05$) lower than those of sensitive phagocytic cells.

Conclusion: As a result of the acquisition of antibiotic resis-

tance, the receptor apparatus changes due to modification of the cell wall.

OP42-Study of Bioeffects of Silver Nanoparticles on Beneficial Fungi in the Environment

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Given the large annual production of silver nanoparticles for a wide range of uses in cosmetics, textiles, disinfection, hygiene, advanced medicine, the fate of nanoparticles released into water and air after use has raised increasing concern. The effects of silver nanoparticles synthesized in the laboratory by reduction with gallic acid on a species of cellulolytic fungi from the environment, with an important role in the degradation of cellulose waste in the biosphere, were studied. The research was focused on some antioxidant enzymes like, catalase and superosidedismutase. Catalase activity increased as evidence of the activation of defense mechanisms against hydrogen peroxide, i.e. the intensification of enzymatic biosynthesis. This process suggested by the 7 day results seems to be much attenuated up to 14 days. Superoxide dismutase activity varies insignificantly both at 7 days and at 14 days, with a slight tendency to decrease with increasing silver nanoparticle concentration. The concentration of malondialdehyde, an indicator of membrane lipid peroxidation, shows a tendency to increase with the concentration of silver nanoparticles, while the content of soluble proteins shows a tendency to decrease after 14 days of fungal culture. Further extension of the present nanotoxicity study is planned on young seedlings from spontaneous vegetation.

OP43-Serological Evidence of West Nile Virus Exposure in Domestic Dogs: Preliminary Findings from Iasi County, Romania

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#Equal work

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West Nile virus (WNV) is a zoonotic arbovirus with a growing presence in Europe, causing recurrent seasonal outbreaks, particularly in southern and central regions. While birds serve as amplifying hosts and Culex mosquitoes as vectors, humans and mammals such as horses and dogs are considered incidental hosts. Although dogs do not play a role in WNV transmission due to low or absent viremia, they may serve as effective sentinels for viral circulation.

This study conducted a preliminary serological survey to evaluate WNV exposure in domestic dogs from Iasi region, north-eastern Romania, using the ID Screen® Pan-Flavivirus ELISA

(IDVet, Montpellier, France). Out of 436 serum samples analyzed, 22.25% (n=97) were seropositive, 76.37% (n=333) negative, and 1.38% (n=6) were doubtful.

The results indicate active WNV circulation in the region and support the inclusion of canine serosurveillance in public and veterinary health monitoring. Further longitudinal studies are recommended to enhance early detection and inform preventive strategies in endemic areas.

This research was supported by a grant from Climate Change Digital Twin Earth for Forecast and Societal Redressement (Grant number: DTEclimate PNRR/2022/C9/MCID/15).

OP44-Preliminary Findings on the Seroprevalence of Crimean-Congo Hemorrhagic Fever Virus in Goat Populations from Southeastern Romania

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Crimean-Congo hemorrhagic fever (CCHF) is an emerging tick-borne zoonotic disease of growing concern in Europe, driven by climate change, animal trade, and expanding *Hyalomma* tick distribution. While animals remain asymptomatic, CCHFV causes severe, often fatal illness in humans. Goats serve as transient amplifying hosts, facilitating virus transmission to ticks and humans.

This study assessed CCHFV exposure in 228 domestic goats from Tulcea County, Romania. Using the ID-Screen® CCHF Double Antigen Multi-species ELISA, a seroprevalence of 5.26% was detected, indicating silent viral circulation despite no reported human cases. These findings align with increasing CCHFV activity in southeastern Europe and underscore the importance of integrated One Health surveillance. Seroepidemiological monitoring of livestock is crucial for early detection of viral circulation and guiding prevention strategies. With ongoing ecological and climatic changes, vigilance is essential to mitigate zoonotic outbreak risks in endemic regions.

This research was supported by a grant from Climate Change Digital Twin Earth for Forecast and Societal Redressement (grant number: DTEclimate PNRR/2022/C9/MCID/15).

OP45-An epidemiological overview of the prevalence of Candida albicans in the human population of Kruja, Albania.

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Candida albicans is a member of the normal microbiota in the gastrointestinal tract, respiratory tract, vaginal area, and mouth. In healthy individuals, it does not cause disease because its growth is suppressed by other microbiota and host immune mechanisms. However, if the normal microbiota or immune competence is disrupted, *C. albicans* may proliferate rapidly and cause candidiasis. *Candida* can also be transmitted sexually and is listed by the CDC as a sexually transmitted infection (STI). No other fungal pathogen produces as diverse a spectrum of disease in humans as *Candida*. Most infections involve the skin or mucous membranes, as *Candida* is a strict aerobe and thrives on such surfaces. Considering what is said above, has been undertaken a study that demonstrates the prevalence of candidiasis infections and their impact on the human population in Kruja, Albania, during the period from January 2021 to December 2023, through an epidemiological overview. For the 1,335 individuals who tested positive in examinations conducted at the National Microbiological Laboratory of Kruja, the role of *C. albicans* was analyzed based on three main locations, gender, age groups, and months of the year during the study period.

OP46-Genotyping and Molecular Analysis of Wheat Germplasm for Resistance to Drought and Leaf Rust

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Genotyping wheat germplasm to identify genes for resistance to leaf rust and drought is crucial for breeding resilient varieties under climate change. Rising temperatures and more frequent droughts can cause yield losses of up to 17% per 1°C increase, making adaptation essential. Phenotypic assessment using the Green Seeker device identified 21 wheat lines with high NDVI values, indicating greater productivity and drought tolerance. Morphological screening revealed carriers of the dominant Hg gene, associated with pubescence and drought resistance, confirming the utility of morphological markers in selection. Pathological evaluation of 600 wheat accessions (383 spring, 217 winter) identified 110 lines resistant to leaf rust. Correlation analysis showed strong positive relationships between grains per spike and grain weight ($R=0.812$), and between 1000-grain weight and grain weight per spike ($R=0.511$), supporting their breeding value. Molecular analysis using functional markers (Vrn, Ppd, Drebl, Lr) identified lines with key stress adaptation genes. Eight promising lines outperformed standards in yield. The Vrn1 gene was present in six lines, Ppd in seven, Drebl in four; Lr10 in two, Lr29 in five, Lr68 in eight.

Three entries had rye translocation 1BL/1RS, and three carried the Lr26/Sr31/Yr9/Pm8 complex, confirming the effectiveness of molecular breeding for resilience.

This research was supported by the Science Committee of Kazakhstan (Grant No. BR 21882024).

OP47-“footprints” – social media meets knowledge discovery in a data sharing environment

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Abstract

There are three trends today that are ready for consolidation and mutual benefit -

- Social Media
- Artificial Intelligence (AI)
- Data Sharing

The advantages to consolidating these three trends under a single umbrella are significant:

1. Reusing raw data for the knowledge discovery potential that is within it recycles the data

- Recycled data is “green”
- Shared data projects can return new IP and publications to the original author for no added effort
- Saves new authors the expense of recreating the data

2. The application of AI across many industries is proving to be transformative, especially for data mining and knowledge discovery.

3. Surrounding these tools with an easy-to-use social media interface places the knowledge discovery potential in the shared data within reach of every researcher. This is especially true for researchers of the Gen X and Gen Z generations who have been raised with social media.

“footprints” is a platform which brings these three trends together and holds promise to reinvent how research work might be supplemented and advanced within a social media environment. In the “footprints” environment data sharing promotes knowledge discover.

OP48-Molecular investigation for *Toxoplasma gondii* and *Leptospira* spp monitoring in freshwater fish as passive carriers

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Recently, global fish consumption has increased significantly

together with food demand.

Also because of climate change, the transmission of re-emergent zoonotic agents is becoming impactful. Recent studies have highlighted the presence of *Toxoplasma gondii* in marine environments as well as in fish that behave as bio-indicators and passive carriers. Conversely, similar studies about another zoonotic ubiquitous pathogen, the *Leptospira* spp, have never been conducted yet. This project wants to fill this gap, by molecular monitoring (qPCR and dPCR) of *T. gondii* and *Leptospira* spp in fish of Umbrian Lakes, as epidemiological ecosystem models. At the beginning of summer an initial quota of fish was sampled and investigated. Prior to the molecular investigation, optimization workflow was carried out. After a comparison among slightly modified different DNA extraction kits using ATCC DNA strains as spike-in, the more performant methods were selected, based on the quantity of analyzed tissues after appropriate homogenization: the QIASymphony/QIAGEN® for pool (muscle, gills and bowels) and QIAamp DNA mini kit/QIAGEN® for kidney. Limit of detection (LOD) in matrix was assessed for *B1* and *LipL32* genes, resulting in about 3 hge (haploid genomic equivalents) and in about 100 hge with a cut-off of 36.8 Cq and 36 Cq, respectively. The TaqMan assays have been proven 100% specific, also after in silico check by BLAST. Research funded by Italian Ministry of Health IZSUM 07/24 RC

OP49-Substitutes for Titanium Dioxide in the Pharmaceutical Industry: Scientific and Regulatory Perspectives

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Abstract

Background: Titanium dioxide (TiO₂) has long been a staple in pharmaceutical oral solid dosage forms, appreciated for its strong whitening properties, ability to mask unpleasant tastes or odors, and chemical stability. Its high refractive index makes it especially effective as an opacifier in tablet and capsule coatings. However, growing safety concerns particularly around its nanoparticulate forms have led to increased regulatory scrutiny. In 2022, the European Commission banned the use of TiO₂ as a food additive (E171), following the European Food Safety Authority's (EFSA) conclusion that its potential genotoxicity could not be definitively ruled out. While its use in medicinal products is still permitted under transitional rules, the decision has sparked a widespread search for safer, pharmaceutically acceptable alternatives.

Purpose: This research explores potential substitutes for TiO₂ in pharmaceutical coatings and solid dosage forms, with a focus on functional performance, toxicological safety, and regulatory feasibility.

Results: The ideal TiO₂ alternative would need to match its whitening and opacifying effects, provide stability under light

exposure, and remain inert in both chemical and biological terms. Several candidates have emerged, including calcium carbonate, magnesium carbonate, zinc oxide, talc, and silica-based excipients. Of these, calcium carbonate and magnesium carbonate show the most promise due to their favorable safety profiles and broad regulatory acceptance. However, both have lower refractive indices than TiO₂, which means they offer less masking ability, often requiring adjustments to formulation design, such as increased coating thickness or different polymer systems. For manufacturers, the transition brings several technical and regulatory hurdles. Replacing TiO₂ may affect the mechanical properties of film coatings, influence light protection, or impact the overall appearance of the product. Regulatory pathways can also be complex, as any excipient change in approved products typically requires formal variation submissions, extended stability studies, and additional documentation. Authorities such as the European Medicines Agency (EMA) and national regulators have issued guidance to support TiO₂-free development, emphasizing the importance of ongoing risk-benefit assessments throughout the reformulation process.

Conclusion: Phasing out titanium dioxide in pharmaceutical products is a multifaceted challenge, but one that is increasingly pressing in light of evolving safety concerns. While no single substitute replicates all of TiO₂'s functions perfectly, certain excipient combinations and new coating strategies are showing encouraging results. Moving forward, continued innovation in excipient science—combined with open dialogue between industry and regulators—will be key to developing effective, safe, and compliant TiO₂-free formulations.

Keywords: Titanium Dioxide Substitutes, Regulatory Perspectives; Pharmaceutical Industry

OP51-Loss of CPL1 Enhances Salt Tolerance through the SOS Pathway but Causes Synthetic Lethality with *sos1* Mutation in *Arabidopsis*

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Salt stress limits plant growth and productivity, yet the roles of transcriptional co-regulators in salinity tolerance remain underexplored. C-terminal domain Phosphatase-Like 1 (CPL1) regulates RNA metabolism and stress-responsive gene expression. Here, we investigated genetic interactions between *cpl1-6* and key salt tolerance mutants (*sos1-1*, *sos3-1*, *hkt1-1*) in *Arabidopsis thaliana*. Under 50 mM NaCl treatment, *cpl1-6*, *cpl1-6sos3-1*, and *cpl1-6hkt1-1* showed enhanced salt tolerance, along with increased expression of salt-responsive genes, transcription factors, and ABA signaling components. Elevated antioxidant enzyme activity was observed in *sos3-1* and *hkt1-1* combinations. In contrast, the *cpl1-6sos1-1* double mutant displayed a severe synthetic phenotype: developmental arrest, failure to complete the life cycle, and floral defects. These plants

formed aberrant flowers with non-viable pollen or unusually thick, short pollen tubes, and only developed flower stalks and open flowers under high humidity. The findings suggest CPL1 negatively regulates salinity tolerance through the SOS pathway and that SOS1 function becomes essential in the absence of CPL1. This interaction is critical for both vegetative stress responses and reproductive development under salt stress.

OP52-Long-Read Whole Genome Sequencing Uncovers Pathogenic Variants Missed by Conventional Diagnostics: A Case Series Using Oxford Nanopore Technology

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Background

Despite the extensive use of clinical exome sequencing (CES), whole exome sequencing (WES), Sanger sequencing, and short-read whole-genome sequencing (srWGS), numerous patients with suspected monogenic disorders remain undiagnosed. These methods may fail to detect complex or non-coding variants. Oxford Nanopore Technologies (ONT)-based long-read whole genome sequencing (lrWGS) is a new approach that enables high-resolution variant detection, including structural variants and deep intronic mutations.

Methods

We applied ONT-lrWGS in six patients with persistent diagnostic uncertainty following the exclusion of CES, WES, and srWGS. The patients presented with neurodevelopmental phenotypes such as global developmental delay, speech apraxia or autism, language developmental delay, and seizures. High-molecular-weight DNA was extracted and sequenced on the PromethION Solo 2 platform. Long-read-oriented tools were applied for variant identification and interpretation.

Results

Pathogenic or likely pathogenic variants were identified in all six patients, including intronic splice-modifying mutations, structural rearrangements, and insertions previously undetectable by short-read methods. All six cases were followed by a conclusive molecular diagnosis, with clinical management and genetic counselling implications.

Conclusion

ONT lrWGS offers unequivocal diagnostic advantages, especially in neurodevelopmental disorder diagnosis, and is a consideration for application in situations with high clinical suspicion but uninformative short-read sequencing.

OP53-Determination African Swine Fever Virus presence in fresh pork meat

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African swine fever virus is a transmissible virus, resulting in important economic consequences. The indirect transmission is common, including by products originating from pigs. The aim of study was to evaluate the presence of ASFV in fresh meat originating from pigs. Nine samples of fresh pork meat were collected from local markets, located in Iasi, Romania. The samples underwent DNA viral extraction and the identification of the ASFV was performed by PCR using the protocol recommended by Agüero et al., 2003. Following the PCR assay, all the samples analyzed resulted to be negative. The validation of the test was assessed by using positive and negative controls. This negative result suggests that in the study area, the verification of animal's status prior slaughtering is correctly done and the products resulted are safe. Many studies have confirmed the role of meat in virus spreading. However, this study has a limitation, given the low number of the tested samples and possibly the low quantity of viral DNA in samples.

Funding: Program of the Ministry of Agriculture and Rural Development of Romania, project ADER 10.1.1. 2024-2026.

OP54-Preliminary Analysis of Oxidative Stress Profile in Skin Samples of *Streptococcus equi* infected Foal compared to Healthy Individual

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Despite the clinical increasing importance of oxidative stress in veterinary medicine, research investigating oxidative stress markers in horses remains remarkably limited. This study addressed this knowledge gap by evaluating oxidative stress dynamics in skin samples obtained from a 7-days-old foal with confirmed systemic *Streptococcus equi* infection compared to a healthy 10-months aborted fetus from twin pregnancy as control. Biochemical assays revealed significantly decreased catalase (44% of control) and superoxide dismutase (58% of control) enzymatic activities and lower levels of reduced glutathione (34% of control) in infected sample compared to control, indicating impaired antioxidant defences. The other oxidative stress markers demonstrated markedly elevation, as revealed by lipid peroxidation and protein oxidative damage (an increase of malondialdehyde and advanced oxidation protein products by 2 and 1.7 times of control, respectively). Histological examinations from both samples confirmed preserved skin integrity, confirming that the biochemical results reflect oxidative stress in the absence of noticeable tissue degenera-

tion. These preliminary findings indicate oxidative imbalance in equine bacterial infections, suggesting disrupted redox homeostasis in *Streptococcus equi* infected foal skin and supporting further research into antioxidant therapies.

OP55-Morphological and Genome Analysis of a Novel *Clostridium perfringens* Phage CPP1_HSI_ASKI Isolated from Wastewater in Türkiye

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Abstract

Clostridium perfringens causes various systemic and enteric diseases affecting humans and animals, posing serious health risks, especially due to antibiotic resistance. Bacteriophages provide a promising alternative therapeutic approach. In this study, we isolated a novel lytic *C. perfringens* phage, CPP1_HSI_ASKI, from wastewater targeting *C. perfringens* type A ATCC 13124. Transmission electron microscopy revealed that CPP1_HSI_ASKI exhibits a short non-contractile tail and icosahedral head, characteristic of podoviruses. The genome is a 17,814 bp linear double-stranded DNA with 28.3% GC content. Among 21 predicted open reading frames, 12 encode functional genes (GenBank accession PP973485). No tRNA, virulence, lysogenic, or antibiotic resistance genes were detected. Phylogenetic analysis indicates CPP1_HSI_ASKI is a novel species within Gregsiragusavirus (family *Guelinviridae*). To our knowledge, this is the first report of a *C. perfringens* phage isolated in Türkiye. These findings highlight its potential for controlling *C. perfringens* infections.

OP56-Valorization of brewery organic waste by products for sustainable livestock feed

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Abstract

This study focuses on the effective management and utilization of solid waste, particularly organic by-products, generated in breweries in Albania. The primary aim is to assess the nutritional potential of brewery spent grains (BSG), hot trub, cold trub, and spent yeast for use in animal feed. The project aims to explore sustainable practices that can reduce waste, lower feed

costs, and contribute to environmental sustainability through the effective use of these by-products.

BSG, spent yeast, and trub are underutilized yet valuable by-products of the brewing process. These materials are rich in proteins, fibers, vitamins, and minerals, making them excellent sources of nutrition for animals. BSG, in particular, is a cost-effective and sustainable option for animal feed due to its high nutritional content and energy value. Furthermore, its incorporation into animal feed not only adds value to brewery waste but also reduces environmental impact by minimizing waste and contributing to a circular economy. The addition of spent yeast and hot and cold trub to animal feed formulation significantly enhances the nutritional profile, providing additional protein, amino acids, vitamins, minerals, and fiber. This adjustment allows for a reduction in traditional ingredients like soybean meals, fish meal, maize meal, and alfalfa. BSG can be used up to 25% especially if it is a fermented one. Spent Yeast rich in protein, amino acids, and B-vitamins, replacing part of the soybean meal and fish meal. Hot trub and cold trub provide protein, fiber, soluble sugars, and antioxidants, replacing some maize meal.

This modified feed formulation ensures a balanced, cost-effective diet, improving the nutritional quality of the feed while reducing reliance on traditional feed ingredients. It supports a sustainable and economical feeding strategy for livestock.

Keywords: Brewery spent grains (BSG), animal feed, organic waste management, nutritional value, spent yeast, hot trub, cold trub.

OP57-The differentiating role of sphingomyelin in the central nervous system

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Sphingomyelin (SM) is involved in brain pathophysiology, as evidenced by its dysregulated metabolism, which appears to be implicated in neurodegenerative diseases. It also plays structural roles, being a major constituent of the myelin sheath. At the intracellular level, SM is involved in the formation of lipid rafts, microdomains of the inner nuclear membrane composed of SM and cholesterol, which serve as platforms for the interaction between SM and vitamin D receptor, essential for vitamin D3 (VD3) activity. These molecules play important roles in brain function and pathophysiology.

Considering the relevance of SM and VD3 for the brain, the aim of this study was to investigate the effect of a SM + VD3-enriched diet for 4 months in rabbits. The results showed a pro-differentiating effect of daily administration of SM + VD3, as demonstrated by an increase in GFAP expression in the white matter of the brain, a marker of neurodifferentiation. Moreover,

an increase in ceramide and hexosylceramide levels was observed, which are molecules relevant for the structure, function and stability of myelin.

Taken together, these findings demonstrate that SM + VD3 promote neurodifferentiation, suggesting a potential role in facilitating the maturation of the nervous system in premature infants or to prevent neurodegeneration.

OP58-A Novel Machine Learning Algorithm for Enhanced Polygenic Risk Score Estimation

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Abstract:

Introduction: Polygenic Risk Scores (PRS) is a statistical measure used to quantify the genetic predisposition to complex diseases based on the cumulative effect of multiple genetic variants. While PRS has shown promise in predictive medicine, its accuracy and generalizability remain limited by methodological constraints and population biases.

Materials and Methods: We developed a novel machine learning-based algorithm integrating some methods PCA or SVM techniques with variant prioritization filters tailored to disease-specific genetic architectures. The model was trained and validated on publicly available genome-wide association study (GWAS) datasets and benchmarked against traditional PRS methods. Preprocessing included imputation, normalization, and principal component analysis to control for population stratification.

Results: The algorithm demonstrated a significant improvement in predictive performance, over classical PRS models in testing cohorts. It outperformed standard linear models, especially in the studied diseases with polygenic signatures.

Conclusions: Our approach highlights the potential of machine learning to enhance PRS estimation by incorporating non-linear interactions and adaptive feature selection. This method could contribute to more accurate risk stratification in personalized medicine.

Keywords: Polygenic Risk Score, Machine Learning, GWAS, Genetic Prediction, Gradient Boosting, Personalized Medicine

OP59-Application of Liquid Chromatography Mass Spectrometry for High Resolution Proteomics in Bovine Ovary Function

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many

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Abstract

This study objective was to identify protein expression in the bovine corpus luteum (CL) across various phases of the estrous cycle (days 1–2, 3–4, 5–7, 8–12, 13–17, and >18) and different stages of pregnancy (months 1–2, 3–4, 5–6, and >7). The CL, a temporary ovarian gland, plays a vital role in hormone secretion and sustaining pregnancy. The primary aim was to examine the temporal dynamics of protein profiles throughout the CL's functional lifespan and to assess their potential impact on reproductive physiology. To achieve this, a proteomic analysis was conducted using high-resolution liquid chromatography-mass spectrometry (LC-MS/MS). We successfully identified around 1900 proteins expressed across all the investigated cohorts. Protein expression data were grouped based on patterns identified by the self-organizing tree algorithm (SOTA), revealing six clusters with shared regulatory trends. Notably, expression changes and protein abundance during pivotal periods, such as the shift from active CL to regression is crucial in determining whether the CL is preserved or undergoes involution. The findings demonstrate that specific proteins are consistently present, with expression levels varying significantly on reproductive stages. We identified signaling pathways like ECM remodeling, ROBO, NOTCH, WNT, Hedgehog, hypoxia response, and RUNX, which work together to support corpus luteum formation and function by guiding structural remodeling, vascular development, luteal cell differentiation, and proliferation. These results underscore the need for further investigation into the molecular mechanisms governing CL function, particularly those influencing luteal maintenance, regression, follicular maturation, and hormonal regulation in cattle.

OP60-Metabolic Response to Ultraviolet Radiation of Some Agroindustrial Plant Species – a Biotechnological Approach

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The experiments were focused on the response of some plant species of agroindustrial interest following vegetal embryos exposure to ultraviolet radiation. We evidenced metabolic changes in young plantlets exposed to UV-C radiation during early ontogenetic stages. Total soluble protein content was found linearly increased with ultraviolet radiation dose. Antioxidant enzymes were found differently changed, with a progressive decreasing trend of superoxidedismutase activity but with non-linear response of catalase. The lipid peroxidation indirect

marker, the malondialdehyde content changed differently for relatively low radiation exposure levels compared to the higher ones quite similar to catalase activity variation which suggested complex processes of plant cells ability to deal with oxidative stress. Box-plot approach was applied to describe the comparative statistical distributions of plant roots and stems that revealed stimulatory bioeffects on plant growth in the case of relatively low energy impact, the photoassimilatory pigments being found changed accordingly. Genetic impact expressed as chromosomal modifications were evidenced in the vegetal embryos metaphase sustaining the use of biotechnological tool based on ultraviolet C radiation exposure.

OP61-Autonomous Vascular Route Opening Device for Military Terrain Conditions

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In situations where access to healthcare services is limited or non-existent, such as field conditions, battlefields or terrorist attacks, delays in the first medical aid for injured people to be applied by healthcare personnel lead to an increase in the loss of lives. In order to develop a solution to this problem and to increase the survival rates of the injured military personnel in the field, this project was initiated in order to develop an easy-to-use and portable device prototype that facilitates the first aid by opening an autonomous vascular access in scenarios where there is no access to medical personnel and does not require the presence of healthcare personnel and can be used in the future by military personnel without medical training, and aims to reduce the loss of lives. The intended device prototype determines the coordinates of the veins with the Near Infrared (NIR) Imaging and transmits it to the automatic needle guidance system inside the vein, and the needle system detects the entry into the vein at the appropriate angle with the pressure sensor and re-adjusted the system in the appropriate position with the feedback mechanism.

Keywords: field conditions; first aid; vascular access; autonomous; Near Infrared (NIR)

OP62-Evaluations on some quantitative parameters of the stocks of *Salmo letnica* and *Salmo ohridanus* as well as on the analytical indicators that express the levels of exploitation of them from the professional fisheries

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Abstract

In this study some notions (or, indicators of the fisheries management) of fishing science [species specific production ratio

(*P/B*); catch per unit effort (*CPUE*) and maximum sustainable yield (*MSY*)] have been applied to the analysis of the commercial catches of 2023, of two endemic trouts (*Salmo letnica* and *S. ohridanus*), from the Ohrid Lake. The assessments on the catches of Ohrid trout and Ohrid belvica resulted in the respective values for the *P/B*-indicator: 0.559/yr and 0.791/yr (using the data on the variable *B*, kg/ha); 0.284/yr and 0.262/yr (using the protocol of Hoening, 1983) as well as 0.151/yr and 0.259/yr (the protocol according to Randall and Minns, 2000). The values estimated for *CPUE* were: *CPUE*_{Tc}=0.520 kg/hr/ou (according to total catches); *CPUE*_{Ot}=0.312 kg/hr/ou (according to Ohrid trout catches); *CPUE*_{Ob}=0.087 kg/hr/ou (according to Ohrid belvica catches) and *CPUE*_{Sal}=0.400 kg/hr/ou (according to salmonid fishes catches). The values resulted from the estimations about *MSY*, were: *MSY*_{Ot}=2.15 kg/ha, in the exploitation of Ohrid trout and *MSY*_{Ob}=0.40 kg/ha, in the exploitation of Ohrid belvica.

Keywords: endemic species, stock, biomass, catch per unit effort, fishing effort.

OP63-Biotechnological advances in lipid-lowering therapies - shaping the future of dyslipidemia treatment

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Dyslipidemia remains one of the most common modifiable risk factors for cardiovascular diseases worldwide, with its prevalence still rising in both developed and developing countries. The widespread use of conventional therapies has significantly improved outcomes in reducing the cardiovascular risk. However, there is still a considerable proportion of patients – especially those in the high and very high-risk population – who fail to achieve the LDL-C targets recommended by clinical guidelines.

Recent biotechnological advances have introduced novel lipid-lowering therapies, such as PCSK9 inhibitors, siRNA-based agents, and other emerging approaches that offer more sustained LDL-C reduction with less frequent dosing. These not only have improved treatment effectiveness but also have significantly increased patient adherence.

This review will explore these novel biotechnological therapeutic options in dyslipidemia management, their clinical relevance, and their role in shaping the future toward a more precise, predictive, and preventive cardiovascular medicine – moving closer to the goals of personalized medicine.

OP64-Valorization of the invasive ascidian *Styela plicata* from mussel aquaculture systems: metabolite profiling and bioactivity screening

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Invasive ascidians pose considerable challenges to aquaculture, often leading to economic and ecological burdens. However, their potential as sources of bioactive compounds offers a unique opportunity to convert these challenges into valuable biotechnological resources. This study aimed to explore the biotechnological potential of *Styela plicata* from a mussel aquaculture in the Albufeira Lagoon (Portugal), by evaluating its chemical profile and biological activities, including antimicrobial, antibiofilm, and anticancer properties. LC-MS/MS metabolite profiling identified 21 major compounds spanning several classes: alkaloids/amines (e.g., benzamil, lepidimoic acid, lyngbyatoxin, becatecarin), lipids/fatty acid derivatives (e.g., cer(d18:0/16:0), stearic acid), nucleosides/nucleobases (e.g., hypoxanthine, uridine), amino acids (tyrosine, phenylalanine), aromatic halogenated 2,3,4,5,6-pentachlorobenzyl alcohol, and sterol 5b-cholestane-3b-ol.

Bioactivity assays revealed that all extracts (SP1-SP3) significantly inhibited *Staphylococcus aureus* biofilm formation without affecting bacterial growth. SP1 showed the highest potency with a minimum biofilm inhibitory concentration (MBIC) of 15.62 µg/mL, while SP3 demonstrated the strongest inhibition (81%) at higher concentrations 250 µg/mL. SP3 also showed cytotoxic activity against HCT-116 colorectal cancer cells.

These findings support the valorization of *S. plicata* as a sustainable source of bioactive compounds, offering ecological and biotechnological benefits. The study promotes its use within circular economy frameworks, transforming a biofouling challenge into a pharmaceutical and industrial opportunity.

Funding: This work was financed by national funds from FCT—Fundação para a Ciência e a Tecnologia, IP, in the scope of the project UIDP/04378/2020 of the Research Unit on Applied Molecular Biosciences—UCIBIO and the project UID/50006/2023 of the Associate Laboratory for Green Chemistry- LAQV REQUIMTE. C.M.P.R. is financially supported by grants from FCT—Fundação para a Ciência e Tecnologia (Grant No PTDC/MED-FAR/3492/2021) and La Caixa Foundation (Grant No LCF/PR/HR21/52410028).

OP65-Aseptic Process Simulation (Media Fill) for Injectable

Manufacturing at Profarma sh.a: Validation of Sterility Assurance Under Routine and Worst-Case Conditions

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Introduction: At Profarma sh.a, maintaining sterility in the manufacturing of injectable drug products is a top priority. To ensure the process consistently meets high standards, a validated Aseptic Process Simulation (APS) commonly referred to as a media fill is carried out. This simulation replaces the actual product with a sterile growth medium, tryptic soy broth (TSB), and replicates the entire aseptic process under conditions that reflect both typical operations and worst-case scenarios.

Purpose: The goal of this study is to demonstrate that the aseptic process, cleanroom environment, and operator practices at Profarma sh.a can reliably prevent microbial contamination during injectable drug production.

Methods: The media fill mimics every critical step of the aseptic process, including component preparation, sterile filtration, vial filling, equipment setup, line clearance, and both routine and non-routine operator interventions. The simulation is conducted using representative batch sizes (1 mL and 2 mL), across normal production shifts and line speeds, while deliberately introducing stress conditions—such as prolonged filling times, slower line operation, and increased operator activity—to challenge the system. After filling, all units are incubated under controlled conditions (20–25°C for 7 days, then 30–35°C for 7 days) and visually inspected for any signs of microbial growth. Acceptance criteria are based on current EU GMP Annex 1 and FDA aseptic processing guidance.

Results: The media fill runs at Profarma sh.a were successfully completed, confirming that the aseptic process remains in a validated state of control. These simulations reinforce confidence in the facility's sterility assurance and are performed not only during initial validation but also annually for requalification and following significant changes in equipment, process, or personnel fully aligned with Profarma sh.a quality risk management approach.

Keywords: Aseptic Process Simulation, Media Fill, Injectable Drug Products, Sterile Manufacturing, Tryptic Soy Broth (TSB)

OP66-Antioxidant Potential of Some Albanian Medicinal Plants and Challenges of Their Inclusion in Semi-solid Preparations

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Abstract:

Albania, due to its favourable climatic conditions, including humidity, temperature and natural biodiversity, is home to a wide variety of medicinal plants. Many of these species have been traditionally used in dermatology and skin care. This narrative review is focused on the antioxidant phytochemicals of selected Albanian medicinal plants such as *Salvia officinalis*, *Hypericum perforatum* L., *Syderitis syriaca* and *Rosmarinus officinalis*. It evaluates the challenges of incorporating their extracts into semi-solid preparations. A literature search was conducted using main databases such as PubMed, ResearchGate and the CAB digital library, identifying research articles, emphasising both phytochemical profiles and formulation barriers. While studies confirm significant antioxidant effects of these plants attributed to their polyphenolic components and essential oils, several formulation-related constraints are evidenced, such as instability of active components, poor solubility and sensitivity to oxidation. Technological approaches including encapsulation methods and nanoemulsion systems are proposed as promising solutions to enhance stability, efficacy and skin penetration. In conclusion, the Albanian medicinal plant resource combined with biotechnological innovation represents a promising binomial for the development of antioxidant-based dermocosmetic products.

Keywords: Albania, medicinal plants, antioxidants, phytochemicals, semi-solid formulations, formulation challenges

OP67-Substitutes for Titanium Dioxide in the Pharmaceutical Industry: Scientific and Regulatory Perspectives

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Abstract

Background: Titanium dioxide (TiO₂) has long been a staple in pharmaceutical oral solid dosage forms, appreciated for its strong whitening properties, ability to mask unpleasant tastes or odors, and chemical stability. Its high refractive index makes it especially effective as an opacifier in tablet and capsule coatings. However, growing safety concerns particularly around its nanoparticulate forms have led to increased regulatory scrutiny. In 2022, the European Commission banned the use of TiO₂ as a food additive (E171), following the European Food Safety Authority's (EFSA) conclusion that its potential genotoxicity could not be definitively ruled out. While its use in medicinal products is still permitted under transitional rules, the decision has sparked a widespread search for safer, pharmaceutically acceptable alternatives.

Purpose: This research explores potential substitutes for TiO₂ in pharmaceutical coatings and solid dosage forms, with a focus on functional performance, toxicological safety, and regulatory feasibility.

Results: The ideal TiO₂ alternative would need to match its whitening and opacifying effects, provide stability under light

exposure, and remain inert in both chemical and biological terms. Several candidates have emerged, including calcium carbonate, magnesium carbonate, zinc oxide, talc, and silica-based excipients. Of these, calcium carbonate and magnesium carbonate show the most promise due to their favorable safety profiles and broad regulatory acceptance. However, both have lower refractive indices than TiO₂, which means they offer less masking ability, often requiring adjustments to formulation design, such as increased coating thickness or different polymer systems. For manufacturers, the transition brings several technical and regulatory hurdles. Replacing TiO₂ may affect the mechanical properties of film coatings, influence light protection, or impact the overall appearance of the product. Regulatory pathways can also be complex, as any excipient change in approved products typically requires formal variation submissions, extended stability studies, and additional documentation. Authorities such as the European Medicines Agency (EMA) and national regulators have issued guidance to support TiO₂-free development, emphasizing the importance of ongoing risk-benefit assessments throughout the reformulation process.

Conclusion: Phasing out titanium dioxide in pharmaceutical products is a multifaceted challenge, but one that is increasingly pressing in light of evolving safety concerns. While no single substitute replicates all of TiO₂'s functions perfectly, certain excipient combinations and new coating strategies are showing encouraging results. Moving forward, continued innovation in excipient science—combined with open dialogue between industry and regulators—will be key to developing effective, safe, and compliant TiO₂-free formulations.

Keywords: Titanium Dioxide Substitutes, Regulatory Perspectives; Pharmaceutical Industry

OP68-Whole-Cell Fiber-Optic Biosensor for Real-Time, On-Site Sediment and Water Toxicity Assessment: Applications at Contaminated Sites Across Israel (SUNDANSE)

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Abstract

Monitoring toxicants in aquatic environments, especially within sediments, is crucial for assessing the impact of pollutants

on ecosystems. Conventional chemical analyses often fail to capture bioavailability, biological relevance, and cumulative effects. In this study, we developed a portable whole-cell fiber-optic biosensor for real-time on-site toxicity monitoring. The biosensor houses a highly sensitive photo-multiplier tube (PMT) that counts photons produced by bacterial reporter cells in response to environmental stressors. The bacterial cells are immobilized within a calcium-alginate matrix on fiber-optic tips, transmitting the photons directly to the PMT. The biosensor was deployed at four potentially contaminated rivers/streams across Israel. Samples were tested by directly submerging the fiber tip with immobilized bacteria into vials containing either water or sediment samples from the tested sites, and the bacterial bioluminescent responses were acquired. Complementary liquid chromatography-mass spectroscopy (LC-MS) and inductively coupled plasma optical emission spectroscopy (ICP-OES) provided chemical characterization. Results revealed various induction factors (I.F.) values, representing the different toxicity levels between the tested sites. The Be'er-Sheva stream was found to be the most contaminated (I.F. = 3.72) compared to the standard inducer, 1% ethanol (I.F. = 1.67). The results demonstrated the biosensor's efficacy in detecting various toxicity levels corresponding to identified contaminants by LC-MS, showcasing its potential integration into environmental monitoring frameworks for enhanced sediment and water quality assessments. Despite its utility, the study notes the system's operational challenges in field conditions, recommending future enhancements for improved portability and usability in remote locations.

Keywords: bioreporter; bioluminescent bacteria; optical-fiber biosensor; water toxicity; sediment toxicity; in-situ monitoring; whole-cell biosensor

OP69-Genetic diversity of 3 Albanian local goat breeds based on 10 microsatellite analysis

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Abstract

The conservation and sustainable use of farm animal genetic resources (AnGR) have become global priorities due to the rapid decline of local breeds and the increasing homogenization of livestock populations. Albania, with approximately 774,000 goats, relies heavily on small ruminants for meat and milk production, particularly in mountainous areas where local breeds remain essential for rural livelihoods. However, the absence of herd books, small and fragmented populations, and unstructured breeding practices pose risks for genetic erosion. This study provides a comprehensive genetic characterization of three Albanian local goat breeds, Velipoja, Dragobia,

and Smokthina, using 10 highly polymorphic microsatellite markers to evaluate allelic diversity, heterozygosity, population structure, gene flow, and inbreeding levels. Across all loci, a high number of alleles and satisfactory levels of genetic diversity were observed, confirming the rich genetic base of Albanian goats. Dragobia goats exhibited the highest allelic diversity, while Velipoja presented several private alleles, underlining their importance for conservation programs. Smokthina goats, although slightly less diverse, maintained good allelic richness. Observed heterozygosity (H_o) was lower than expected heterozygosity (H_e) in all breeds, suggesting potential inbreeding, small effective population sizes, or non-random mating patterns. The overall inbreeding coefficient ($F_{IS} = 0.143$) indicated a significant heterozygosity deficit. Population differentiation among breeds was remarkably low (global $F_{ST} = 0.018$), with AMOVA results showing only 1.89% of total genetic variation attributed to differences among breeds. Pairwise genetic distances and high gene flow estimates (N_m ranging from 8.09 to 28.80) confirmed substantial admixture, reflecting traditional breeding practices where bucks are frequently exchanged between herds. STRUCTURE and factorial correspondence analyses further supported weak breed clustering and extensive genetic overlap among populations. This genetic baseline provides a foundation for national breeding policies and supports FAO-aligned strategies for sustainable management of Albania's goat biodiversity.

Key words: Genetic diversity; Goat breeds; Population structure; Inbreeding; Conservation genetics; Gene flow;

POSTER PRESENTATION ABSTRACTS

PP1-Challenges in transfection of the halophytic microalga *Dunaliella salina*

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During a SINO-MALTA project funded by Xjenza Malta, the local national contact point for European projects, we attempted to genetically modify the *Dunaliella salina* halophytic microalga in order to express a peptide antibiotic produced as a derivative of the zebrafish yolk protein phosvitin, in order to allow scale up biological production. Following a review of the literature, four methods were identified as successful methods for such transfection, most of which used the herbicide glufosinate (phosphinothricin). These included electroporation, glass beads-mediated transfection, osmotic shock-based transfection and lithium acetate based transfection.

The *Dunaliella salina* strain obtained from a commercial collection was inherently resistant to high doses of glyphosate making the herbicide useless in selection of transformants. For this reason, we eventually switched to puromycin resistance.

The four published methods, two of which described successful transfection rates of more than 1% all appeared to be ineffective in transfecting the *Dunaliella*, despite trying different background salinity levels and cellular concentrations. A modification of the calcium phosphate methodology commonly used in mammalian cell transfection proved more successful than any of these methods and is now being further developed in the lab.

PP2-Predicting wheat yield for multiple cultivars based on agroclimatic factors

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Abstract:

This study aimed to assess the yield of four durum wheat cultivars (ODYSSEO, SARAGOLA, IRID, and MAESTRALE) using two machine learning techniques: Classification and Regression Trees (C&RT) and Random Trees (RT). The C&RT analysis demonstrated that the annual average temperature (A.A.T.) is the dominant factor influencing yield across all cultivars. For the SARAGOLA, IRID, and MAESTRALE cultivars, yield increased significantly when A.A.T. exceeded 17.25°C, particu-

larly when emergence density was optimal. Conversely, the ODYSSEO cultivar displayed sensitivity to both A.A.T. and seeds per spike, with higher yields associated with A.A.T. above 17.25°C and seeds per spike exceeding 33.6. The RT analysis confirmed the importance of A.A.T. and emergence density, highlighting their strong predictive power. The models provided enhanced robustness and generalization capacity by reducing prediction variance, making them reliable tools for yield prediction. These findings underscore cultivar-specific responses to agroclimatic conditions, where ODYSSEO is influenced by both A.A.T. and seeds per spike, while SARAGOLA, IRID, and MAESTRALE demonstrate a critical interaction between A.A.T. and emergence density. The integration of RT models improves prediction accuracy and offers valuable insights for developing precision agriculture strategies tailored to environmental conditions.

PP3-Genetic Variability of *Callinectes sapidus*: Evidence of a Species Complex.

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The Atlantic blue crab, *Callinectes sapidus*, is an invasive species in the Mediterranean, threatening biodiversity and ecosystems. This study explores its distribution dynamics and evolutionary history through phylogeographic and phylogenetic analyses of 667 mitochondrial Cytochrome c Oxidase subunit I (COI) gene sequences. Of these, 36 were newly collected from under-investigated Mediterranean sites, while 631 were obtained from literature, representing global populations. Results identified two distinct but closely related genetic groups, potentially representing sister species and suggesting, for the first time, the existence of a species complex for *C. sapidus*: one predominantly found in South and Central America and the other in North America and the Mediterranean. Mediterranean populations exhibited general mitochondrial homogeneity,

indicating a recent introduction. Turkish populations showed early signs of differentiation, likely due to a longer-established presence in the region. Our findings improve understanding of the species genetic variation, offering valuable insights into its taxonomic status thus supporting management strategies.

PP4-Bridging predictive modeling and traditional statistics for clinical risk factor identification: an innovative framework for precision medicine

Valentina Agelvis, Andres Paredes, Sofia Godoy, Rafael Valdivieso and Lilibeth Niño

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The identification of clinical risk factors remains a cornerstone in the prevention and management of high-burden diseases such as dengue, diabetes, and cardiovascular disorders. While traditional statistical models provide transparency and ease of interpretation, they are limited in handling nonlinear interactions and high-dimensional datasets. In contrast, machine learning (ML) methods achieve superior predictive performance but face barriers to clinical adoption due to their “black-box” nature. This review proposes a novel hybrid framework that leverages the interpretability of classical statistics with the predictive accuracy of ML. By systematically comparing recent applications in dengue risk stratification, metabolic complications, and cardiovascular events, we highlight scenarios in which each method excels and where their integration may overcome current limitations. Our synthesis demonstrates that statistical models remain invaluable in hypothesis-driven analyses and small clinical cohorts, whereas ML achieves substantial gains—up to 20% higher AUC-ROC—in large datasets with complex variables. The originality of this proposal lies in the clinical translation: hybrid models that embed regression coefficients within predictive pipelines could provide both accuracy and interpretability, facilitating acceptance by healthcare professionals and regulatory bodies. We argue that the future of clinical risk factor prediction will not rely on the dominance of one approach over the other, but on their convergence within precision medicine strategies.

Keywords: Clinical risk factors; Hybrid modeling; Machine learning; Statistical models; Precision medicine; Artificial intelligence.

PP5-Evaluating Bryne's classification for prognostic purposes in feline squamous cell carcinoma

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Feline squamous cell carcinoma (SCC) represents a highly aggressive malignancy, particularly in oral and cutaneous forms. The aim of this study was to assess the prognostic value of Bryne's classification system for feline oral and cutaneous SCC in a subset of neoplastic samples collected from ten European breed cats (8 females and 2 males). Most tumors originated in the auricular area, followed by the oral cavity. Senior cats were predominant. The tumors were evaluated using Bryne's parameters: degree of keratinization, nuclear polymorphism, number of mitoses, and pattern of invasion. The mean total score was 10, classifying tumors as moderately differentiated.

There were no statistically significant correlations between tumor location (oral versus cutaneous) and total score or between diagnosis and total score. Similarly, age and sex showed no significant association with the total score.

While Bryne's classification provides a structured solution to grading feline SCC, tumor severity as measured by this system was not significantly affected by age, sex, or tumor location in this study. A broader range of biological and molecular investigations is needed to find effective prognostic markers in feline SCC.

PP6-Use of Predictive Computational Models for Clinical Risk Factors Analysis in Dengue

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Abstract

Dengue represents a major global public health challenge, with millions of cases reported annually, especially in tropical and subtropical regions. Early identification of clinical risk factors is essential to prevent progression to severe forms such as dengue hemorrhagic fever. In this context, predictive models based on computational techniques such as machine learning (ML) have emerged as promising tools for risk stratification, clinical prognosis, and therapeutic decision-making. This article reviews recent advances in the application of ML techniques in predicting clinical risk factors for dengue, highlighting their integration with biotechnological approaches to improve epidemiological surveillance and personalized medicine.

PP7-Surface Wettability Modification with the Development of Structural Features of Transparent Conductive Oxide Thin Films Prepared by Sol-Gel Technique

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Abstract

Transparent conductive oxides (TCOs) are smart materials

characterized by their wide band gap, high transparency in the visible region (400–700 nm), and excellent electrical conductivity. These properties make them suitable for a wide range of applications, including photovoltaic cells, light-emitting diodes, gas sensors, and flat panel displays (FPDs). Sol-gel-derived coatings are of particular interest, as they can modify surface properties, enhance protection, and provide functional advantages in intelligent system technologies. The sol-gel technique is a cost-effective, simple, and scalable method for synthesizing homogeneous and conformal TCO thin films.

In this study, oxide precursor solutions of copper, aluminum, zinc, tin, and titanium (0.1 M) were synthesized using the sol-gel method. Thin films were prepared by dip-coating with 10 layers, followed by annealing at 500 °C for 1 hour. The surface wettability of the films was investigated through contact angle measurements, which revealed the characteristic surface interactions of the TCO coatings with water droplets. It is observed that the amount of TiO₂ in the solution directly effects the wettability properties of TCO thin films. With increasing TiO₂ percentage, the contact angle values are decreased.

Keywords: Thin films, TCO, Sol-gel method, Contact angle

PP8-Exploring the therapeutic value of EU-GMP certified Cannabis sativa L. in Alzheimer's-related neuropathic pain: preclinical evidence

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Chronic pain affects over 45% of individuals with Alzheimer's disease (AD), yet the underlying mechanisms linking pain and neurodegeneration remain poorly defined. Both conditions are multifactorial and may involve dysregulation of the endocannabinoid system (ECS), which represents a promising therapeutic target. Persistent pain has been associated with accelerated cognitive decline and increased dementia risk. However, the role of the ECS in AD patients experiencing chronic pain is largely unexplored, and clinical evidence supporting cannabinoid-based interventions is limited. This preclinical study investigates the therapeutic potential of an EU-GMP certified Cannabis sativa L. product (Cannabixir® Medium Flos) in a rat model of AD with comorbid neuropathic pain. Animals received 5 mg/kg in a chronic intermittent dosing schedule. Cognitive and nociceptive outcomes were assessed using clinical observation, behavioral tests and tissue analysis to examine cognitive and nociceptive changes. Results indicate that Cannabixir® Medium Flos was well tolerated and led to improvements in mechanical and thermal pain sensitivity, alongside

histological markers suggestive of neuroprotection and cognitive benefit. These preliminary findings support the hypothesis that cannabinoid-based therapies may modulate neuroinflammatory and nociceptive pathways, warranting further investigation into their potential application in neurodegenerative diseases with comorbid chronic pain.

Funding: This research was funded by a grant of the Ministry of Research, Innovation and Digitization, CNCS - UEFISCDI, project number PN-IV-P2-2.1-TE-2023-0879, within PNCDI IV and by a project under The Health Program (PS) 2021-2027, Policy Objective 1, Priority 5, project title "Development of translational research for vaccines, serums and other biological drugs - Acronym CANTAVAC 2.0", SMIS code 326920.

PP9-Transcriptomic biomarker development pipeline – Monitoring off-label therapy in anaplastic thyroid cancer in extracellular vesicles

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Abstract

Extracellular vesicles (EVs) are membrane-enclosed particles secreted by all cells and present in all biofluids, where they protect RNA from degradation. EV-associated cell-free RNA holds great promise as a biomarker source in liquid biopsies. Our group has developed and published a pipeline for the development and analysis of such EV-associated transcriptomic biomarkers and successfully applied it in several studies. Here, we illustrate the use of our pipeline, using an example from off-label treatment of anaplastic thyroid cancer with vandetanib. Cal62 cells were treated *in vitro* with different concentrations of vandetanib, followed by concentration and characterization of EVs from the supernatant. We applied dimensional reduction and pathway analysis to cellular RNA sequencing and label-free proteomics data of the cells and EVs to identify biomarker candidates for the early evaluation of therapy success. Ultimately, we propose eight transcripts as an EV-associated biomarker signature, which we successfully validated in the cellular and cell-free RNA. At each stage of the showcased pipeline, we highlight key bioinformatic tools, potential pitfalls, and considerations for optimizing biomarker discovery. Finally, we outline critical challenges in validating RNA biomarker signatures using RT-qPCR.

PP10-Experimental Application of Induced Pluripotent Stem Cells (iPSCs) in the Treatment of Autoimmune Thrombocytopenia: Benefits, Limitations, and Potential Risks

Marsela SHANI¹, Treisi GOXHAJ²

Introduction: Induced Pluripotent Stem Cells (iPSCs) are cells generated through the genetic reprogramming of mature somatic cells, with significant potential in tissue regeneration, disease modeling, and cell therapy. They represent a valuable alternative to embryonic pluripotent stem cells due to the absence of ethical dilemmas and the possibility of genetically personalized treatment.

Objective: To explore the potential application of iPSC-based therapy in the treatment of a clinical case of persistent autoimmune thrombocytopenia resistant to conventional therapies, as well as to analyze the biological risks associated with this experimental approach.

Methodology: A clinical case of a 36-year-old patient with immune thrombocytopenic purpura (ITP) onset in childhood, treated with immunoglobulin therapy and splenectomy at the age of six. The patient presents with symptomatic disease relapse and severe thrombocytopenia. A proposed intervention involves the use of iPSCs generated from the patient's fibroblasts, reprogrammed using Oct3/4, Sox2, Klf4, and c-Myc factors to produce functional megakaryocytes and restore healthy thrombopoiesis.

Results: The therapy potentially avoids the need for surgical intervention or long-term immunosuppression. However, the risk of teratoma formation, immune rejection from incompletely differentiated cells, and leukemogenic transformations poses a major challenge, necessitating rigorous evaluation of cellular purification protocols prior to transplantation.

Conclusions: The use of iPSCs in the treatment of autoimmune hematologic disorders remains under investigation. Further in-depth studies are required to ensure full differentiation control, oncological safety, and the avoidance of immune responses against induced cells. Despite these challenges, iPSCs offer a real opportunity for personalized therapies with significant impact on the future of regenerative medicine.

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PP11-How Smart Are AI Tools in Classifying BRCA1 Missense Variants?

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Abstract

Background:

BRCA1 is one of the most extensively studied cancer susceptibility genes, and its variants are relatively well annotated in public databases such as ClinVar. This study evaluates the classification performance of four AI-based tools-ChatGPT, Claude, DeepSeek, and Gemini-for BRCA1 missense variants.

Materials and Methods:

Missense variants in BRCA1 were selected from ClinVar. Only variants with at least two-star review status (Multiple Submitters) were included. Filtering criteria included: (1) Selection of missense SNVs; (2) Stratification into four ClinVar-based categories: *Pathogenic only*, *Likely Pathogenic only*, *VUS only*, and *Likely Benign/Benign*; (3) Random selection of five variants per group using Random.org. All AI tools were instructed to base their classifications solely on biological features and population frequency (via gnomAD), without referencing clinical databases such as ClinVar, Franklin, or VarSome.

Results:

All models showed strong agreement in pathogenic classifications. DeepSeek generally aligned well with ClinVar, except for one likely benign variant misclassified as likely pathogenic. Gemini demonstrated variable outputs for benign variants—ranging from *VUS* to *benign/VUS*—with only one misclassified as *pathogenic*. ChatGPT showed a more conservative trend by overusing *VUS*. Claude favored specificity, reclassifying one likely pathogenic variant as likely benign.

Conclusion:

AI models show promising potential in supporting variant interpretation; however, expert review remains essential to ensure clinical accuracy and patient safety.

PP12-Reinterpreting MEFV Variants of Uncertain Significance: A Five Step In Silico and Structural Pipeline in 125 Patients

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Background: Familial Mediterranean Fever (FMF) is caused by MEFV alterations, yet variants of uncertain significance (VUS) often complicate clinical interpretation. Standardized re-evaluation integrating in silico tools and structural context may improve diagnostic yield and reproducibility.

Materials and Methods: We retrospectively analyzed 125 patients tested for MEFV between December 2020 and June 2025 using an amplicon based NGS workflow (RefGen; Illumina). Variants were processed via Sophia DDM® (Pepper®

/hg19) and annotated with Ensembl VEP according to ACMG/AMP and local expert criteria. A five step pipeline was applied: 1.Population frequency filtering (gnomAD), 2.Multi tool in silico prediction (SIFT, PolyPhen 2, MutationTaster), 3.Domain mapping (B30.2/SPRY focus), 4.3D structural appraisal for selected VUS, 5.Evidence collation for standardized VUS reinterpretation. Copy number analysis was excluded.

Results: Fourteen distinct variants were observed. •P/LP: M694V (13), R761H (4), K695R (3), A744S (2), V726A (2), I591T (2 LP) •VUS: R202Q (39; 2 hom, 28 het, 8 compound/multi het), G196W, R329H, P124=, E148Q, E477G, I591T Multi tool concordance identified some VUS as “potentially damaging,” while structural mapping highlighted functionally relevant sites.

Conclusion: A lightweight, clinic ready pipeline enables standardized and transparent triage of MEFV VUS in FMF and is adaptable to other monogenic autoinflammatory genes.

PP13-miR-3179 can be therapeutic microRNA for LUNG carcinoma?

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Abstract

Background: Cancer cell invasion is a multistep process. MicroRNAs (miRNAs) have an important role in the regulation of invasion and metastasis by targeting associated genes. In this study, we aim to investigate the relationship between the genes which, targeting by miR-3179 and cellular invasion ability.

Methods: We performed in silico analysis to identify key signaling pathways associated with miR-3179 target genes. Relevance scores for invasion were determined based on mechanistic contributions to cell motility, tissue infiltration, and metastatic potential.

Results:

Analysis of the pathways affected by miR-3179 revealed that Leukocyte Transendothelial Migration stood out as the most strongly linked to invasive behavior, receiving the highest score (5 out of 5). This pathway is directly involved in helping tumor cells pass through the endothelial layer, a key step in entering the bloodstream and spreading to other parts of the body. In addition, several other pathways—such as cAMP signaling, phagosome, osteoclast differentiation, and neutrophil extracellular trap (NET) formation—were also found to be significantly related to invasion, each scoring 4 or higher. These pathways are known to affect how cells move, adjust their internal structure, and respond to signals from their environment, all of which are essential for cancer progression and metastasis. Collectively, five pathways closely tied to invasive behavior were

identified, with an average relevance score of 4.2 out of 5. In addition, seven other pathways also showed moderate to high involvement in invasion-related processes. Interestingly, about 70% of the pathways influenced by miR-3179 were associated with a medium or high level of invasive activity, suggesting a strong connection between this miRNA and the potential for metastasis. One pathway, Osteoclast Differentiation, stood out in particular, raising the possibility that miR-3179 may have a role in promoting bone metastasis. Likewise, its impact on immune-related processes—such as Neutrophil Extracellular Trap (NET) Formation—points to a broader regulatory effect on how tumor cells interact with their environment.

Conclusion:

These findings indicate that miR-3179 may play a broad regulatory role in cancer cell invasion. By influencing key biological routes tied to movement, immune interaction, and barrier crossing, miR-3179 could be a valuable marker of metastatic behavior. Its involvement in several pro-invasive processes also suggests that it may hold potential as a therapeutic target in aggressive cancers, especially those of the lung carcinoma.

PP14-Chromosomal Aberrations in Healthy Oocyte Donors in Northern Cyprus: A Cohort Study

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Background and Aim:

Chromosomal integrity is a critical factor in oocyte donation, directly impacting reproductive outcomes. This study aimed to examine the prevalence and types of chromosomal aberrations in phenotypically healthy oocyte donors in Northern Cyprus between October and December 2023.

Methods:

A cohort study was conducted involving 321 phenotypically healthy female oocyte donors aged 18–35. Peripheral blood samples were collected from four genetic laboratories and analyzed at the Near East University Hospital Genetics Laboratory (NEUHGL) using standard karyotyping techniques. The prospective phase took place from October to December 2023, and retrospective analyses were conducted in January 2024.

Results:

The mean age of donors was 25.94 ± 3.55 years. Normal karyotypes (46,XX) were observed in 97.8% of participants. Chromosomal aberrations were detected in 2.2% of cases, consisting of structurally balanced rearrangements involving chromosome 9: pericentric inversion [inv(9)(p11;q13)] and heterochromatic polymorphism 46,XX,9qh+. No statistically significant association was found between age and chromosomal aberration type.

Conclusion:

The study demonstrates a low incidence of chromosomal abnormalities among healthy oocyte donors in Northern Cyprus, potentially attributed to the young and phenotypically diverse donor population. Further studies with expanded genomic analysis and demographic profiling are recommended to explore potential associations with ethnicity, region, or reproductive health.

Keywords:

Chromosomal Aberration, Oocyte Donors, Karyotyping, Northern Cyprus, Reproductive Genetics

PP15-Sphingomyelin and RNase-resistant RNA in the microdomains of the inner nuclear membrane: a role in transcriptional regulation

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Abstract

The role of sphingomyelin and cholesterol in specific microdomains of the inner nuclear membrane suggests their involvement in regulating double-stranded exonuclease-resistant RNA (dsRNA). This idea supports the growing view that nuclear lipid microdomains are not merely structural elements but also play a part in signaling and regulatory pathways that influence RNA stability and processing. The goal of this study was to investigate how sphingomyelin

and cholesterol contribute to safeguarding nuclear RNA from degradation and to identify the RNA species located within the lipid microdomains. Our approach was based on enzymatic hydrolysis of nuclear lipid microdomain RNA by sphingomyelinase or phosphatidylcholine-dependent phospholipase C followed by RNA extraction, library preparation and sequencing of all RNAs present in nuclear microdomains. Only the application of sphingomyelinase resulted in RNA vulnerability to RNase digestion. Compared to whole nuclei, nuclear lipid microdomains were enriched in retained introns, small nuclear RNA, and long intergenic non-coding RNA, with a particularly high abundance of miRNA. The high miRNA content (20%) in nuclear lipid microdomains can be attributed to specific nuclear circular RNAs, where exons are circularized along with retained introns, forming exon-intron circular RNAs (EiRNAs) that function as miRNA sponges. The presence of ciRNA, a class of circular RNA composed exclusively of introns, was also confirmed. According to functional analysis, RNase-resistant RNAs associated with nuclear lipid microdomains seems to participate to chromatin organization and brain pathophysiology. In summary, nuclear lipid microdomains serve as regulatory key sites for transcription, where circular RNAs, miRNAs, and double stranded mRNA, each resistant to RNase, are stabilized by nuclear sphingomyelin.

PP16-The overexpression of Toll-like receptors 4 and 8 in lung biopsies of human non-small cell lung carcinoma suggests: a putative role as positive prognostic indicator

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Purpose

Lung cancer remains the leading cause of cancer-related deaths worldwide and is primarily classified into two main types: non-small cell lung cancer (NSCLC), which arises from epithelial cells, and small cell lung cancer (SCLC), which originates from neuroendocrine and hormone-secreting cells.

Emerging evidence has established a causal relationship between inflammation and innate immunity in the development of NSCLC. This study aimed to assess the expression of Toll-like receptors (TLR4 and TLR8) in peripheral blood mononuclear cells (PBMCs) and lung tissue from NSCLC patients, with the

goal of identifying potential prognostic markers for the disease. Patients who underwent surgical treatment for NSCLC with anatomical resections, as well as those with benign conditions, were included in the study. The expression levels of TLR4 and TLR8 were measured using real-time PCR in PBMCs and immunohistochemical analysis in lung tissue. A preliminary in silico analysis was performed, extracting data from 1,194 tissue arrays of both healthy and cancerous samples from the Genevestigator database. Additionally, the study explored the correlation between TLR gene expression and patient survival outcomes. Bioinformatics analysis indicated that the downregulation of TLR4 and TLR8 is associated with improved survival in lung adenocarcinoma (LUAD) and lung squamous cell carcinoma (LUSC). However, no significant differences in the gene expression of TLR4 and TLR8 were found between the case and control groups in PBMCs. A positive correlation was observed between the expression levels of both receptors. Notably, immunohistochemical analysis revealed that TLR4 and TLR8 expression was higher in the lung tissues of NSCLC patients compared to the control group, as demonstrated by increased staining intensity and a higher number of positive cells. In conclusion, although the exact role of TLRs remains unclear, this study highlights the potential involvement of TLR4 and TLR8 in the pathogenesis of NSCLC. Our findings suggest that these receptors may play a role in improving overall survival, which could serve as a positive prognostic marker for the disease in NSCLC.

PP17-Neuroplasticity as a key mechanism in functional recovery following traumatic brain injury

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Abstract: Neuroplasticity refers to the brain's ability to reorganize its structure and function in response to injury or environmental stimuli. This adaptive capacity plays a crucial role in recovery from traumatic brain injury (TBI), enabling the brain to compensate for lost functions by forming new neural connections. Recent studies highlight that both structural and functional plasticity such as axonal sprouting, dendritic remodeling, and synaptic reweighting are influenced by various factors including age, injury severity, and rehabilitation strategies. Biotechnological advances have further contributed to understanding neuroplastic mechanisms through the development of molecular imaging, neurotrophic factor delivery, and stem cell-based therapies. These innovations not only enhance diagnostic precision but also offer promising therapeutic approaches to stimulate endogenous plasticity.

This abstract discusses the fundamental mechanisms of neuroplasticity, the role of targeted interventions, and the potential of biotechnology in improving outcomes for individuals with TBI. Understanding and harnessing

neuroplasticity is essential for developing effective strategies for brain repair and long-term functional recovery.

PP18-From Lab to Bedside: A Game-Changing Miniaturized Plasmapheresis Unit Bridging Rat and Human Therapies

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Therapeutic plasma exchange (TPE) is a cornerstone intervention for various autoimmune and renal conditions, with the global plasmapheresis market valued at approximately USD 1.5 billion in 2024 and projected to reach 3.5 billion by 2035. Despite this, there is a complete absence of commercially available TPE devices designed for use in subjects under 20 kg, severely limiting preclinical research models. Addressing this critical gap is essential for advancing translational research and device innovation.

Developed at the Advanced Research and Development Center for Experimental Medicine (CEMEX), our TPE platform is a groundbreaking, miniaturized plasmapheresis system tailored for conscious rodents. Uniquely TLR 4-5 certified, it ensures biosafety compliance and regulatory readiness. This closed-circuit unit enables up to 95% plasma exchange without anaesthesia, leveraging a four-line system for continuous flow and real-time cardiovascular monitoring via implanted telemetry sensors. Validated in both young and aged rats, the device demonstrated excellent biocompatibility and operational safety without hemodynamic instability or clotting.

The mini TPE station introduces a transformative platform for preclinical plasmapheresis, bridging the translational divide between rodent models and human therapy. By enabling safe, reproducible TPE in subjects under 20 kg, it opens new avenues for translational research and the advancement of extracorporeal therapies in experimental models and clinical veterinary practice.

Funding: This research was funded by a project under The Health Program (PS) 2021-2027, Policy Objective 1, Priority 5, project title "Development of translational research for vaccines, serums and other biological drugs - Acronym CAN-TAVAC 2.0", SMIS code 326920.

PP19-Optimizing algae bioreactors for sustainable biofuel production: A review of design and performance

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Abstract

The escalating global energy demand necessitate the development of sustainable energy sources. Algae present a highly promising source for biofuel production due to their rapid growth rates, high lipid content, and ability to utilize non-arable land and wastewater. However, the commercial viability of algal biofuels remains largely hindered by the high capital and operational costs. Algae bioreactors offer significant advantages over open pond systems in terms of productivity and resource efficiency.

This review will examine the advancements in algae bioreactor design and performance specifically for sustainable biofuel production. We will delve into various bioreactor configurations and critically assess their strengths, limitations, and suitability for different algal species and target biofuel products. Key operational parameters, including light intensity and distribution, CO₂ supply, nutrient management, temperature control, and mixing strategies, will be thoroughly discussed in relation to their impact on biomass yield, lipid accumulation, and overall process efficiency. Furthermore, this review explores emerging technologies and strategies, such as genetic engineering for enhanced strain performance, and advanced control systems aimed at improving economic feasibility and environmental sustainability. Finally, we will highlight the current challenges and identify future research directions crucial for transitioning algal biofuel production from laboratory-scale promise to industrial reality.

PP20-Pharmacokinetic Profiling of 1-(3-Chloropropyl)-3-Substituted Isatin Derivatives Using *In Silico* ADMETlab and SwissADME Evaluation

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The continuous emergence of antimicrobial resistance underscores the need for novel chemotypes with optimized pharmacokinetic profiles. Isatin and its derivatives have attracted significant attention due to their broad-spectrum biological activity. In this study, we evaluated a focused series of 1-(3-chloropropyl)-3-substituted isatin derivatives, in which the isatin core is functionalized at N-1 with a 3-chloropropyl group and at C-3 via imine formation with various primary amines, including aniline, 4-aminomorpholine, 2-, 3-, and 4-aminopyridine, as well as two 1,3,4-thiadiazole derivatives bearing either a fluoromethyl or a chlorophenyl substituent. Additionally, halogen substitutions (Cl, Br, I, or F) were introduced at position 6 of the isatin ring to explore their influence on pharmacokinetic behavior.

The resulting set of 35 compounds was subjected to *in silico* ADME/T evaluation using SwissADME and ADMETlab. Most molecules conformed to Lipinski's rule of five and showed high predicted human intestinal absorption, favorable Caco-2 permeability, and inhibition of P-glycoprotein without efflux

liability. Distribution profiles suggested strong plasma protein binding and limited blood-brain barrier penetration. The compounds exhibited moderate clearance and predicted half-lives compatible with oral bioavailability. Several molecules were predicted to inhibit CYP3A4 and CYP2C9 enzymes, indicating possible metabolic liabilities.

These results highlight the potential of 1-(3-chloropropyl)-3-substituted isatin derivatives as orally bioavailable candidates, and demonstrate the value of *in silico* ADMET screening in early drug development pipelines. The present findings also provide a foundation for further structure-activity relationship (SAR) studies and the rational design of bioactive isatin analogues with improved pharmacokinetic profiles.

Keywords: isatin derivatives; pharmacokinetics; *in silico*; ADMET; CYP inhibition

PP21-Antibiotic resistant genes detection utilizing an electrochemical biosensor

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Food safety is a global priority to guarantee safe products to the final consumers, especially against pathogenic bacterial risks. *Staphylococcus aureus* is a zoonotic pathogen commonly found in farm animals' meat, in particular cattle and pig, but it can also be isolated from milk and dairy food products. This bacterium causes severe gastroenteritis and intoxication; furthermore, the development of antibiotic-resistant strains makes treatment more complex. Monitoring methicillin-resistant *S. aureus* (MRSA) contamination in food at the basis of food production is necessary, but traditional detection methods are often time-consuming and costly. This study aims to develop a rapid detection method for MRSA utilizing an electrochemical biosensor combined with a newly designed 5'-thiol modified DNA probe. The probe was evaluated for its specificity to the *mecA* gene, one of the most diffused genes responsible for resistance to the β -lactam antibiotic group. The calibration curve allowed to detect MRSA DNA between 0.0001 and 1 ng/ μ l in less than 20 minutes of incubation. Applications of the biosensor on extracted DNA from meat and milk products bought from local supermarkets and farms in Northeastern Italy successfully differentiated contaminated food products from safe ones, ensuring implementation of corrective actions and control of antibiotic resistance spread.

PP22-Geobotanical Study and Preservation of Rare and Endangered species *Crataegus ambigua*

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The ongoing loss of plant species-particularly those that are endangered or endemic-represents a critical threat to global biodiversity. This study presents a geobotanical assessment and the development of *ex situ* conservation strategies for *Crataegus ambigua* C.A.Mey. ex A.K.Becker, an endangered species within the *Rosaceae* family. Field research conducted on the Mangyshlak Peninsula in Kazakhstan has revealed a concerning trend: the progressive decline of *C. ambigua* populations and associated biodiversity. This decline is driven by a combination of factors, including vulnerability to pathogens and insect pests, senescence of mature plants, low population density, poor natural seed set, and larger-scale environmental pressures such as climate change. To counteract these threats, we have established an in vitro collection for the short- and medium-term conservation of seeds, embryos, and shoot cultures. For long-term preservation, we employ cryogenic techniques targeting seeds and embryonic axes, complemented by traditional seed storage at -20°C. These integrated conservation approaches are designed to safeguard the species' genetic diversity, ensuring its availability for future use in plant breeding programs and for the propagation of planting material aimed at restoring declining populations in natural habitats.

Keywords: *Crataegus ambigua*, geobotanical study, *in vitro* collection, cryobank, planting stocks

Funding: This research was funded by the Ministry of Science and Higher Education of Kazakhstan Republic (Project BR28713087).

PP23-Geobotanical study of endemic Rose species of Kazakhstan for biodiversity conservation

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Kazakhstan's diverse ecosystems and unique climate foster the development of endemic *Rosa* species with specific adaptive traits. This project focuses on the rare and understudied *Rosa cinnamomea* L., listed in the Red Data Book of Kazakhstan as *Rosa pavlovii* Chrshan., underscoring its conservation value. To date, studies of Kazakhstani wild roses have primarily addressed geobotanical and anatomical traits, lacking detailed international descriptor-based assessments. Recent field surveys in the Almaty region revealed poor population conditions, including significant insect and disease damage and a high proportion of aging plants of some rose species. Only two habitats of *R. pavlovii* are currently known. An expedition to one site in East Kazakhstan failed to locate any individuals, raising serious

concerns about the species' survival in the wild. In response, *in vitro* collections have been initiated for the long-term conservation of the *Rosa* gene pool. These efforts aim to preserve genetic diversity and support future propagation programs to restore declining populations in natural habitats. The data generated will inform targeted conservation strategies for Kazakhstan's wild roses.

Keywords: Rose species, *Rosa pavlovii*, geobotanical study, *in vitro* collection, cryogenic bank

Funding: This research was funded by the Ministry of Science and Higher Education of Kazakhstan Republic (Project BR28713087).

PP24-Pollutant Categories at Vlora Bay & Data on Biototoxicity

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Abstract

Vlora Bay, located along the southern Albanian coastline, represents a critical ecological and economic zone with increasing exposure to environmental threats. The growing anthropogenic pressure on this marine ecosystem underscores the urgency to evaluate the current levels of contamination and their potential biological impacts. This study reviews the main categories of pollutants in the area reported to date, including those coming from industrial discharges, maritime activity, urban runoff, and agricultural inputs, and evaluates the cytotoxicity in water samples using luminescent *Vibrio fischeri* according to ISO 11348-3:2007. This bioassay method offers a rapid and sensitive approach to detecting the impact of toxic substances, contributing to a broader understanding of environmental risks. By highlighting both the environmental significance of Vlora Bay and the challenges it faces, this study aims to support informed decision-making and promote conservation efforts in the region.

Keywords: Vlora Bay, water pollution monitoring, environmental analysis, cytotoxicity, bioluminescent microorganisms.

PP25-A review on pollutant categories at North Adriatic coastline in Albania & Possible Environmental Biotech Solutions

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Abstract

The Albanian Adriatic coastline represents an ecologically and economically significant region currently facing increasing pressures from untreated discharges originating from indus-

trial, agricultural, tourism-related, and urban activities. Understanding pollutant levels and their sources is essential to protect marine ecosystems, maintain water quality, and guide sustainable development. This study focuses on two key sites along the Adriatic coast: the Durrës coastline, characterized by intense urban and port activities, erosion, riverine and chemical pollutants; and the Lezha coastline, influenced by riverine inputs, industrial discharges, port, urban, and agricultural pollutants. Objectives of the study were to summarize findings on main categories and level of pollutants, as well as to identify potential biotech approaches for monitoring their impact and/or for water environment remediation. Findings aim to support the use of standardized monitoring protocols, inform effective pollution control and mitigation strategies, and contribute to evidence-based management policies to safeguard the long-term ecological health and sustainable use of Albania's coastal and marine environments.

Keywords: pollutants, water quality, remediation, biotech approaches

PP26-Probiotics and Synbiotics Affect the Proliferation and Oxidative Stress in Colon Cancer and Neuroblastoma Cell-In-vitro Analysis

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Abstract

The human gut microbiome plays a crucial role in maintaining health, influencing various physiological processes through its complex interactions with the host. Among the strategies to modulate this microbiome, probiotics and synbiotics have garnered significant attention for their potential health benefits. The current study designs optimizes and tests a novel probiotic and synbiotic formulation consisting of three metabolically active probiotics *Lactobacillus plantarum*, *Lactobacillus fermentum* and *Bifidobacteria infantis* together with a novel polyphenol-rich prebiotic, *Triphala*. Additionally, the effect of such probiotics and synbiotics on HT-29 and SH-SY5Y cells proliferation and oxidative stress were studied. The results showed that there were no significant differences in cell proliferation of HT-29 and SY-5Y cells after incubated with probiotic and synbiotic formulations for 6 hours. Moreover, after 24 hours, the synbiotic treatment increased the proliferation of SH-SY5Y cells by two-fold. Further, the reactive oxygen species (ROS) level was significantly decreased in HT-29 and SH-SY5Y cells treated with synbiotics compared to the control. Altogether, the present study suggested that probiotic and synbiotic treatments were safe to the cells, shown in the proliferation and oxidative stress levels in both human colon cancer and neuroblastoma cells.

Keywords: Probiotics, synbiotics, proliferation, oxidative stress, HT-29 cells, SH-SY5Y cells

PP27-Genetic Diversity and Evolutionary Patterns of FCoV Strains in Symptomatic and Asymptomatic Cats in Romania

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Feline coronaviruses (FCoVs) are globally prevalent pathogens in domestic and wild cats, causing mild or asymptomatic infections. In some cases, it can progress to feline infectious peritonitis (FIP), a fatal disease. This study investigated the genetic diversity and evolutionary patterns of FCoV strains in symptomatic and asymptomatic cats in Romania. Feces, blood, and body fluids samples were collected from 11 cats suspected of FIP and 11 clinically healthy cats. Amplification targeting the nucleocapsid gene identified 12 amplicons, with subsequent sequencing revealing mutations and deletions. Insertions were present in only three cases. Phylogenetic analysis using maximum parsimony showed two major Romanian FCoV clusters, with evidence of geographic clustering and potential links to strains from other countries. Detection of similar viral sequences in both symptomatic and asymptomatic cats indicates ongoing circulation of genetically related strains, including potentially virulent variants with unclear pathogenic significance. These findings highlight the importance of ongoing molecular surveillance of FCoV strains and support the nucleocapsid gene as a target for diagnostic and epidemiological evaluations. The study underscores the need for continued monitoring to better understand FCoV evolution and its implications for feline health.

Key words: feline coronaviruses, nucleocapsid, phylogenetic analysis

PP28-Epidemiological Analysis of African Swine Fever in Romania During 2017-2025

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African swine fever (ASF) is a severe viral infectious disease of pigs and wild boars, with a fatality rate up to 90% or higher and it is transmitted through contact with infected animals, ingestion of infected pork products or contact with fomites, either via mechanical vector, such as the soft tick of *Ornithodoros spp.* Since the first confirmed case of ASF in Romania on July 31, 2017 and until June 18, 2025, 7064 outbreaks were reported in pigs and 3882 in wild boars, according to the Animal Disease Information System and European Food Safety Authority. Ma-

jority of the cases were confirmed in pigs, as follow: in 2017 (n=2), 2018 (n=1164), 2019 (n=1728), 2020 (n=1063), 2021 (n=1660), 2022 (n=327), 2023 (n=736), 2024 (n=220) and 164 outbreaks in 2025, until June 18. In wild boars, ASF was confirmed one year later in 2018 (n=182), continuing in 2019 (n=693), 2020 (n=910), 2021 (n=1044), 2022 (n=450), 2023 (n=289), 2024 (n=186) and 2025 (n=128). As ASF represents a global threat for the pig industry, strict biosecurity measures are necessary to keep it under control.

Funding: Program of the Ministry of Agriculture and Rural Development of Romania, project ADER 10.1.1 2023-2026.

PP29-In Vivo Repair of Cranial Defects with Boron-Doped Spongin Scaffolds

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In this study, biohybrid scaffolds were developed using spongin isolated from the marine sponge *Sarcotragus foetidus* (Sf), a Mediterranean Demospongiae species. This sponge features a nanofibrous, 3D spongin-based skeleton enriched with collagen and scleroproteins, offering excellent mechanical strength. Its porous, interconnected structure and ECM-like bioactive surface support cell adhesion and migration, making Sf a promising scaffold for bone regeneration. To enhance osteoconductivity and mechanical properties, Sf scaffolds were functionalized with hydroxyapatite (HAp) and boron-doped HAp (B-HAp). In vivo experiments were conducted on 40 immunocompetent male Wistar Albino rats with bilateral 5 mm cranial bone defects. Bone regeneration was evaluated at 20 weeks postoperatively. Harvested calvarial bones were fixed and analyzed histologically and via micro-CT. Quantitative micro-CT analysis revealed that the Sf/B-HAp group achieved a bone volume/total volume (BV/TV) of ~73%, compared to ~81% in the autograft and ~43% in the control group. Bone mineral density (BMD) was highest in the autograft (~0.80 g/cm³), followed by Sf/B-HAp (~0.70 g/cm³), indicating a ~40% improvement over the control. Among all groups, Sf/B-HAp scaffolds showed near-complete defect bridging, closely approximating the autograft group. No infection or foreign body reaction was observed.

This work has been financially assisted by Hacettepe University Scientific Research Projects (Grant No: THD-2024-21273).

PP30-Seasonal assessment of water composition in Albania and its suitability for lager and ale beer styles

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Abstract

Water is a primary raw material in brewing, and a comprehensive understanding of its chemical composition and pH is essential for producing high-quality beers. This study investigated the seasonal variation in water chemistry to identify the most suitable natural sources for craft brewing in Albania. Water samples were collected from 12 major natural springs across four representative months October, January, April, and July. Each sample was analyzed for key physicochemical parameters, including pH, total hardness, Ca²⁺ ions, concentrations of carbonates and bicarbonates, concentrations of chloride, as well as potential contaminants such as heavy metals and pathogenic microorganisms. One-way ANOVA was applied to assess statistically significant seasonal differences. The results indicated that most of the surveyed water sources possess highly favorable chemical profiles for craft beer production, particularly for Lager and Ale styles, where sensory characteristics are strongly influenced by the balance of specific ions in the brewing water. **Keywords:** natural water, seasonal variation, craft beer, water chemistry, water quality.

PP31-Can Automatic Cell Counters Be Used to Assess the Number of Stromal Cells Isolated from Adipose Tissue?

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Introduction/Objectives

Mesenchymal stromal cells (MSCs) are multipotent and widely explored in regenerative medicine. Adipose tissue offers a readily available source of human adipose-derived MSCs (hAD-MSCs). This study assessed how manual and automated cell counting methods affect the yield, viability, and early culture performance of isolated cells.

Methods

Subcutaneous adipose tissue was collected from 10 patients during liposuction and stored at 4 °C for up to 24 hours. hAD-MSCs were isolated by collagenase digestion (n=50), and cell number and viability were evaluated using manual (trypan blue, haemocytometer) and automated (acridine orange/propidium iodide, Luna-FL) methods. Apoptosis was analyzed by flow cytometry, and immunophenotyping confirmed the MSC identity.

Results and Conclusions

The results showed that the choice of counting method significantly influenced initial yield and viability but had minimal effect on cultured hAD-MSCs.

Acknowledgments

The present work was supported by the National Center for Research and Development in Poland under Agreement no STRATEGMED1/235368/8/NCBR/2014 (Smart AUCI project) within the Strategic Programme STRATEGMED "Prevention practices and treatment of civilization diseases."

PP32-Use of a natural exogenous photosensitizer for Photodynamic Inactivation (PDI) on pathogens

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Blue Light (BL) is part of the electromagnetic spectrum, ranging from 400 - 480 nm (1). This technology operates through the combined actions of three main components: light, oxygen, and a photosensitizer (PS). A PS is a molecule that could be naturally present inside bacteria (endogenous) or externally added (exogenous), which can absorb light at a specific wavelength and be excited. Among the exogenous PS there is curcumin, a natural compound, used in the food industry (such as colourant and/or flavouring agent). An important aspect of curcumin is its photodynamic properties.

Light excites the PS and through different pathways, Reactive Oxygen Species (ROS) are produced and they could attack microbes, damaging bacterial cell components (i.e., DNA, proteins, membrane, lipids) and leading to cell death.

This study aims to evaluate the effectiveness of curcumin as a natural preservative against two major foodborne microorganisms, *L. monocytogenes* and *E. coli*, by testing the microbial inactivation kinetics under different wavelength conditions within the 400-500 nm.

0.5 µM curcumin for 30 min tests resulted in *Escherichia coli* reduction of -4 log by all tested conditions; while *Listeria monocytogenes* showed an inactivation of -3.30 log and -5.50 log depending on wavelengths. The photodynamic technology using natural exogenous PS is an important approach for reducing food-related microorganisms.

PP33-Evaluating Bryne's classification for prognostic purposes in feline squamous cell carcinoma

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Feline squamous cell carcinoma (SCC) represents a highly aggressive malignancy, particularly in oral and cutaneous forms. The aim of this study was to assess the prognostic value of Bryne's classification system for feline oral and cutaneous SCC in a subset of neoplastic samples collected from ten European breed cats (8 females and 2 males). Most tumors originated in the auricular area, followed by the oral cavity. Senior cats were predominant. The tumors were evaluated using Bryne's param-

eters: degree of keratinization, nuclear polymorphism, number of mitoses, and pattern of invasion. The mean total score was 10, classifying tumors as moderately differentiated.

There were no statistically significant correlations between tumor location (oral versus cutaneous) and total score or between diagnosis and total score. Similarly, age and sex showed no significant association with the total score.

While Bryne's classification provides a structured solution to grading feline SCC, tumor severity as measured by this system was not significantly affected by age, sex, or tumor location in this study. A broader range of biological and molecular investigations is needed to find effective prognostic markers in feline SCC.

PP34-The Morphology and Molecular Phylogeny of *Ulva* spp. (Ulvaceae, Chlorophyta) from Çakalburnu Lagoon, İzmir Bay

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Green macroalgae of the genus *Ulva* are globally distributed and are the most common macrofouling algae, often attaching to marine structures like docks and frames. These algae can form dense blooms known as green tides, which wash ashore and decay, harming coastal ecosystems and deterring tourism. Green tide events have been reported in the Çakalburnu Lagoon, İzmir Bay, making it a key site to investigate the origins and development of such blooms.

Morphological identification of *Ulva* species is difficult due to their high variability, necessitating precise molecular methods. This study aimed to assess species diversity and morphological variation of *Ulva* in İzmir Bay using both molecular and morphological approaches. DNA barcoding was conducted by sequencing the 18S rRNA and tufA genes. Sequence data were analyzed using the NCBI BLAST program to determine species identity. The results confirmed the presence of *Ulva lactuca* Linnaeus 1753 and *Ulva ohnoi* Hiraoka & S. Shimada 2004, with both identified as holotype representatives of *U. lactuca*. Collected and identified samples have been preserved in the Ege University Culture Collection herbarium for further study. Study was a part of Cost CA20106 and supported financially by the TUBITAK under project number 123Y090.

Keywords: *Ulva* spp., molecular and morphological identification, DNA isolation

PP35-Integration of whole-slide imaging, QR-based tracking and quantitative analysis in preclinical histology

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CEMEX, the integrated research and development center of Grigore T. Popa University of Medicine and Pharmacy, has over 40 years of experience in biomedical research, focusing on pharmacology, pain therapy, and translational sciences. Renovated and digitally transformed in 2016, CEMEX is now a national leader in preclinical R&D, emphasizing traceability, animal welfare, and digital innovation. Within this ecosystem, we developed a streamlined histology workflow combining whole-slide imaging (WSI), QR code tracking, and quantitative digital analysis. Tissue cassettes and slides were labeled with QR codes linked to a centralized animal database. Slides were digitized using high-resolution WSI systems and associated with metadata. Quantitative image analysis was performed in QuPath. Integration with IoT-enabled tracking devices ensured real-time monitoring of sample status and location. The system ensured traceability, minimized identification errors, and enabled remote, multi-user access. QR and IoT integration improved organization, and software-assisted quantification yielded reproducible, objective metrics. Our work aligns with recent directions in research supporting digital pathology for improved workflow, standardization, and data quality. Uniquely, our pipeline applies this model to animal research with integrated metadata and IoT-based tracking. This digital workflow supports scalable, reproducible, and collaborative histological evaluation in animal-based research, in line with CEMEX's commitment to innovation and transparency.

Funding: This work was supported by a grant from the Ministry of Research, Innovation and Digitalization, CNCS-UE-FISCDI, project number PNIII-P1-1.1-PD-2021-0466, within PNCDI III and by Romania's National Recovery and Resilience Plan (PNRR), Pylon III, Section I8. Development of a Program to Attract Highly Specialized Human Resources from Abroad in Research, Development and Innovation Activities, PNRR-III-C9-2023-I8, Project "Modelling negative symptom domains neurobiology: a transdiagnostic, translational study", code CF 46/ 28.07.2023; and by a project under The Health Program (PS) 2021-2027, Policy Objective 1, Priority 5, project title "Development of translational research for vaccines, serums and other biological drugs - Acronym CANTAVAC 2.0", SMIS code 326920.

PP36-Secretome dynamics of human Adipose-derived Mesenchymal Stem/Stromal Cells: The role of confluency and culture conditions

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Regenerative potential of mesenchymal stromal/stem cells (MSCs) can be mediated by the release of extracellular vesicles (EVs). Adipose-derived MSCs (AD-MSCs) are a promising source of EVs due to their high yield and accessibility, but EV variability caused by culture parameters poses a challenge for therapeutic standardization.

This study examined how the culture conditions (confluency level, passage and medium) affect the human AD-MSC secretome, focusing on EVs.

hAD-MSCs were isolated from lipoaspirates and cultured in two types of GMP-grade media. Conditioned media were collected at 50%, 75%, and 100% confluency across early passages (II-IV). EVs were isolated using centrifugation, ultrafiltration, and Size Exclusion Chromatography.

AD-MSC-EVs size and concentration were assessed using TRPS, while EVs- and MSC-specific surface markers were analyzed via Western blot and nanoflow cytometry.

Substantial differences in EV yield, size, and marker profiles were observed. Notably, EVs phenotype varied between media despite comparable cellular expression. These findings emphasize the need for rigorous standardization of MSCs culture protocols in EV-based therapies.

This research was supported as part of the 'ANFIBIOM' project carried out within the 02.02 First TEAM programme of the Foundation for Polish Science, co-financed by the European Union under the European Funds for Smart Economy 2021–2027 (FENG).

PP37-Distribution of Serotonin Receptor Polymorphisms rs6311 and rs6313 in a Nonclinical Adolescent Cohort

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Serotonin (5-hydroxytryptamine, 5-HT) is an important neurotransmitter that modulates a broad spectrum of functions, including cognition, learning, memory, reward processing, sleep, mood, anxiety, and depression [1]. The last are described to be multifactorial conditions influenced by genetic, environmental, and psychosocial factors. Some studies have demonstrated a significant association between genetic variants of serotonin receptors and vulnerability to psychiatric disorders, particularly anxiety and depression [2]. However, limited research has examined their association in nonclinical adolescent populations. This study belongs to the *SMART project* (CUP: J53D23008110006) funded by the NextGenerationEU and it is aimed to investigate the distribution of rs6311 and rs6313 serotonin receptor polymorphisms, in a cohort of non-clinical adolescents (n = 143) of high schools in the Umbria

region, Italy. Genotyping was performed using RT-PCR. The results revealed that the G allele is the major allele for rs6311 and the C allele is the major allele for rs6313. Regarding the rs6311 polymorphism, 54% of subjects were heterozygous A/G, 28.5% homozygous G/G, and 17.5% homozygous A/A. A similar distribution was found for rs6313: 54% of subjects were heterozygous C/T, 27.8% homozygous C/C, and 18.2% homozygous T/T. The two polymorphisms are in fact in nearly complete linkage disequilibrium (the A and G alleles of rs6311 correspond respectively to the T and C alleles of rs6313). Only two subjects presented a different allelic distribution.

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PP38-Use of Predictive Computational Models in Determining Clinical Risk Factors in Dengue

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Abstract

Dengue represents a major global public health challenge, with millions of cases reported annually, especially in tropical and subtropical regions. Early identification of clinical risk factors is essential to prevent progression to severe forms such as dengue hemorrhagic fever. In this context, predictive models based on computational techniques such as machine learning (ML) have emerged as promising tools for risk stratification, clinical prognosis, and therapeutic decision-making. This article reviews recent advances in the application of ML techniques in predicting clinical risk factors for dengue, highlighting their integration with biotechnological approaches to improve epidemiological surveillance and personalized medicine.

PP39-Performance enhancement of bacterial bioreporters for the detection of trace explosives

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Landmines and explosive remnants of war pose a global problem which claims numerous casualties long after the

conflict has ended. Current approaches for the location of landmines, such as metal detection, require physical presence at the minefield and therefore involve high risk to personnel; these methods are also costly, time consuming, and have a high rate of false positive results. The development of alternative technologies for efficient remote detection of buried explosive devices is thus urgently needed.

Most landmines contain 2,4,6-trinitrotoluene (TNT) as the main explosive component, as well as its production by product 2,4-dinitrotoluene (DNT). Over time, the more volatile DNT leaks out of the landmine casing and accumulates in the soil above it where it can be detected.

For future detection of buried landmines, we have developed *Escherichia coli*-based microbial bioreporters. These sensor strains harbour a gene promoter (*yqjF*) as a sensing element, along with its transcription factor gene (*yhaJ*). In the presence of DNT/TNT metabolites, the *yqjF* gene promoter is activated, and drives the transcription of a microbial bioluminescence *luxCDABEG* reporter gene cassette. Using several molecular biology techniques, we be able to substantially enhance the bioreporter's activity.

PP40-A refined biotechnological methodology for integrative animal monitoring using the OxyletPro-Physiocage system

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Abstract

Technological advances in animal biotechnology are significantly improving both research quality and animal welfare by reducing stress and minimizing human intervention. In line with the 3Rs principles (Replacement, Reduction, Refinement), the OxyletPro-Physiocage system offers a sophisticated, non-invasive platform for monitoring laboratory animals within their home cages. This digital system allows for the simultaneous assessment of key parameters such as respiratory metabolism, food and water intake, activity, and rearing, all under controlled and standardized environmental conditions. By eliminating the need for frequent handling and reducing external stressors, the system improves the reproducibility and precision of physiological and behavioral data. This is particularly beneficial in sensitive research areas such as neuroscience and mental health, where stress can significantly affect outcomes. Moreover, the system's high-throughput design enables efficient phenotyping while minimizing animal distress and procedural severity.

The OxyletPro-Physiocage system exemplifies how innovative biotechnological tools are refining experimental methods and

promoting ethical standards in animal research. By enhancing data integrity and supporting animal welfare, this technology represents a meaningful advancement in the field of animal biotechnology.

Funding: This research was funded by a project under The Health Program (PS) 2021-2027, Policy Objective 1, Priority 5, project title "Development of translational research for vaccines, serums and other biological drugs - Acronym CAN-TAVAC 2.0", SMIS code 326920.

PP41-Resilient Native Flora on Mine Lands: Linking Phytoremediation Strategies to Bioeconomic Opportunities

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Abstract

This study explores the phytoremediation potential of native tree species naturally colonizing abandoned mine lands in Portugal. Species such as *Pinus*, *Eucalyptus*, and *Quercus* have demonstrated resilience to metal-contaminated, nutrient-poor soils, enabling their use in soil stabilization and pollution attenuation. Through field observations and metal accumulation analysis, we found that while these trees show moderate metal uptake compared to herbaceous species, their high biomass and adaptability make them suitable for phytostabilization and selective phytoextraction in peripheral contamination zones. Importantly, harvested biomass presents bioeconomic opportunities when metal content is managed within safe thresholds. Options include bioenergy generation (incineration, biofuels), phytomining, biochar production, and application as adsorbents in wastewater treatment. This work underscores the dual benefit of ecological restoration and resource recovery, advocating for an integrated approach that balances environmental remediation with sustainable economic use. Proper risk assessment is essential to ensure environmental and health safety in biomass utilization strategies.

Keywords: Bioenergy, Biomass offtake, Economic revenue, Environmental remediation, Phytoremediation.

PP42-Development of *in vitro* technique for elimination of Raspberry bushy dwarf virus

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Raspberry bushy dwarf virus (RBDV) is one of the most common and harmful raspberry pathogens, significantly reducing yield of the crop and quality of berries. The efficiency of various methods for RBDV eradication in Malinovaya Gryada variety *in vitro* plant was compared. Thermotherapy, chemotherapy and cryotherapy, as well as combinations of these techniques, have been tested. Thermotherapy of aseptic plants was carried out in a growth chamber at alternating temperatures (16 h at 38°C, light intensity 25 $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$; 8 h at 24–26°C, darkness) for two weeks. Chemotherapy was carried out by *in vitro* plant culture for 4 weeks on Murashige-Skoog medium with 30 mg/L of ribavirin. For cryotherapy of shoot tips, the PVS2 vitrification technique was used. *In vitro* plants were tested for viruses by multiplex TaqMan real-time PCR. It was found that thermotherapy and chemotherapy alone, as well as the combination of these treatments with cryotherapy, did not result in RBDV elimination. Only when chemotherapy was used in combination with thermotherapy, RBDV was not detected in 37.5% of *in vitro* plants. The highest percentage of RBDV-free plants was obtained using the combined technique: chemotherapy + thermotherapy + cryotherapy, while RBDV elimination was confirmed in 66.7% plants.

This research was funded by the Ministry of Science and Higher Education of Kazakhstan Republic (Program BR28712539).

PP43-Effect of A New Formulation Based on Sphingomyelin and Vitamin D3 On Cognitive Functions of Phenylketonuria Patients

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Phenylketonuria (PKU) is an inherited metabolic disorder caused by a mutation in the gene encoding phenylalanine hydroxylase, leading to an accumulation of phenylalanine. This buildup is responsible for neurological impairments, including motor dysfunction, seizures and intellectual disability and possible skin manifestations. Recent studies have highlighted the essential role of dietary sphingomyelin, ceramide, and sphin-

gosine-1-phosphate in maintaining brain health.. The work was aimed to evaluate the effect of dietary lipid fraction enriched in sphingomyelin and vitamin D3 content in improving the cognitive disorders of PKU patients. 17 patients (10 males and 7 females, aged > 18 years) affected by PKU on diet therapy, diagnosed at newborn screening and/or with late diagnosis, were recruited by the Inborn Errors of Metabolism Unit, Department of the Women and the Child San Paolo Hospital - ASST Santi Paolo e Carlo, University of Milan . Baseline (T0) data served as the control for each participant.. The cognitive disorders were assessed with MMS and Cognifit test. 6 mL of whole blood was collected from each patient. After centrifugation at 3000 rpm, 4 mL of plasma was used for sphingolipid-omic analysis. The results showed that cognitive improvement after the intervention was most evident in patients with mild to moderate cognitive impairment at baseline. In the same patients, sphingomyelin, ceramide and, in particular, sphingosine-1-phosphate were increased. The results lead us to reflect on the connection between changes in sphingolipid metabolism and improvement in cognitive activities. Financial support from Buona s.p.a. company Sesto Fiorentino, Italy.

PP44-Genetic diversity and population structure in wild *Prunus* species of Kazakhstan

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Cherry is one of the most popular stone fruit crops. Four species of wild cherry grow in Kazakhstan: *Prunus fruticosa* Pall., *Perythrocarpa* (Nevski) Gilli, *Pgriffithii* var. *tianshanica* (Pojark.) Ingram, and *P. verrucosa* Franch. Wild cherry species ingenious to Kazakhstan and Uzbekistan offer valuable genes for breeding drought- and frost-tolerant varieties and dwarf rootstocks.

163 accessions from *Pfruticosa*, *Perythrocarpa*, *Pgriffithii* var. *tianshanica*, and *P. verrucosa* were assessed using morphological descriptors and 13 SSR genetic markers. STRUCTURE analysis revealed hybrids in *P. griffithii* var. *tianshanica*, *P. erythrocarpa* and *P. verrucosa*. The highest percentage of hybrids was found in *P. griffithii* var. *tianshanica* (34.4%), which occurs with *P. verrucosa* and *P. erythrocarpa*. Identical genotypes were identified in four species investigated in this study. The most (54.8%) genetically identical accessions were found in *Pfruticosa*. The highest genetic diversity was observed in *P. verrucosa*, while the lowest in *Pfruticosa*. AMOVA showed that most genetic variation (81%) existed within species rather than among them (19%). Cluster analysis revealed a clear separation between *Pgriffithii* var. *tianshanica* and *Pfruticosa*, whereas *Perythrocarpa* and *P. verrucosa* showed close genetic relationships.

Understanding genetic diversity and population structure, along with identifying hybrid and identical genotypes is crucial

in developing effective conservation strategies and breeding programs.

This research was funded by the Ministry of Science and Higher Education of Kazakhstan Republic (Program BR28712539).

PP45-Optimizing Conditions for the Extraction and Saponification of Carotenoids from *Ulva* sp. in İzmir Bay

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Ulva sp. (associated with algal blooms) contains green pigments; thus, it is classified within the phylum Chlorophyta. Additionally, it commonly inhabits Mediterranean coastal areas with favorable temperatures. In recent years, nitrogen (N) and phosphorus (P) levels have increased in İzmir Bay due to population growth and intensified industrial activities; consequently, *Ulva* sp. has proliferated uncontrollably in the Bay. *Ulva* sp. contains various valuable compounds, including polysaccharides, chlorophyll, carotenoids, proteins, and lipids. Among these, carotenoids represent tetraterpenoid lipophilic pigments that occur naturally in red, yellow, and orange colors. Beyond their pigmentary role, carotenoids exhibit a wide range of biological activities, including anti-inflammatory, antimicrobial, antioxidant, and UV-protective properties, making them promising candidates for cosmetic applications. In this context, the optimum conditions for carotenoid extraction and saponification from *Ulva* sp. in İzmir Bay were determined. The carotenoid contents were found to range between 0.10 and 0.23 mg/g. After the saponification procedure, carotenoid levels were determined with HPLC-DAD. The potential use of these carotenoids as cosmetic raw materials will be investigated in subsequent experimental studies.

TUBITAK supported this study under Grant Number 124M210. The authors thank TUBITAK for their support.

Key words: *Ulva* sp., İzmir Bay, carotenoid, extraction, saponification.

PP46-Anaplasma spp. infection in cattle and water buffaloes, in Romania: serological preliminary data

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Anaplasmosis is one of the most common tick-borne diseases worldwide caused by *Anaplasma* species (Rickettsiales: Anaplasmataceae) causing diseases in humans and animals. It is also associated with considerable economic losses in livestock.

Little is known about *Anaplasma* spp. infection in ruminants in Romania. Therefore, a preliminary cross-sectional serological study was conducted to investigate the infection with *Anaplasma* spp. in cattle and water buffaloes (*Bubalus bubalis*), in different geographical areas (in Northeast, Center, Southeast) of Romania. For this, serum samples were collected from cattle (n=182) and water buffaloes (n=30) and subjected to a competitive enzyme linked immunosorbent assay (cELISA) detecting an epitope of major surface protein 5 (MSP5) of *Anaplasma* spp. An overall seropositivity rate of 42.3% (95% CI: 35.03-49.84) in cattle and 20.0% (95% CI: 7.71–38.57) in buffalo was recorded, with seropositive animals in all the study areas. Significant difference ($p < 0.05$) of mean seroprevalence, varying from 22.2% (95% CI: 13.26-33.57) to 72.0% (95% CI: 57.50-83.77) was registered according to the cattle's originating area. The findings revealed natural exposure to *Anaplasma* spp. infection of both cattle and buffaloes in the investigated areas and emphasize on the need for further studies, including on the potential risks of veterinary and public health relevance.

PP47-Preliminary Analysis of Oxidative Stress Profile in Skin Samples of *Streptococcus equi* infected Foal compared to Healthy Individual

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Despite the clinical increasing importance of oxidative stress in veterinary medicine, research investigating oxidative stress markers in horses remains remarkably limited. This study addressed this knowledge gap by evaluating oxidative stress dynamics in skin samples obtained from a 7-days-old foal with confirmed systemic *Streptococcus equi* infection compared to a healthy 10-months aborted fetus from twin pregnancy as control. Biochemical assays revealed significantly decreased catalase (44% of control) and superoxide dismutase (58% of control) enzymatic activities and lower levels of reduced glutathione (34% of control) in infected sample compared to control, indicating impaired antioxidant defences. The other oxidative stress markers demonstrated markedly elevation, as revealed by lipid peroxidation and protein oxidative damage (an increase of malondialdehyde and advanced oxidation protein products by 2 and 1.7 times of control, respectively). Histological examinations from both samples confirmed preserved skin integrity, confirming that the biochemical results reflect oxidative stress in the absence of noticeable tissue degeneration. These preliminary findings indicate oxidative imbalance in equine bacterial infections, suggesting disrupted redox homeostasis in *Streptococcus equi* infected foal skin and supporting further research into antioxidant therapies.

PP48-Integrated Biorefinery Approach for the Valorization of *Ulva* sp. in İzmir Bay as a Sustainable Source of Value-Added Products

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Ulva sp. proliferated excessively in İzmir Bay, harming the marine ecosystem. Although it had been collected for Bay cleaning, the biomass was not utilized. This interdisciplinary study aimed to valorize *Ulva* through food applications, biogas, and bioplastics, following a zero-waste biorefinery approach.

Collected *Ulva* samples were prepared as biomass for further analyses. Bioactive compounds were extracted using ultrasound-assisted ethanol extraction. Following heavy metal and microbiological assessments, the extracts were used as natural colorants in two model food products. Extraction residues were evaluated for biogas production via Biomethane Potential (BMP) tests and were also incorporated into bioplastic formulations with the aim of producing flexible, soft, tensile-resistant, and smooth architectural materials. This integrated valorization strategy highlighted the potential of *Ulva* biomass in sustainable product development, offering an eco-friendly approach for marine biomass management and supporting circular bioeconomy principles.

This study was supported by COST (CA20106) and TUBITAK (Grant No. 123Y090).

Key words: İzmir Bay, *Ulva*, biorefinery, extraction, biogas, bioplastic.

PP49-Prevalence and dynamics of ticks infesting small ruminants in a region of Southern Romania

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Tick infestations have a major impact on sheep health and their production, directly, as hematophagous parasites, and indirectly, as vector for pathogens, some of them being causative agents of emergent zoonotic diseases. In recent decades, an increasing abundance of tick populations have been reported in many parts of Europe, posing increased risks for tick-borne pathogens. Knowledge on the presence and geographical distribu-

tion of tick species in a particular area is essential for effective control of ticks and tick-borne diseases. Therefore, this study aimed to provide insights into diversity and dynamics of tick species infesting small ruminants, in Southern Romania. For this, sheep and goats from eleven herds in different locations of Prahova county were examined, during of 2019-2024. Overall, 7348 ticks were collected and subjected for morphological identification. Subsequently, the following species, with their overall prevalence, were identified: *Haemaphysalis punctata* (57.37%), *Dermacentor marginatus* (29.96%), and *Ixodes ricinus* (12.66%). The annual dynamics of ticks in the investigated area showed a higher abundance in April for *H. punctata* and *D. marginatus*, and in May for *I. ricinus*. These findings showed high prevalence and diverse ticks infesting small ruminants in the area, and highlight the need for appropriate control measures to be applied.

MALDI-TOF, urine cultures, *Escherichia coli*

PP50-Potential Impact of Antibiotic Resistance of Gram-Negative Pathogens in Urinary Infections in Tirana, Albania, in 2024, After the COVID-19 Pandemic

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Healthcare globally has been significantly affected by the COVID-19 pandemic, which is changing not only how antibiotics are used but also the landscape of antibiotic resistance, particularly concerning Gram-negative bacteria. The threat from antibiotic resistance is especially notable in Gram-negative bacteria like *Klebsiella pneumoniae* and *Escherichia coli*. This study aims to provide vital insights while evaluating the prevalence and trends of antibiotic resistance against these pathogens identified in urine cultures from the year 2024, after the COVID-19 pandemic, in the Tirana district of Albania. By employing MALDI-TOF mass spectrometry for the rapid identification of bacteria and the VITEK system to assess antibiotic resistance, we managed to analyze various resistance profiles in these pathogens.

Our findings reveal a significant increase in the prevalence of strains producing extended-spectrum beta lactamases (ESBL), with *Klebsiella pneumoniae* showing particularly high resistance levels to second-generation cephalosporins. Meanwhile, *Escherichia coli* demonstrated an alarming rise in resistance to aminoglycosides and fluoroquinolones. Consequently, treatment options have become quite complex, necessitating careful therapeutic considerations for both types of bacteria.

Furthermore, the emerge of cases with resistance to carbapenem classes cannot be overlooked. This study highlights an urgent need for stringent monitoring of antibiotic resistance, coordinated antimicrobial programs, and the integration of the latest rapid identification techniques for pathogens, including MALDI-TOF mass spectrometry.

Keywords: Antibiotic Resistance, Gram-negative bacteria,

PRESENTATIONS AT SATELLITE EVENT: CA RECROP WORKSHOP

CA1-Metabolome profiling for a better selection of winter wheat cultivars (*Triticum aestivum* L.) tolerant to heat stress.

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Abstract

Durum wheat is essential for human dietary needs, and various environmental stresses can severely hinder the expression of its yield potential and influence the qualitative traits of the grain. Among others, the elevated temperatures, as a form of abiotic stress, can significantly affect the concentrations of plants primary and secondary metabolites. The aim of this study was to investigate the possible HT stress memory at wheat plants exposed to two subsequent HT (30°C) treatments (T1 and T2) during pre-anthesis based on their metabolic profiles. For this, three weeks old plantlets were exposed at 30°C for 1hr, then kept in control conditions for 48hrs, and subsequently exposed to a second HT treatment of 30°C for 1hr. GC-MS and HPLC-MS were used to analyze primary and secondary metabolic profiles. Over 27 compounds of primary metabolites and almost 16 of secondary metabolites had cv-specific variable quantities. An elevation in the majority of the examined metabolites was observed in "T1", although some of the compounds like biotin, catechin or epigallocatechin gallate did not change in their amount. Primary metabolites exhibited cv-specific variation. Acids and sugars like malic acid, d-fructose, and ethanolamine were present in very low quantities (nearly 0) in both T1 and T2. In contrast, aminoacids like silanol, L-aspartic acid, cadaverine, glycolic acid, and asparagine are found in greater quantities in T1 than in T2. Almost all secondary metabolites displayed significant changes in their compounds. Epigallocatechin gallate, procyanidin, and chlorogenic acid were entirely absent (0 concentration) in T2. The remaining compounds (13) exhibited variations between T1 and T2 across cultivars.

In conclusion, metabolomics is an important tool to enhance our understanding of heat stress affect in *Triticum aestivum* L., and possible memory in metabolomics level.

Keywords: metabolomics, primary and secondary metabolism, heat stress, wheat

CA2-Investigating Drought Intergenerational Memory in Legumes using Chickpea as a Model

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Abstract

Drought stress, caused by climate change is a critical challenge to legume productivity, including chickpea. The purpose of this work is to gain insight into the complex and hidden mechanisms of intergenerational memory to this abiotic stress using chickpea as model species for legumes. Our approach followed the classical forward genetics approach that integrates multi-omics methodologies with biochemical, morphological and phenotypic analysis. Results clearly showed a molecular mechanism of stress memory aiming at conferring offspring a beneficial adaptation to drought stress while it might compromise filial fitness in absence of stress. Drought stress significantly affected specific leaf area (SLA), photosynthesis rates and plant biomass. Plant filial generation of stressed parents followed a conservative plant growth behavior focused on efficiently managing stress response with a consequent advantage in comparison to plants derived by parents that never experienced drought stress. Offspring of stressed parents (G1S) showed higher levels of scavenging mechanisms against re-

active oxygen species (ROS) as well as upregulation of genes involved in detoxification of reactive oxygen species and proline biosynthesis compared to those of control parents (G1C). Methyloome profiles were affected by intergenerational memory as shown by the reduction of genome-wide DNA methylation in response to drought stress in parental generation contrarily to the increase observed in offspring of stressed parents. Differentially methylated genes involved in abiotic stress responses remained in G1S even under optimal irrigation regime. An inherited drought stress memory was also observed at metabolic level. Key drought stress-related metabolites (proline, tryptophan, alanine, fructose) were higher in offspring of stressed parents compared to control ones. Our findings provide valuable insight into the complex mechanisms governing intergenerational plant stress memory to identify key molecular targets for developing climate-smart legume varieties using sustainable breeding strategies.

Keywords: Plant intergenerational stress memory, chickpea, drought stress, DNA methylation, omics approaches.

CA3-Micro and macro morphology for fusarium detection at wheat cultivars in use in albania and more

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Abstract

Fusarium head blight (FHB), often known as scab or tombstone, constitutes a major fungal disease that affects wheat, barley, oats, and several other small cereal grains, in addition to corn. This affliction can also affect both wild and cultivated species, although wheat is the crop that suffers the most severe consequences. It is among the most prevalent, abundant, and significant genera of soil microfungi identified as pathogens affecting a variety of plant species. The ascomycete fungus, *Fusarium graminearum*, is the predominant causative agent of Fusarium head blight (FHB). *F. graminearum* generates ascospores (sexual spores) and conidia (asexual spores), which can act as inocula for the disease FHB. At the same time, grains infected with *Fusarium* frequently exhibit contamination by mycotoxins, including trichothecenes (TRIs), fumonisins, and zearalenones. Thirty-two winter wheat cultivars (*Triticum aestivum* L.) in use in Albania were selected to be morphologically characterized by macro and microscopy means. Nineteen colonies identified visually as belonging to *Fusarium* genera were grown in PDA plates, and colony morphology and structure were further investigated via stereomicroscopy. Their pigmentation, and morphological traits such as the presence of macroconidia, microconidia, sporodochia, and chlamydospores revealed notable morphological similarities among the isolates. The most common species of *Fusarium* genus found in the Albanian wheat cultivars were *F. graminearum*, *F. culmorum*, *F. avenaceum*, *F. poae*. Twenty seven out of thirty-two cultivars tested were infected by at least one of the four *Fusarium* species

investigated in this study.

Keywords: wheat, Fusarium Head Blight, colony morphology

CA4-Multi-omics insights into chilling injury responses in peach (*Prunus Persica*) fruit

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Abstract

Peach fruit deteriorate quickly at ambient temperature and therefore cold storage is widely used to slow these processes and decay development. However, chilling injury (CI) limits the storage life of peaches under low temperature. It has been widely reported that the expression of CI symptoms evidenced as undesirable softening, flavor loss, mealy texture, and internal reddening. Although the genetic background of peaches is limited, there are differences between cultivars in their CI tolerance. Here, we employed a multi-omic approach (transcriptomics, epigenomics, proteomics and metabolomics) in the mesocarp of a CI-sensitive peach cultivar at various pre-conditioning stages. Using this approach we identified potential genes, proteins and metabolites that are involved in cold responses and possibly in CI symptoms. Specifically, we characterized cold-related hub responses, among which we focus on selected cold-responsive transcription factors. To link these TFs with CI, we evaluated their expression at pro-symptomatic and CI symptomatic stages in 30 peach cultivars that exhibited distinct CI phenotypes. We have also screened 118 cultivars from the peach reference collection, PeachRefPop, located in Naoussa Greece, to identify CI-related donor germplasm. Consequently, we performed whole genome resequencing of all above cultivars to identify small variants (SNPs and InDels). Our genome-to-phenome association analyses uncovered potential genetic markers controlling CI, providing valuable targets for molecular breeding. This work underscores the breeding potential of peach genetic resources and paves the way for enhanced postharvest fruit quality in perennial tree crops.

CA5-Molecular strategies for thermotolerant pollen: a

translational perspective

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Abstract

Pollen germination and pollen tube growth are among the most heat-sensitive stages of plant reproduction. High temperatures induce a global downregulation of translation while promoting the selective synthesis of proteins required for cellular survival and protection against protein misfolding. In *Arabidopsis thaliana*, the *eif3m1/eif3m2* double mutant exhibits impaired pollen germination, compromised tube integrity, and increased seed abortion even under normal conditions. Unexpectedly, however, *eif3m1* single mutants display improved pollen germination and enhanced tube stability under heat stress, outperforming the wild-type Col-0. This thermotolerant phenotype is associated with the upregulated expression of the eIF3M1 paralog eIF3M2, which drives elevated HSP70 mRNA and protein levels. Overexpression of eIF3M2 enhances HSP70 expression, while its knockdown reduces HSP70.1 promoter activity and increases pollen tube bursting under elevated temperatures. Moreover, eIF3M2 physically interacts with both HSP70 and eIF4G proteins. Together, these findings identify an eIF3M2–HSP70 regulatory module as a key determinant of pollen tube thermotolerance, preserving membrane integrity and supporting fertilization and seed set under heat stress. This mechanism reveals a novel strategy by which plants safeguard reproductive success under climate-induced temperature extremes.

Acknowledgement:

The authors acknowledge the financial support from European Cooperation in Science and Technology COST Action RECROP (CA22157), the European Regional Development Fund (ERDF) Programme Johannes Amos Comenius project TowArds Next GENERation Crops (TANGENC) (reg. no. CZ.02.01.01/00/22_008/0004581) and the Czech Science Foundation GACR grant no. 24-10653S.

Keywords: pollen thermotolerance, translation regulation, eukaryotic translation initiation factor 3, heat shock proteins

CA6-Genetic background-dependent cold stress response in maize

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Abstract

Cold stress is a severe constraint in early sowing for the stabilization of maize yield in changing climate conditions. The aim of this research was to study the molecular basis of cold response in genetically disparate maize inbred lines-Lancaster and Non-Lancaster-offered for hybrid combinations. RNA-Seq-mediated expression profiling showed 77 DEGs between the two groups, some involved in photosynthesis, signal transduction, and sulfur metabolism. Cold responsiveness of some selected DEGs-Chloroplast ATP-sulfurylase, CIPK15 kinase, and Calvin cycle CP12-was validated at different time points after exposure to stress, showing differential expression depending on the genetic background. Furthermore, cold tolerance physiological assessment agreed with the molecular profiles, determining that some Non-Lancaster lines had higher potential for adaptation. The present findings provide molecular targets for marker-assisted selection and hence development of cold-tolerant hybrids, paving way for climate-resilient agriculture and food security in the region.

Keywords: RNA-seq, differential gene expression, cold stress, maize, climate change

CA7-Interaction of Biological and Physical Factors in Optimizing Microclimatic Conditions for the Preservation and In Vitro Conservation of Indigenous Grapevine Cultivars Kallmet, Vlosh and Shesh i Zi

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Abstract

In this study, in vitro preservation and conservation methods were applied to the minimal growth of explants of autochthonous cultivars Kallmet, Vlosh and Shesh i Zi. The preservation of plant material of grapevine cultivars was carried out with the minimal growth methods in the field (3 months; 6 months; 9 months). The data show that the cultivar Shesh i Zi has the highest percentage of 93% of bud survival and 81.2% bud regeneration percentage in the 3-month period compared to the 6-month and 9-month treatment periods. Another minimal growth method is soil modification without the presence of phytohormones, where the best result in the percentage of bud regeneration of 85%, resulted for the cultivar cv. Shesh i Zi, and for cv. Vlosh with 60.6% for the 3-month treatment. Another method used for the preservation and conservation of buds consists of lowering the temperature (4°C) and in dark conditions, where the best results were obtained in the percentage of bud regeneration for cv. Vlosh with 80% and Shesh i Zi with 77.1% for the 3-month treatment period, which is considered the best, compared to 6 months and 9 months, where plants under minimal in vitro growth conditions are characterized by low regenerative potential.

Keywords: conservation, regeneration, cv. shesh i zi, vlosh, kallmet

CA8-Leveraging stress tolerance mechanisms of resurrection plants for climate-resilient crop breeding: the role of modern technologies

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Abstract

Climate change presents significant challenges to plant productivity, necessitating the development of resilient crop varieties capable of withstanding extreme environmental conditions. Resurrection plants such as *Ramonda serbica* and *Ramonda nathaliae* offer valuable insights into stress tolerance mechanisms that can inform modern breeding strategies. These species demonstrate remarkable abilities to recover from desiccation and tolerate freezing stress through enhanced antioxidant capacity, stress-induced protein accumulation, and efficient regulation of photosynthesis—traits that are highly desirable for improving crop resilience. In our research, the application of innovative technologies—including gas exchange measurements using CIRAS-4 and LI-COR 6800 systems, 3D multispectral scanning, and CropReporterTM and Western Blot biochemical analysis, enabled a detailed physiological and molecular characterization of *Ramonda* species. These technologies provided significant added value by deepening our understanding of stress response mechanisms at both the physiological and protein expression levels, highlighting potential pathways for practical application in crop improvement. Integrating such stress tolerance traits into crop breeding programs can lead to the development of climate-resilient cultivars with improved resistance to drought, freezing, and oxidative stress. Modern breeding approaches, including marker-assisted selection, genomic prediction, and genetic engineering, offer effective tools for introducing protective traits into economically important crop species. Enhancing the expression of key protective proteins, such as dehydrins, early light-inducible proteins (ELIPs), and light-harvesting complex (LHC) proteins, could significantly improve photosynthetic efficiency and environmental adaptability. By leveraging the natural resilience of species like *Ramonda*, plant breeding can play a transformative role in advancing sustainable agriculture under climate change. Such innovations are essential for ensuring stable food production in cold-prone and arid regions, ultimately contributing to global food security in the face of increasing environmental stress.

Keywords: Resurrection plants, drought and freezing stress, climate change, crop breeding, innovative technologies

CA9-Can I put some logic inside my sensor plants?

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Functional sensing, which evaluates plant health through genotypic responses, offers a compelling alternative to traditional agricultural monitoring. Recent advances in synthetic biology have enabled the design of genetic circuits that perform Boolean logic operations *in vivo*, allowing detection of multiple stimuli via a single reporter. However, most plant circuits to date focus on altering plant traits through irreversible genetic changes, limiting their use for real-time sensing. Here, we introduce a proof-of-concept reversible genetic logic circuit in tobacco plants using Cas6-mediated translational repression. The system functions as a 2-input NOR gate, with estradiol and ethanol as inputs and green fluorescent protein (GFP) as the output. When either input is present, inducible promoters activate Cas6 expression, leading to cleavage of GFP mRNA and inhibition of its translation. Tobacco plants transiently expressing the constructs showed reduced GFP fluorescence—two- to four-fold lower—when exposed to at least one inducer, as observed through confocal microscopy. This approach highlights the potential of reversible genetic circuits for real-time functional sensing in plants, laying the groundwork for future development of dynamic, multiplexed biosensors for agricultural applications.

CA10-Revealing protein phosphorylations in male gametophyte by phosphoproteomic approaches

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In angiosperms, mature pollen represents a quiescent stage of the male gametophyte, with a desiccated cytoplasm enclosed by a tough cell wall. Pollen grains have to survive harsh environmental conditions in order to safely deliver the genetic material to the female gametophyte. Upon pollination, pollen rapidly rehydrates and becomes metabolically active, initiating germination and rapid pollen tube growth—a highly dynamic process involving protein synthesis, metabolic reprogramming, and signaling with female reproductive tissues. Given the reversible nature of protein phosphorylation, we focused on its regulatory role during male gametophyte development. We will share insights from various phosphoproteomic studies conducted across several species, including *Arabidopsis thaliana*, tobacco, maize, and kiwifruit. By comparing these datasets, we've identified common regulatory phosphoproteins and conserved signaling patterns. Special attention was given

to the phosphorylation of eukaryotic translation initiation factor subunits, which are key regulators of protein synthesis. We extended our analysis to root hairs, revealing striking phosphoproteomic similarities and suggesting that common molecular mechanisms govern polarized cell growth in diverse plant cell types. The presentation will be part of RECROP workshop, and we acknowledge the financial support from the Ministry of Youth, Sports and Education OP JAK (CZ.02.01.01/00/22_008/0004581), and Czech Science Foundation (23-07000S).

Keywords: male gametophyte, protein phosphorylation, tobacco, regulation of translation

CA11-Integrated Methodological Approach -A Success Story On The Investigation Of *Fsc* At Local Wheat Cultivars During Early Development

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Abstract

Identifying *Fusarium Complex Species* (FCS) is essential for understanding this fungal pathogen diversity, for the disease management, and for the selection of wheat cultivars naturally resistant to it. The study aimed the identification of FSCs naturally present in three wheat cultivars (Urma, Vittoria, and Artico) in use in Albania, based on the *Tef1α* gene. The last encodes a protein essential for positioning aminoacyl-tRNA on the ribosome during translation and is a highly reliable species-level marker, with no detected non-orthologous copies and universal primers now available for its entire phylogenetic range. *Fusarium* single cultures were isolated from seeds of the cultivars grown on PDA medium, total DNA was extracted from hyphae, the *Tef1α* gene fragments were PCR amplified, and amplicons were sequenced via DNBSEQ Short-read library preparation (DNA fragmentation; Size selection; End repair and "A" tailing; Adapter ligation; Product size selection; PCR reaction; Library QC.; Bioinformatic Analysis). Sequences were analyzed using the Fusaroid-ID and NCBI databases. Hierarchical clustering (UPGMA) of the results allowed the construction of two dendrograms, one based on presence/absence, and the other on species abundance. Specific FCSs and dominant species for each cultivar were identified (FIESC, FFSC, FOSC, FFBSC, FNESC, FTSC, FSAMSC) with FIESC and FFSC as the most dominant. In conclusion, the study demonstrated the diversity of *Fusarium* species in local wheat cultivars and the importance of molecular tools for accurate pathogen identification.

Keywords: gene fragments, PCR, sequencing, hierarchical clustering

CA12-Expression of *Rca* genes in *Fusarium*-infected wheat during early development

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Abstract

Fusarium is a widespread and economically significant genera of soil microfungi known to infect numerous plant species, particularly cereals such as wheat and other small grain cereals. This study aimed to investigate the early transcriptional response of wheat to *Fusarium* infection by analyzing the expression of RuBisCo activase genes, *Rca1B* and *TaRca1*. These genes encode nuclear-encoded chloroplastic chaperones essential for modulating RuBisCo activity, especially under environmental stress. Three local wheat cultivars (Urma, Vittoria, Toborzo) were studied during early vegetative growth stages (3 and 4 weeks old). Total RNA was extracted from leaf tissue prior to anthesis, and gene-specific transcripts were amplified using the SuperScript™ III One-Step RT-PCR System (Invitrogen™). Amplification resulted in seven *Rca1B* fragments (90 bp–1.3 kbp) and four *TaRca* fragments (50–224 bp); the expected 224 bp *Rca1B* product was consistently detected, while the 1.4 kbp *TaRca* product was absent. UPGMA dendrograms (Past 4.0 software) revealed cultivar-specific clustering patterns. Expression differences were observed across cultivars and infection status: Vittoria showed reduced *Rca1B* expression under infection, while Urma remained unaffected. *TaRca* was over-expressed in infected samples. In conclusion, results suggest cultivar-specific response to *Fusarium* infection with respect to the expression of different transcripts and their concentrations for both *Rca1B* and *TaRca* genes. These findings highlight genotype-specific expression responses to *Fusarium* stress and suggest potential molecular markers for breeding stress-resilient wheat varieties.

Keywords: gene expression, RuBisCo activase, RT-PCR, *Fusarium*

CA13-Rapid Identification of Quiescent Fungi in Fruits: A New Approach to Minimize Postharvest Losses

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Abstract

Postharvest decay, responsible for up to 50% of global fruit and vegetable losses, is often caused by latent infections of fungal pathogens such as *Colletotrichum*, *Botrytis*, and *Alternaria*. These pathogens invade unripe fruit and remain quiescent until ripening, making them invisible to conventional inspection methods during harvesting, packaging, or shipping. Early, sensitive detection is critical for minimizing spoilage and improving postharvest decision-making. Recent developments in loop-mediated isothermal amplification (LAMP), particularly reverse transcription LAMP (RT-LAMP), enable the detection

of pathogen-specific RNA biomarkers during the quiescent stage of infection. One RT-LAMP assay targeting the enoyl-CoA hydratase (ECH) transcript of *Colletotrichum gloeosporioides* provides visual results within 23 minutes using just 1 pg of RNA. The assay has been adapted into a low-cost, field-deployable paper-based format using cellulose membranes and a basic heat source, demonstrating high specificity and sensitivity down to 0.5 pg RNA. The approach has also been expanded to *Botrytis cinerea* using a heat-dried RT-LAMP formulation in 384-well plates. This format offers femtogram-level sensitivity, long-term reagent stability at room temperature, and suitability for both laboratory and on-site use. High-throughput adaptations using standard plate readers now enable the simultaneous screening of hundreds of samples, greatly increasing operational efficiency in postharvest facilities. These innovations support rapid, scalable, and affordable detection of latent fungal infections, allowing producers to make informed decisions about storage, distribution, or processing. By identifying high-risk produce early, these systems offer a practical strategy to reduce food losses, improve supply chain quality, and strengthen food security through targeted postharvest management.

Keywords: Biosensors, loop-mediated isothermal amplification (LAMP), fungal pathogen, fruit, point of care technology (POCT), paper-based analytic devices (PADs).

CA14-Histone Acetyltransferase GCN5 and the Associated Coactivator ADA2b Interplay with Plant Hormones Biosynthesis and Signaling in Arabidopsis

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Abstract

GCN5 is a well-characterized histone acetyltransferase in plants that functions in coordination with the transcriptional coactivator ADA2b within multiprotein complexes like SAGA (Spt-Ada-Gcn5 acetyltransferase), playing a critical role in the regulation of gene expression. Loss-of-function mutations in GCN5 and ADA2b in *Arabidopsis thaliana* result in a range of pleiotropic developmental defects, including dwarfism, aberrant root and floral morphogenesis. Phytohormones are central regulators of plant development, orchestrating processes from embryogenesis through to reproductive maturity. Notably, GCN5 and ADA2b have been implicated in regulating multiple hormonal pathways by modulating the expression of genes involved in hormone biosynthesis and signaling. Quantitative analyses revealed that the levels of key phytohormones—such as auxin, gibberellins, jasmonic acid, and abscisic acid—were markedly decreased in the inflorescence meristem of *gcn5* and

ada2b mutants. Transcriptomic profiling further demonstrated downregulation of a broad set of genes associated with both the biosynthetic and signaling components of these hormonal pathways in the mutant lines. Collectively, genetic, hormonal, and transcriptomic data converge to support that GCN5–ADA2b module functions as a positive regulator of multiple hormone-mediated developmental pathways, particularly during floral development.

This work is supported by the Hellenic Foundation for Research and Innovation (H.F.R.I.) Grant number 3026 to KV.

Keywords: Histone acetylation, floral meristem, hormones, biosynthesis, signaling, transcriptomics

CA15-Micro and Macro Morphology for Fusarium Detection At Wheat Cultivars in Use in Albania And More

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Abstract

Fusarium head blight (FHB), often known as scab or tomb-stone, constitutes a major fungal disease that affects wheat, barley, oats, and several other small cereal grains, in addition to corn. This affliction can also affect both wild and cultivated species, although wheat is the crop that suffers the most severe consequences. It is among the most prevalent, abundant, and significant genera of soil microfungi identified as pathogens affecting a variety of plant species. The ascomycete fungus, *Fusarium graminearum*, is the predominant causative agent of Fusarium head blight (FHB). *F. graminearum* generates ascospores (sexual spores) and conidia (asexual spores), which can act as inocula for the disease FHB. At the same time, grains infected with *Fusarium* frequently exhibit contamination by mycotoxins, including trichothecenes (TRIs), fumonisins, and zearalenones. Thirty-two winter wheat cultivars (*Triticum aestivum* L.) in use in Albania were selected to be morphologically characterized by macro and microscopy means. Nineteen colonies identified visually as belonging to *Fusarium* genera were grown in PDA plates, and colony morphology and structure were further investigated via stereomicroscopy. Their pigmentation, and morphological traits such as the presence of macroconidia, microconidia, sporodochia, and chlamydospores revealed notable morphological similarities among the isolates. The most common species of *Fusarium* genus found in the Albanian wheat cultivars were *F. graminearum*, *F. culmorum*, *F. avenaceum*, *F. poae*. Twenty seven out of thirty-two cultivars tested were infected by at least one of the four *Fusarium* species investigated in this study.

Keywords: wheat, Fusarium Head Blight, colony morphology

CA16-Hairy roots as a powerful tool to study hormonal and abiotic stress response

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Abstract

Hairy root cultures are a versatile system with many applications, including the production of recombinant proteins and valuable secondary metabolites, as well as the functional characterisation of genes. We have developed efficient transformation protocols for the spring cultivars of *Brassica napus* and *Brassica rapa* using hairy roots. We have generated various reporter lines, including new fluorescent reporters that monitor the response of the plant hormones auxin and cytokinin to abiotic stress stimuli. Furthermore, we have developed a pipeline for gene editing and hairy root regeneration in *B. napus*, with the aim of creating transgene-free, gene-edited plants. Since oilseed rape is an allotetraploid species (AACC, $2n=38$), mutating homoeologs from both subgenomes is necessary to overcome functional genetic redundancy. Using optimised CRISPR/Cas9 vectors, we generated multiple mutant lines in four *B. napus* TRYPTOPHAN AMINOTRANSFERASE (*BnaTAA1*) auxin biosynthetic genes. In conclusion, we have initiated a functional analysis of *BnaTAA1* and a study of the auxin biosynthesis pathway in oilseed rape using hairy root cultures. We offer transformation services for selected oilseed rape cultivars to generate CRISPR-edited plants and reporter lines. Funding sources: GA23-06140S by the Czech Science Foundation and TANGENC (TowArds Next GENeration Crops) CZ.02.01.01/00/22_008/0004581 of the ERDF Programme Johannes Amos Comenius by MEYS.

Keywords: *Brassica napus*, hairy root, gene editing, plant transformation, plant regeneration

CA17-From Understanding Heat Stress Response to Developing A Thermoresilient Tomato

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Abstract

Heat stress poses a major challenge to tomato production, particularly affecting reproductive success and fruit yield. In the face of rising global temperatures, our research aims to decode the molecular networks that enable heat stress mitigation in tomato. We focus on the role of Heat Shock Factors (HSFs) and their associated gene networks in orchestrating gene expression programs under high temperatures. Using a combination of functional genomics and cell biology, we investigate how HSFs integrate stress signals and engage in tissue-specific regulatory interactions. Special attention is given to the transition

between stress response activation and recovery, highlighting the temporal control of gene expression. In addition to HSFs, we have also identified splicing factors that play central role in heat stress sensitive alternative splicing. The activity of two balances the basal and acquired thermotolerance capacity. Our findings uncover developmental stage-specific sensitive traits and adaptive mechanisms that can be utilized to improve tomato resilience to high temperatures.

Keywords: thermotolerance, heat stress response, transcription, RNA splicing, crop resilience, tomato

CA18-Movement protein-mediated approaches in the development of virus-resistant transgenic plants

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Abstract:

Plant viruses continue to threaten global food security by causing widespread losses in crop yield and quality. Traditional control methods are often ineffective, especially against rapidly evolving viruses. A promising alternative lies in genetic engineering approaches that disrupt the fundamental processes viruses use to spread within their host. Central to many plant virus infections are movement proteins (MPs), non-structural viral components that enable the virus to move between plant cells via plasmodesmata. These proteins alter the size exclusion limits of these intercellular channels, allowing viral genomes or particles to pass through. Due to their minimal genomes, plant viruses are forced to hijack specific cellular pathways that depend on direct interactions between viral MPs and host proteins. By exploiting this dependency, transgenic plants can be engineered to express interfering proteins such as mutated MPs that still bind to target sites (plasmodesmata) but cannot function properly, that sequester or inhibit viral MPs. This interference can restrict virus movement, delay symptom onset, or prevent systemic infection. Because this strategy targets a conserved mechanism common to many plant viruses, it offers potential for broad-spectrum resistance. Movement protein-mediated resistance represents a powerful and targeted approach for developing virus-resistant crops through molecular biotechnology.

Keywords: plant virus, movement protein, plasmodesmata, genetic engineering, transgenic resistance, virus-host interaction, broad-spectrum resistance.

CA19-Does *Fusarium* infection impact the epigenetic memory of wheat to repeated HT?

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HS is accompanied by other abiotic and biotic stresses, which contribute to plants performance. Here we describe how three wheat cultivars (*T. aestivum* L.), both *Fusarium* infected (inf) or not (non-inf), were used to evaluate its possible role on the memory to HT 30°C applied twice ($T^{1,2}$) to three-week old plants. Root and shoot length, fine root cells death, RWC, pigments, carbohydrates, and Rubisco activase expression were evaluated. Results showed higher synthesis of carotenoids at inf plants. Synthesis of pigments were cv-specific, higher for T^2 than T^1 . Carbohydrates were higher at inf, with T^1 values higher than T^2 . RWC was lower at inf, and cv-specific for $T^{1,2}$. Shoot length was reduced at inf plants, and HTs had positive effect to both. Root length was impacted in cv-specific manner. Alive root tip cells were less for inf plants, and higher after T^2 . *Rca* expressions were not modified by infection. In conclusion, *Fusarium* impacts the memory of wheat to repeated HT in a cv-specific manner, which has to be considered for selection purposes.

FULL TEXTS

FT1-Potential Impact of Antibiotic Resistance of Gram-Negative Pathogens in Urinary Infections in Tirana, Albania, in 2024, After the COVID-19 Pandemic"Arjeta Xheka^{1*}, Klementina Puto²¹University of Tirana, Faculty of Natural Sciences, Department of Biotechnology, Albania²University of Tirana, Faculty of Natural Sciences, Department of Biotechnology, Albania

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Abstract

Healthcare globally has been significantly affected by the COVID-19 pandemic, which is changing not only how antibiotics are used but also the landscape of antibiotic resistance, particularly concerning Gram-negative bacteria. The threat from antibiotic resistance is especially notable in Gram-negative bacteria like *Klebsiella pneumoniae* and *Escherichia coli*. This study aims to provide vital insights while evaluating the prevalence and trends of antibiotic resistance against these pathogens identified in urine cultures from the year 2024, after the COVID-19 pandemic, in Tirana district of Albania. By employing MALDI -TOF mass spectrometry for the rapid identification of bacteria and the VITEK system to assess antibiotic resistance, we managed to analyze various resistance profiles in these pathogens. Our findings reveal a significant increase in the prevalence of strains producing extended-spectrum beta lactamases intermediates with *Klebsiella pneumoniae* showing particularly high resistance levels to second and third -generation cephalosporins. Meanwhile, *Escherichia coli* demonstrated an alarming rise in resistance to aminoglycosides and fluoroquinolones. Consequently, treatment options have become quite complex, necessitating careful therapeutic considerations for both types of bacteria. Furthermore, the emergence of cases with resistance to carbapenem classes cannot be overlooked. This study highlights an urgent need for stringent monitoring of antibiotic resistance, coordinated antimicrobial programs, and the integration of the latest rapid identification techniques for pathogens, including MALDI-TOF mass spectrometry.

Keywords: Antibiotic Resistance, Gram-negative bacteria, MALDI-TOF, urine cultures, *Escherichia coli*

Introduction

Urinary tract infections (UTIs) are a common yet troublesome health issue that affects countless individuals worldwide. They

are the most common bacterial infectious diseases encountered in clinical practice and account for significant morbidity and high medical costs. With antibiotic resistance on the rise, treating these infections is becoming increasingly challenging. Infections caused by antimicrobial-resistant organisms are not only difficult to treat, there is also always an increased change of severe illness and even death due to these infections.[1] As we have navigated through the COVID-19 pandemic, the landscape of treating these infections has changed dramatically. Antibiotic resistance is becoming a major hurdle, making it tougher to find effective treatment. The main cause of UTIs are infections caused by *Escherichia coli*, responsible for 75% of uncomplicated UTIs and 65% of complicated UTIs.[2] *Klebsiella pneumoniae* is also a Gram- negative bacteria that has emerged as a major pathogen responsible for both community-acquired and nosocomial UTIs, particularly in immunocompromised individuals and those with chronic underlying conditions. In this study, we're turning our focus to Tirana, Albania, to explore how gram- negative pathogens like *Klebsiella pneumoniae* and *Escherichia coli* are developing resistance in UTIs cases, exhibiting markedly increased resistance to a variety of antibiotics.

Methods

Our research aims to evaluate the prevalence and trends of antibiotics resistance within these critical pathogens, based on urine cultures collected from 2012 patients during 2024 in Tirana, Albania.

Study site:

The investigation was conducted across multiple healthcare facilities with the urban district of Tirana.

Sample collection and isolation of pathogen:

Urine cultures were systematically collected from patients presenting with symptoms indicative of urinary tract infections. A total of 2412 urine samples were collected for both culture and sensitivity, from different Microbiology laboratories in Tirana, using same methods of Antibiotic Susceptibility Testing. Patients collected midstream urine specimens in sterile cups. Colony counts of more than 10^5 CFU/mL were considered significant.

After barcoded, the samples were sent to the microbiology laboratory for further analysis.

Urine samples were inoculated onto Uricult Plus slide immediately after collection. Those samples that needed to be stored prior to inoculation, had been refrigerated at 2°C - 8°C for no more than 24 hours.

Uricult Plus is a dipslide culture method for diagnosing urinary tract infections by demonstrating microbes in urine. This dipslide is based on three agar media. One side of the plastic slide is covered with green CLED agar medium and the other with reddish- brown MacConkey agar and a colorless Enterococcus medium [3]

CLED is a non-selective differentiating medium in which *S. aureus* colonies grow, which are presented in yellow color. Colonies of *E. coli* grow on CLED and MacConkey grounds. Only enterococci and some streptococci grow on Enterococcus selective medium.

After totally immersed agar surfaces into freshly voided midstream urine, the tubes were placed upright in the incubator 37°C for 16-24 hours.

Escherichia coli is a lactose-fermenting bacteria and on selective media like CLED and MacConkey, this is shown by a color change to yellow or pink/purple, respectively.

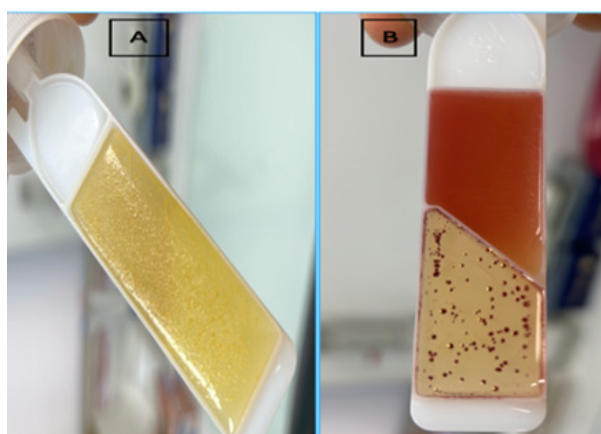


Figure 1. *Escherichia coli*, cultivated on Uricult Plus dipslide at 37°C during 24h. *E. coli*-strains grow on CLED agar (A side) and the color of the medium is changed from green to yellow since *E. coli* ferments lactose and on MacConkey agar (the upper part of the B side) forms pink-red colonies.

Pathogens identification and laboratory techniques:

Bacterial growth of $\geq 10^5$ CFU/mL was considered significant for UTIs.

A finally bacteria identification was performed by MALDI-TOF mass spectrometry, allowing identification of microorganisms within a few minutes down to the species level. It was a simple, fast identification technology capable of analyzing many samples at the same time [4],[5]

This advanced technology was employed for the rapid identification of bacterial species, significantly enhancing diagnostic efficacy.



Figure 2. The colony are placed on a MALDI target plate in order to be identified. The device irradiates the target plate with a laser. Compass software automatically generates MALDI-TOF Spectrum. To identify the sample, the acquired MALDI mass spectral fingerprint is compared with the stored database.

VITEK 2, an automated system was also utilized in our research to determine antibiotic susceptibility profiles of the identified pathogens.

To determine bacterial susceptibility to antibiotic agents, minimum inhibitory concentrations were determined using the ID-AST cards.

A sufficient number of colonies was suspended in sterile saline (0.45%) and adjusted to a 0.5 McFarland turbidity standard using the Densitometer. The inoculated tube was placed in a cassette on the VITEK 2 Smart Carrier Station. The sample number was entered and associated with an ID and AST card (Figure 3). The sample accession numbers and card identification bar code numbers were scanned, and the information was stored on the cassette memory chip. The SCS cassette with the cards and the test tubes was placed on the VITEK 2 instrument where the inoculation of the AST cards was automatically performed by the instrument [6].



Figure 3. Equipment used in the antimicrobial susceptibility testing workflow: basic inoculum preparation tools, densitometer for inoculum verification and AST cards

Our research was focused on gram negative bacteria and antibiotic susceptibility testing was performed on all isolates using AST-N437 panel according to the manufacturer's instructions. The card we used were AST-N437. The cards contained well preloaded with 18 different antibiotics at fixed concentrations. The antibiotic panel tested included: AMK, AMP, AUG, CAZ, CIP, FOX, FTX, FUR, GEN, IMP, KEF, NAL, OFL, PPT, SXT, TIC, TOB and ETP. After inoculation with a bacterial suspension the cards were placed in the VITEK 2 instrument. (Figure 4). This instrument checked bacterial growth and reported MICs and susceptibility categories once testing was completed. Results were integrated into the laboratory information system and communicated to clinicians as MIC Sensitive/ Intermediate/ Resistant.



Figure 4. VITEK 2 instrument

Data analysis:

Microsoft Excel was used for data collecting and coding. A rigorous statistical approach was adopted to analyze resistan-

lines. Intermediates results were excluded from the analysis. No genotype data (ESBL status) were collected or analyzed.

Results and discussions

For over 12 month's period from January to December 2024, a total of 2412 urine samples from different patients in Tirana region were recorded. Microbiological proof of gram-negative infections was found in about 63,4% of the samples. Isolates were for 18 antibiotics susceptibility.

Among 680 *Klebsiella pneumoniae* isolates, susceptibility was categorized as susceptible or resistant (intermediates excluded). Overall susceptibility varied notably by antibiotic. The highest susceptibilities were observed for FUR (597/680; 87.79%), whereas the highest resistance was seen for FTX (560/680; 82,35%), AUG (520/680; 76.47%) and AMP (470/680;69.12%) exhibited markedly high resistance levels to second and third generation cephalosporins, thus posing a challenge to effective treatment strategies. This resistance is particularly concerning given the reliance on these antibiotics for common clinical interactions. (Chart 1).

The *Escherichia coli* highlight a different resistance profile compared with *Klebsiella pneumoniae*, with notably higher resistance to fluoroquinolones demonstrated a troubling rise in resistance rates to fluoroquinolones and beta-lactams like ampicillin. Among 850 *E. coli* isolates overall susceptibility varied by antibiotics. The most favorable susceptibility was observed for FTX (470/850; 55,3%), CAZ (447/850; 52.6%) and FUR (441/850; 51.9%) whereas the greatest resistance was seen for CIP (700/850; 82.4%) and AMP (700/850; 82.4%). Complete susceptibility data are summarized in chart 2. This trend raises significant concerns regarding the efficacy of these antibiotics, which are widely used in treating UTIs and other bacterial infections.

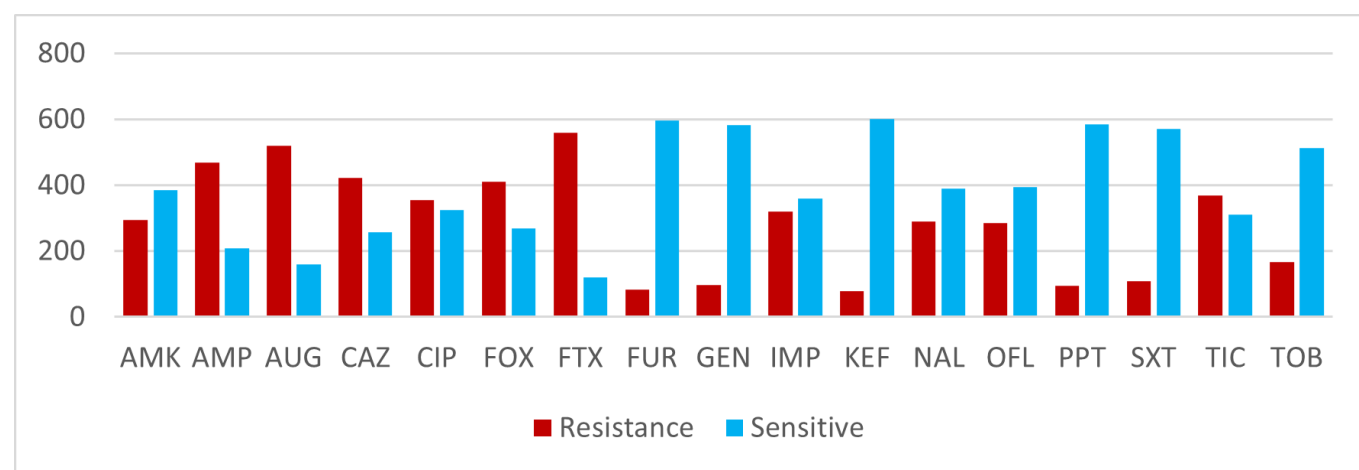


Chart 1. *Klebsiella pneumoniae* antibiotic susceptibility

ce patterns across various antibiotic classes, specifically focusing on β -Lactam, second and third generation cephalosporins, aminoglycosides, fluoroquinolones and carbapenems. Susceptibility interpretation followed the local/CLSI guide-

Additionally, the emerge of resistance to carbapenem antibiotics emerges as a serious threat to therapeutic options. The complexities involved in managing infections caused by these resistant strains need careful evaluation and optimization of

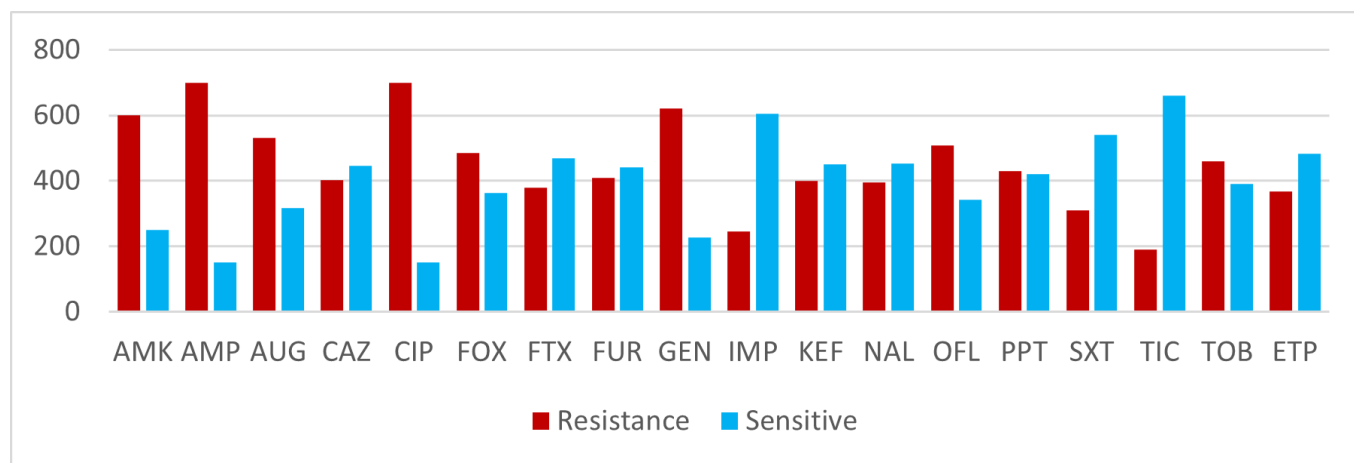


Chart 2. *Escherichia coli* antibiotic susceptibility

treatment strategies. Comparing our results with each other we evaluated that Imipenem had a very high efficacy in *E. coli* (85.1%) but more modest in *Klebsiella* (52.9%) and also Ticarcillin with very high efficacy in both, but comparable levels (*E. coli* 85.6%, *Klebsiella* 45.6%). The least favorable activity was observed for Amikacin and Ciprofloxacin (29% and 18% respectively). There is no genotype data available in this dataset (e.g., ESBL genes,). As a result, we cannot correlate phenotypic resistance to specific resistance determinants. We need to mention also the fact that had been some limitation in our research. The data report selected are only susceptible (S) and resistant (R) categories; no intermediates are shown and no genotype data is available, which constrains deeper mechanistic interpretation. The sample sizes differ between species and this should be considered in comparison. Resistance patterns might also be influenced by contextual factors such as patient location, specimen source, prior antibiotic exposure and also comorbidities.

Conclusions

The findings of this study highlight a concerning increase in antibiotic resistance among Gram-negative pathogens. The documented rise in resistance to critical β -lactam antibiotics complicates infections management, emphasizing the urgent need for careful selection of empirical therapy. Notably, while many commonly utilized antibiotics, such as Cefotaxime and Ceftazidime, exhibit significantly reduced efficacy, Nitrofurantoin remains a viable therapeutic option for uncomplicated urinary tract infections. Importantly, this investigation is conducted in the context of a post COVID-19 landscape, where shifts in healthcare practices and antibiotic usage patterns may influence resistance trends. Regular monitoring of antibiotic resistance and the development of effective stewardship programs are essential for ensuring that treatment options remain effective and for improving patient care in the changing healthcare landscape. The absence of ESBL genotype data limits in

terpretation of resistance mechanisms. These findings underscore the need local surveillance and inclusion of genotypic data

in future work.

Abbreviations:

AMR: Antimicrobial Resistance
MDR: Multi-Drug Resistance
UTIs: Urinary Tract Infections
AST: Antibiotic Susceptibility Testing
AMK: Amikacin
AMP: Ampicillin
AUG: Amoxicillin/Clavulanate
CAZ: Ceftazidime
CIP: Ciprofloxacin
FOX: Cefoxitin
FTX: Cefotaxime
FUR: Nitrofurantoin
GEN: Gentamicin
IMP: Imipenem
KEF: Cephalexin
NAL: Nalidixic acid
OFL: Ofloxacin
SXT: Sulfamethoxazole/ Trimethoprim
TIC: Ticarcillin
TOB: Tobramycin
ETP: Ertapenem

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FT2-EVALUATIONS ON SOME QUANTITATIVE PARAMETERS OF THE STOCKS OF *SALMO LETNICA* AND *SALMO OHRIDANUS* AS WELL AS ON THE ANALYTICAL INDICATORS THAT EXPRESS THE LEVELS OF EXPLOITATION OF THEM FROM THE PROFESSIONAL FISHERIES.

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Abstract

In this study some notions (or, indicators of the fisheries management) of fishing science [species specific production ratio (P/B); catch per unit effort ($CPUE$) and maximum sustainable yield (MSY)] have been applied to the analysis of the commercial catches of 2023, of two endemic trouts (*Salmo letnica* and *S.ohridanus*), from the Ohrid Lake. The assessments on the catches of Ohrid trout (*S.letnica*) and Ohrid belvica (*S.ohridanus*) resulted in the respective values for the P/B -indicator: 0.559/yr and 0.791/yr (using the data on the variable B , kg/ha); 0.284/yr and 0.262/yr (using the protocol of Hoening, 1983) as well as 0.151/yr and 0.259/yr (the protocol according to Randall and Minns, 2000). The values estimated for $CPUE$ were: $CPUE_{Tc}$ =0.520 kg/hr/ou (according to total catches); $CPUE_{Ot}$ =0.312 kg/hr/ou (according to Ohrid trout catches); $CPUE_{Ob}$ =0.087 kg/hr/ou (according to Ohrid belvica catches) and $CPUE_{Sal}$ =0.400 kg/hr/ou (according to salmonid fishes catches). The values resulted from the estimations about MSY , were: MSY_{Ot} =2.15 kg/ha, in the exploitation of Ohrid trout and MSY_{Ob} =0.40 kg/ha, in the exploitation of Ohrid belvica.

Keywords: endemic specie; stock; biomass; production rate per unit biomass; catch per unit effort; maximum sustainable yield; halieutic; fishing effort.

Introduction

Although fishery research has a long history at Ohrid Lake there is not much evaluations on the quantitative data from catches. Some information exists from the grey literature, however, it is often relates to annual or periodic catches only (Spirkovski and Talevska, 2002; Avramoski et al. 2003). The overfishing confirmed by this authors for two salmonid fishes requires scientific assessments on their stocks. In particular, fishing effort should be recorded at all times and taken into consideration when analyzing catch data. Recognizing the annual fluctuations in the total catches and the catches by different species in the both border areas of Ohrid Lake, spatial and temporal comparisons and assessment of stock developments over time require detailed information on the effort undertaken for data collection. It is crucial, therefore, to not only report on catches but to also calculate the catch per unit of effort ($CPUE$). Recording the fishing effort should become part of each monitoring program (Palluqi and Spirkovski, 2017).

The assessments on the real situation of the halieutic resources, in general and the fish stocks, in particular, as well as the annual evaluations on the catches of target species of commercial fisheries, are necessary prerequisites for respecting the principle of responsibility in exploitation of ichthyic species and guaranteeing the regeneration of fish stocks. In different scientific publications on the global fishing situation, are analysed human and natural factors that have caused the depletion of the stocks and the reduction of catches for some of the main target fish species. Thus, since 1996, the world's global catch is declining.

ing (Pauly and Zeller,2016).This expansion went along with tremendous build-up in fishing effort (Tickler et al.,2018),and massive declines of fisheries biomass (Costello et al., 2016) defined as the weight (whole-body, wet weight) of the in-water part of fish (and invertebrates) populations that is vulnerable to fishing gears (henceforth referred to as 'biomass').This decline in biomass of demersal species went along with an often radical modification of the ecosystems and habitats in question,caused by trawling (Palomares et al.,2020).

Systematic evaluation on a stock is a condition for knowing the factors that promote fluctuations in their quantitative indicators. There are several definitions about the notion of the "stock". According to Palomares et al.,(2020) the 'stock' or exploited population is defined as that part of the total biological/ecological population in situ,i.e., in the water body, that is vulnerable to the fishing gears used and hence potentially exposed to fisheries exploitation. Stock assessment studies the status of a fish stock as well as the possible outcomes of different management alternatives. It tells us if the abundance of a stock is below or above a given target point and by doing so lets us know whether the stock is overexploited or not; it also tells us if a catch level will maintain or change the abundance of the stock. Stock assessment includes aspects not only related to the resource abundance such as whether the stock is depleted or close to its maximum biomass, but also in regards to other important aspects of fish population dynamics such as the current levels of mortality and expected levels of future recruitment, or even economically relevant features such as likely changes in catch per unit effort (Musik and Bonfil,2005).

Calculations on the biomass index (B ,kg/ha) and on the species-specific production rate per unit biomass (P/B ,per year) ratios,are important elements in the fish stock's assessment. At a population level, techniques for measuring fish production rate (elaboration of fish biomass per unit area and per unit time) are described by Ricker (1975) and others, and fish production is routinely calculated for fisheries management (assessment of exploited stocks) (Randall and Minns.2002). According to several authors (Boudreau and Dickie,1989; Downing and Planete,1993; Randall et al.,1995;Randall and Minns,2000) specific or population production (i.e., production per unit biomass, P/B) varies with fish size, however, and a more accurate estimate of production is possible if both biomass and fish size are used as predictors.

In fact, the models we have chosen to calculate the P/B index include the use of several variables that represent the "length (L ,cm)" and the "weight (W ,g)" indicators. Such variables were the asymptotic length (L_{∞} ,cm),the length at first maturity (L_m ,cm) as well as the average weight (W ,g) in the largest length-class and the weight at first maturity (W_m ,g). It is important to pointed out a feature of the results that were obtained from the calculation of the P/B ratio,applying different protocols. Commenting on the findings of Randall and Minns (2000),we note that from 9 species that were analyzed,in 7 of them the value calculated for the P/B ratio was greater when the calculation was based on the "field" variables. In the brook

trout (*Salvelinus fontinalis*) the average value of P/B_{field} was 0.82 (0.55-2.0),while the values for P/BW and P/BZ were respectively 0.66 and 0.49 (Randall and Minns,2000).

The interpretation of catch and effort data, and the construction of indices of resource abundance based on these data, remains an integral part of the stock assessment process for many fisheries (Campbell,2004). Catch per unit effort (CPUE) and Maximum Sustainable Yield (MSY) are two notions in the fisheries science, which are of particular importance during the assessments of the stocks and analyses of the commercial catches. CPUE measures only the component of the population that is vulnerable to the gear; it may be proportional to this component of the population, but not to the total population. The proportion of the population that is vulnerable to the fishery depends on gear selectivity, size and age of fish, horizontal and vertical distribution of fish, and fishing practices (Maunder et al.,2006).

A comprehensive fish inventory and also fish stock assessments have never been performed on Lake Ohrid fish (Palluqi and Spirkovski,2017). This paper is a component of a study on the analysis of species specific annual catches, including for the first time in the Albanian literature on the fisheries, some parameters that are characteristic for the science that regulates the rational and responsible application of this economic activity.

Materials and Methods: The main data for this study were taken from Fisheries Management Organisation of Pogradec (FMOP) and the Ministry of Agriculture and Rural Development (MARD). This data were the statistics of the 2023 about the total fish catches and the catches of the Ohrid trout and Ohrid belvica (Table 1) in the Albanian part of Ohrid Lake (Figure 1a).

Table 1. Fish production (in kv and in % of the total production) from FMO-Pogradec, according to the three taxonomic groups present in the catches (2023).

Ancient Lake Ohrid, the oldest extant lake in Europe (Wagner

Evaluation unit	Salmonidae	Cyprinidae	Anguillidae	Total
	Ohrid trout and Ohrid belvica			
kv	933+200=1133	376.3	46	1555.3
%	59.98+12.86=72.84	24.21	2.95	100

et al.,2009), is an oligotrophic waterbody located in the Western Balkans and shared by the riparian countries Albania and Macedonia. Its large size, geographical isolation, depth, water quality and long geological history provided excellent preconditions for development of a diverse and unique fauna and flora. Many animal and plant species inhabiting Ohrid Lake are endemic to this region (Palluqi and Spirkovski,2017). In the Ohrid Lake fishing has been performed by local people from both riparian countries for many years. At present eleven fish species are commercially used, of which Ohrid trout, Ohrid belvica, eel, common carp, and bleak receiving special interest

(Palluqi and Spirkovski,2017).

The main parameters estimated in this study for Ohrid trout and Ohrid belvica's stocks were:species specific production ratio (P/B),catch per unit effort ($CPUE$) and maximum sustainable yield (MSY).In principle,in the estimation of the values of the parameter P/B our study was carried out following the timeline and the status of the Ohrid trout and Ohrid belvica's stocks that distinguished the protocol advised by Randall and Minn (2000).According to this protocol specific production (P/B) is based on a 1-year time frame (annual production divided by mean annual exploited biomass),and it applies to populations in steady state (not increasing or decreasing in abundance with time).The protocols followed for calculations,were:

•The values of the exploited biomass (B ,kg/ha) for Ohrid trout and Ohrid belvica were estimated by knowing the values of annual catches of these two fishes (kg) and the total area of the fishing region,in the Albanian part of Ohrid Lake (ha).The calculation of the species specific production ratio (P/B) was performed by following three alternative protocols:

a)The first protocol initially requires the calculation of the annual productivity (P ,kg/ha,yr) of the respective fish population.The calculations were performed based in the real value of the exploited biomass (B ,kg/ha) and the value of the average weight of the fish (W ,g) in the largest length-class,identified from the periodic samples taken from the commercial catches-,using a empiric equation according to Downing and Plante (1993): $\log_{10}P = 0.32 + 0.94 \log_{10}B - 0.17 \log_{10}W$.Further was estimated the value of the P/B ratio for the stock of the respective fish specie.

Figure 1.a.Three sections of the FMOP on the Albanian coast



of Ohrid Lake (the image from Palluqi and Spirkovski,2017);**b.** The fishing boats and some fishermen;**c.**Salmonids caught by professional fishermen;**d.**Hooks with artificial (imitation) bait (News24-youtube.com/watch app).

b)The main variable in this protocol is the average weight in the first maturity (W_m).For this calculation we applied the empiric formula according to Randall and Minns (2000): $\log P/B = 0.12 - 0.35 \log W_{mat} + 0.18H$.This formula is applicable to

fishes that populate lakes ($H=0$) and rivers ($H=1$).Were used the previously estimated values of the variable W_m in Ohrid trout (Kamberaj et al.,2024) and Ohrid belvica (Kamberaj et al.,2025).

c)The main variable in this protocol is the maximum theoretical lifespan (t_{max}).The calculations were performed according to the formula proposed by Hoening (1983):

$$P/B = 4.22 t_{max}^{-0.982}$$

The maximum theoretical age (t_{max}) was estimated previously in Ohrid trout (Kamberaj et al.,2024) and Ohrid belvica (Kamberaj et al.,2025).

For fish populations in lakes,most P/B ratios varied between 0.2 and 5.0, and were inversely related to maximum size of the fish in the populations and positively related to lake productivity (Downing and Plante,1993).

The calculation of the daily yield (D_y ,kg/day), according to the specific operating elements,is carried out using a general formula:

$$D_y(x) = (C/Da)/N$$

$D_y(x)$ -daily yield per operating element (kg/day/x); C -total catch or the catch of a target species (kv or kg); Da -number of active fishing days in a respective year; N -the category of "operating element" (in number of elements-for example the number of operating units or fishing groups).

The "operating elements" were:operating units (ou),long-lines (ll) and hooks (h).

To calculate the value of the catch per unit effort ($CPUE$),we applied the formula according to Sweke et al.(2015): $CPUE = C/Nou*Da*t$

C -annual total catch (or annual catch of a target fish species) (kg); Nou -number of "operative unity" (according to MB-ZHR,2022) or fishing groups; Da -number of active days (in the sense of active fishing) in respective year (day/yr); t -number of the hours in active fishing in a day.

The Maximum Sustainable Yield (MSY) was calculated according to Gulland (1971): $MSY = 0.5 MBo$

M -natural mortality (yr); Bo -biomass of unexploited (or quasi unexploited) stock, or a stock's theoretical carrying capacity (kg/ha)

According to Fish Base (2023) the approximate calculation of the parameter Bo ,can be performed using the formula: $B = SLBo$

B -exploited biomass of a stock (kg/ha); SL -the selectivity of the respective fishing gear

To estimate the values of natural mortality (M) was applied the formula according to Hoenig (1983): $\ln(M) = 1.44 - 0.982 * \ln(t_{max})$

t_{max} -maximum theoretical lifespan (Kamberaj et al.,2024;Kamberaj et al.,2025)

To estimate the average value of the selectivity (or relative retention) (SL) of the spinner hooks,we used the selectivity curves of hooks numbered 2, 3 and 4,which were calculated from Ateşşahin et al.(2015),in the experimental fishing trips of rainbow trout (*O.mykiss*).The evaluations were made for those coordinates of the selectivity curves that included the

length-classes over 30 cm,since the minimum size allowed for the exploitation of the Ohrid trout is 32 cm while for the Ohrid belvica,30 cm (MBZHR, 2022).

The different mathematical operatins and statistical analyses were performed with computer's program IBM SPSS Statistics 21.0 (2019) and the Microsoft Office Exel Software version 2010. The largest length size (L_{max}) was estimated from field samples by using the 10 largest individuals in large samples (Pauly,1984).FiSAT II (Gayanilo et al.,2005) was applied to solve the principal empiric equations.

Results:

The values of P/B ratio:In the Table 2 we have set the variables which are included in the protocols for calculating the species specific production ratio (P/B) in the two exploited stocks,that of Ohrid trout (*S.letnica*) and that of Ohrid belvica (*S.ohridanus*).

Table 2.The variables used in the different models for the calculation of the species specific productivity index (P/B ,yr).

Year	Biological indicators	According to total catch	Ohrid trout (<i>Salmo letnica</i>)	Ohrid belvica (<i>Salmo ohridanus</i>)
2023	Biomass index (B ,kg/ha)	13.07	7.857	1.681
	Average weight (W_g) in the largest length-class	-	1125	250
	Asymptotic length (L_{∞} ,cm)	-	53.46*	37.01**
	Length at first maturity (L_m ,cm)	-	32.95*	23.67**
	Weight at first maturity (W_m ,g)	-	494.90*	103.89**
	Maximum theoretical age (t_{max} ,yrs)	-	15.6*	16.97**

*According to Kamberaj et al.(2024);**According to Kamberaj et al.(2025)

In the Figures 2 and 3 are shown the differences in the values of the species specific productivity index (P/B ,yr) for the stocks of Ohrid trout (Figure 2) and Ohrid belvica (Figure 3),estimated using three different protocols.

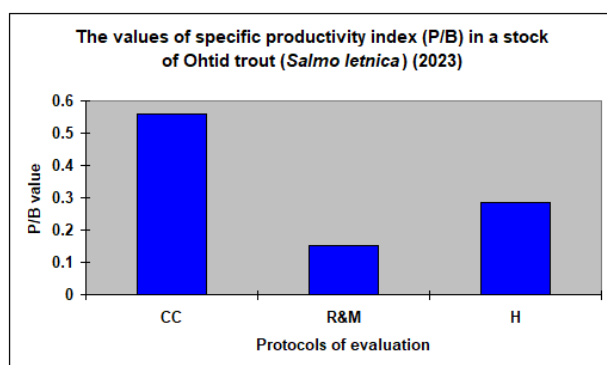


Figure 2.The differences in the values of the species-specific productivity index (P/B ,yr),for a stock of Ohrid trout exploited in the Albanian part of Ohrid Lake,estimated applying three different protocols of calculation [CC-According to commercial catches (or biomass index,B) of 2023;R&M-According to the protocol of Randall and Minns,2000);H-According to the protocol of Hoening,1983].

The diagrams confirmed that the calculation of P/B ratio using the data about the annual commercial catches (kg) (or the values of exploited biomass B ,kg/ha),resulted in the highest values of this parameter (0.559/yr,in Ohrid trout's stock and 0.791/yr,in the Ohrid belvica's stock).The results obtained from the application of both other calculation models were almost the same when applying the protocol according to Hoening (1983) (0.284/yr in Ohrid trout's stock and 0.262/yr,in the Ohrid belvica's stock) and different when the estimations were carried out according to the protocol of Randall and Minns (2000) (0.151/yr in Ohrid trout's stock and 0.259/yr,in the Ohrid belvica's stock)

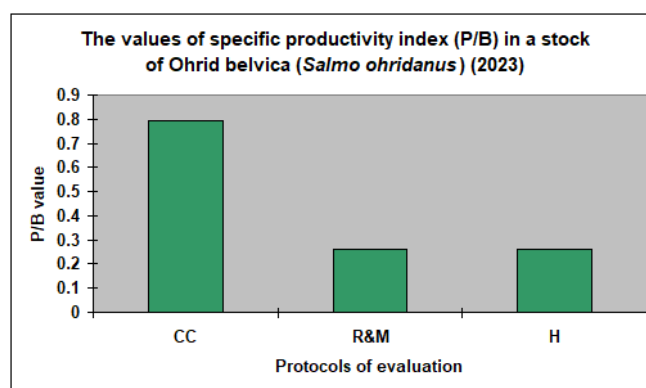


Figure 3.The differences in the values of the species-specific productivity index (P/B ,yr),for a stock of Ohrid belvica exploited in the Albanian part of Ohrid Lake,estimated applying three different protocols of calculation.

The values of the yields:The Table 3 included some variables used in the calculation of the parameters that inform about the yields of the catches,according to some operating elements.

Table 3.The variables used in the estimation of the fishing yields.

Variables	Value
Days in active fishing (Da)	170
Number of operating units (Nou)	220
Number of long-lines per operating unit	3
Number of hooks in a long-line	50
Hours in fishing in a day (t)	8

*The number of hooks ($n=150$) per operating unit is determined by the Albanian Law on the Fisheries (MBZHR,2022).

In the Table 4 we have summarized the values of the daily yield of the catches (Dy ,kg/day),estimated for the total catch $DyTc$,the catches of the Ohrid trout ($DyOt$) and the catches of Ohrid belvica ($DyOb$),for three operating elements (fishing operating unit (ou), a hook's long-line (ll) and a hook (h)).

Table 4.The values estimated for the daily yield (Dy ,kg/day) according to three operating elements (operating units*,long-lines and hooks),based on the statistics of the catches of 2023.

Catches	Amount (kg)	Daily yield per operating unit (Dy ,kg/day/ou)	Daily yield per a long-line (Dy ,kg/day/ll)	Daily yield per a hook (Dy ,kg/day/h)
Total catch	155 530	4.158	-	-
Ohrid trout catch	93 300	2.495	0.832	0.0170
Ohrid belvica catch	20 000	0.535	0.178	0.0036

*"operating unit" (MBZHR,2022);**there are no results for Dy_{ll} and Dy_h ,in the

calculations based on total catches,due to the using of different fishing gears.

The values estimated for the catch per unit effort (CPUE):The diagram in Figure 4 presents the results of the calculations for the values of the parameter catch per unit of effort (CPUE),estimated according to the four indicators of the fish catches;total fish catches ($CPUE_{Tc}=0.520$ kg/hr/ou),the catches of Ohrid trout ($CPUE_{Ot}=0.312$ kg/hr/ou),the catches of Ohrid belvica ($CPUE_{Ob}=0.087$ kg/hr/ou) and the catches of the two salmonids taken together ($CPUE_{Sal}= 0.400$ kg/hr/ou).

For some reasons related to the management of the catches, it is very important to evaluate the differences between the values of the CPUE-variants that resulted from this study. It is noticeable that the value of $CPUE_{Tc}$ is only 1.3 times greater compared to the value of $CPUE_{Sal}$.These differences confirm that the fishing effort that was applied during the 2023 in the catches of two endemic trouts in Ohrid Lake was higher compared to the fishing effort applied in the catches of other fish species (cyprinids and European eel).

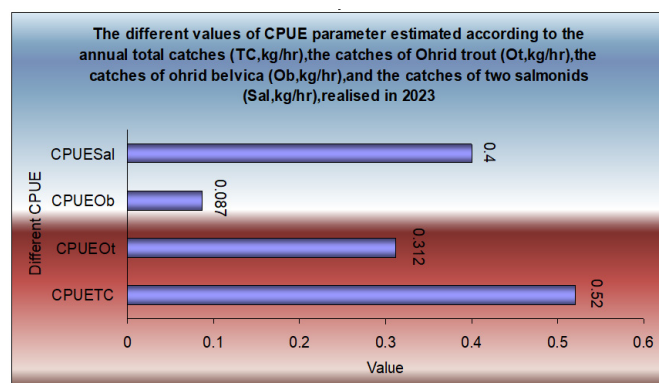


Figure 4.The values of the catch per unit effort (CPUE,kg/hr/ou) estimated for a operating units (ou),on the data about the total annual catches of 2023,the catches of Ohrid trout,Ohrid belvica and the complessive annual catches of these two salmonids.

The values estimated for the Maximum Sustainable Yield (MSY):Table 5 contains the variables that are included in the formulas for calculating MSY values for two target species of commercial fishing,Ohrid trout and Ohrid belvica,which are exploited in Lake Ohrid.

Table 5.The variables used for the estimation of the Maximum Sustainable Yield (MSY),in the exploitation of two salmonid fishes in Ohrid Lake.

Fish species	Natural mortality (M ,yr)	Exploited biomass (B ,kg/ha)	Unexploited biomass (B_0 ,kg/ha)	Selectivity coefficient (s) of the hooks ($TL>30$ cm)*
Ohrid trout (<i>S.letnica</i>)	0.30	7.857	14.3	0.55
Ohrid belvica (<i>S.ohridanus</i>)	0.26	1.681	3.0	0.55

*The estimations of the approximative values of selectivity were carried out according to Ateşşahin et al.(2015),as well as according to the determinations of MBZHR (2022) on the minimum sizes of Lake Ohrid's salmonids allowed for exploitation.

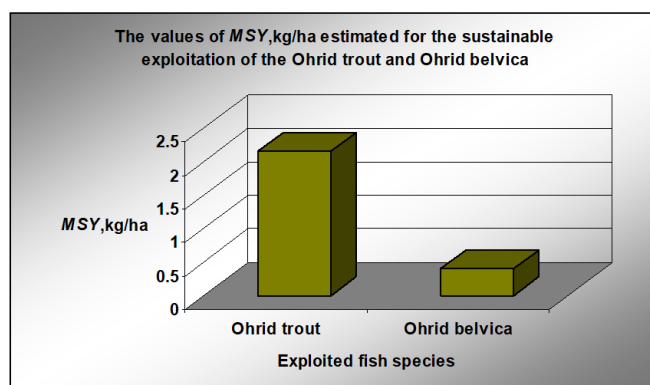


Figure 5.The results of the calculation of MSY,kg/ha using the evaluations on the stock's theoretical carrying capacity (B_0 ,kg/ha) and the exploited biomass of a stock (B ,kg/ha),based on the data about the annual catches of *Salmo letnica* and *S.ohridanus*.

According to the values calculated for MSY ($MSY_{Ot}=2.15$ kg/ha and $MSY_{Ob}=0.40$ kg/ha) it results that the current levels of the exploitation for salmonids are from 3.5 to 4.0 times higher compared to the values that are required to guarantee the regeneration of their stocks.On the other hand,the real ratio

between the annual catches of the Ohrid belvica (in kg) and the catches of the Ohrid trout are 1.0:4.7, while according to the values estimated for the *MSY* the right ratio in the exploitation of these two species, at least as stated by the current situation of their stocks, should be 1.0:5.4.

Discussion:

The lack of the assessments on the stocks of target fish species of commercial fishing as well as scientific analyzes on their catches has been pointed out before. Informations about Lake Ohrid fish stocks and condition of the fish is scarce. While many papers refer to an overfishing of the stocks (UNESCO, 2004; Watzin, 2003; Spirkovski, 2004a; Kostoski et al., 2010), there is rarely any quantitative data in the scientific literature supporting this statement (Spirkovski, 2004b; Palluqi and Spirkovski, 2017). However, a study carried out by Bllaca and Kolaneci (2023) creates an opportunity to be informed about the situation of the indicators of exploitation and to confront the results and opinions. On the other hand, we will focus on the "behaviors" of the indicators we have evaluated, making comparisons with nearby fish species.

According to our analysis on the results of quantitative indicators of the catches, it results that the ratios of catches between the three taxonomic groups present in the total production were: 72.84% (salmonids); 24.21% (cyprinids) and 2.95% (anguillids). These values confirm that the two endemic trouts are the dominant species of commercial fishing that is carried out in the Albanian part of Ohrid Lake. Before, Spirkovski and Talevska (2002), analyzing the catches of the period between 1930 and 1957, in the Macedonian part of Ohrid Lake, had claimed that the lake has occasionally been characterised as typical salmonid water or "lake of trout". However, these authors, evaluating the catches in later years (1969-1999), had found that the dominance of salmonids had been replaced by the dominance of cyprinids. According to the decreased trout participation in the fish catchment structure, the previous categorization of Lake Ohrid like "lake of trout" can be easily changed in "lake of cyprinids", especially of bleak (Spirkovski and Talevska, 2002). It seems that the situation we have found, which is characterized by the marked increase in the presence of salmonids in the fish catches, was started after the first twenty years of the 2000s. According to the total catches of 2015, the ratio between cyprinids and salmonids was 54.3% (only the bleak 43.3% of total catches) with 45.7% (Elmasllari, 2015). We think that the significant increase in the catches of salmonids in the Albanian part of Ohrid Lake, from about 400 kv that was in 2015 to 1085 kv in 2022 and 1133 kv in 2023 (MBZHR, 2024) is not caused by the increase in the quantitative indicators of the Ohrid trout and Ohrid belvica's stocks but due to the increase in fishing effort. According to our findings the value of $CPUE_{Tc}$ was 0.520 kg/hr/ou, and from this value 0.400 kg/hr/ou belonged to the catch per unit effort of the salmonid fishes ($CPUE_{Sal}$). We judge that among the variables included in the calculation of the fishing effort (Δf), the number of licensed operating units (or fishing groups) (ou) has the greatest impact on the values of the quan-

titative indicators of the fisheries. According to the available statistics, in Albanian part of Ohrid Lake this variable from 2015 to 2023 has subjectively increased in a measure of 27.5% (or with 60 ou).

We mention the fishing effort, as this indicator of the catches management is simultaneously also a variable in the classic equation for calculating the catch (ΔC) (Gulland, 1969). The classic catch equation expresses catch as a proportion of abundance (N/A), and this proportion varies with the amount of effort ($\Delta C = q \cdot \Delta f \cdot N/A$) (Hubert and Fabrizio, 2007). This means that the variability in time for the catches of salmonids in Ohrid Lake is not only caused by the fluctuation in abundance (N/A , indv/ha) or biomass (B_0 , kg/ha) of their stocks but also by the unstudied changes that have affected the operating elements used in the estimation of effort. Size structure indices and catch per unit effort (C/f) are commonly used by fisheries managers to draw inferences about fish population dynamics. These indices are best used in conjunction with a suite of diagnostic information, including fish growth, condition, and recruitment, as well as data from catches (Craig Bonds and Van Zee, 2010). These authors pointed out that in an effort to control the status of the exploited stocks and increase fish growth rates, fishery managers responded by changing the harvest regulation, by relying on catch per unit effort (C/f) and proportional size distribution (PSD) data, as these indices remained consistent concomitant to significant changes.

Regardless of the unit of measurement, comparing the values that we obtained from the calculation of $CPUE$ for the two salmonids ($CPUE_{Ot} = 0.312$ kg/hr/ou or $CPUE_{Ot} = 2.496$ kg/day/ou (according to Ohrid trout catches) and $CPUE_{Ob} = 0.087$ kg/hr/ou or $CPUE_{Ob} = 0.696$ kg/day/ou (according to Ohrid belvica catches) with the values that were obtained in the study carried out by Bllaca and Kolaneci (2023) ($CPUE = 2.2$ kg/day/boat, for the catches of Ohrid trout and 0.5 kg/day/boat), for the catches of Ohrid belvica, they were relatively similar (ou and boat are equivalent unities because each operating unit uses a fishing boat). The differences in the values that we pointed out must be related to the fact that we analyzed the annual catches of 2023, while in the other work, the catches of the first six months of the 2023, were analysed.

According to Bllaca and Kolaneci (2023) the $CPUE$ for some species has increased, which may be an indication that we have had an increase in the reserve for this species. We think that it is true that the catch (in unity of the weight) is an indicator for biomass (or fish reserve), but on the condition that the fishing effort (including the category of fishing gear) remains unchanged between two or more intervals of calculations. Assumptions of the classic catch equation (Gulland, 1969) are (1) the population is in equilibrium; (2) units of effort operate independently (one unit of fishing gear does not interfere with other units); (3) q (catchability of fishing gear) is constant throughout the sampling period; and (4) every individual in the stock has the same probability of capture (Seber, 1982).

As we mentioned above citing Hubert and Fabrizio (2007), the ratio between the catches and abundance change in depending

on the applied effort. An underlying assumption of using C/f as an index of abundance is that the number of fish captured is proportional to the amount of effort expended. Although the proportional relation between C/f estimates and abundance is convenient, it is not universal. The temporary concentration in limited aquatic spaces or profundity, for different fractions of a stock (as also happens in lake salmonids), which in reality may not be abundant, a fact that occurs in areas of intensive grazing or in the area of reproduction, and intensive exploitation of these fractions from the fishermen creates wrong impressions on the real abundance of the stock as a whole. Therefore, the estimates about the relationship between the catches and the stock's abundance must take into consideration the specific characteristics of the stocks.

After the estimations of the values of the parameter "species specific production ratio", applying three alternative protocols, we found that both in the Ohrid trout and Ohrid belvica stocks, the values of the P/B ratio were higher when the real (or field) exploited biomass data (B) were used in calculations. Both methods (using in the calculation W_{mat} or t_{max}) underestimated on average the actual specific production coefficients as measured in the field (Randall and Minns, 2000). In order to guarantee a more realistic assessment, if population specific trait (such as W_{mat}) are known for a particular population and area, they should be used to estimate P/B (using the allometric equation) rather than the generic species P/B coefficients. On the other hand, P/B ratios can be validated by intercorrelation of the two methods and by comparison with published empirical data (Randall and Minns, 1995; Randall and Minns, 2000). The method using P/BW is favoured because the predictor population trait (size-at-maturity or maximum size) is often available from population studies of age and growth and because the empirical relationship between animal size and P/B is well founded in the literature (Peters, 1983; Randall and Minns, 2000).

We must mention the fact that the value resulted from the calculation of the P/B ratio for the Ohrid trout stock, when the protocol according to Randall and Minns (2000) was applied (using the weight at first maturity, W_m), was $P/B = 0.151/\text{yr}$. This value was smaller compared to the minimum limit value ($0.2/\text{yr}$) determined by Downing and Plante (1993). But this result does not constitute an error or an exception, as according to Randall and Minns (2000) in 37% of cases the calculated value for the P/B ratio turns out to be $<0.2/\text{yr}$. However, we can note the fact that in the original paper of Randall and Minns (1995), to calculate the P/B ratio was used the average weight of a fish species (W , g) captured at the transect, rather than a species constant weight-at-maturity (W_m , g). The formula of allometric relationship between P/B (y) and W (x) was: $P/B = 2.64 W^{-0.35}$ (Randall and Minns, 2002). Using our data about the average fish weight (W , g) calculated in Ohrid trout (O_t) and Ohrid belvica (O_b), according to the evaluations of the samples taken from commercial catches of 2023, the values calculated for the P/B ratio in the stocks of these two species were: $P/BO_t = 0.286/\text{yr}$ and $P/BO_b = 0.499/\text{yr}$. This protocol gives for Ohrid trout a value of P/B that was between the limits of 0.2 - $5.0/\text{yr}$.

Conclusion:

It is important to emphasize that the results of this paper are preliminary and as such they should be calibrated with further investigations. The current situation of exploitation of two trout's stocks, endemic from Ohrid Lake, dictates the need to determine the real values of the fishing effort, which was imposed without applying scientific protocols. The multi-annual evaluations on the catches, which should also include the assessments about the state of the stocks, are necessary in order to obtain real values for those scientific parameters that will be necessary in the management of fisheries. We hope that the values of the parameters that are calculated in our work to serve as guidelines for future studies

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FT3-LENGTH-WEIGHT RELATIONSHIP AND CONDITION FACTORS OF THE STOCKS OF *ALBURNUS SCORANZA* AND *SQUALIUS CEPHALUS* FROM ALBANIAN PART OF OHRID LAKE

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Abstract

Common chub and Scoranza bleak, as well as 19 other species and subspecies are components of the native ichthyofauna present in Ohrid Lake. Based on the analyzes of the samples taken from the catches of these two fishes, in the years 2023 and 2024, we had estimated the values of the coefficients a and b in LWRs as well as the values for three types (K , K' and K_n) of condition factors. The values of the coefficients in the LWRs for the common chub's stock, were: a) For all the 11-month period of the study $W = 0.0077TL^{3.1587}$ $r = 0.968$; b) in the active grazing period $W = 0.0045TL^{3.2709}$ $r = 0.921$ and, c) after the breeding season $W = 0.0135TL^{2.8266}$ $r = 0.925$. The respective values in the Scoranza bleak's stock, were: a) $W = 0.0132TL^{2.728}$ $r = 0.968$; b) $W = 0.0094TL^{2.901}$ $r = 0.934$ and, c) $W = 0.0173TL^{2.6486}$ $r = 0.907$. As for the condition factors, the highest average value was calculated for $K = 2.079 \pm 0.029$, in the common chub's stock during the active grazing period. The lowest average value was calculated again for $K = 0.685 \pm 0.032$, in the Scoranza bleak's stock, immediately after the breeding season.

Keywords: Ohrid lake, Scoranza bleak, common chub, izometry and allometry of the growth, condition factor, grazing period, breeding period.

Introduction

The Scoranza bleak is endemic to the Southeastern Adriatic Ecoregions (Marić, 2019; Pešić et al., 2020). According to Marić (1995) as well as Talevski et al. (2009) the Scoranza bleak inhabits only Ohrid – Drim – Skadar system. In an assessment about the degree of the risk of extinction for the ichthyc species Miloshevic and Talevski (2016) had classified the common chub (Figure 2) and Scoranza bleak (Figure 3) as "less endangered" fish species (category LC). The populations of the chub and the bleak, in the large lakes of the Western Balkans (the Shkodra, Ohrid and Prespa lakes), in addition to the faunal values, presents also economic values, while they are target species for commercial fishing. In the last two years (2023 and 2024), the catches of the common chub and Scoranza bleak taken together, in the Albanian part of Ohrid Lake, comprised 9.65% of the total annual catches (MBZHR, 2025).

Ahirwal et al. (2017) had realized a summary from the scientific literature in which they discovered the importance of the estimation of the coefficients in the length-weight allometric relationship, for knowing the state of the fish populations. Length-weight-relationship (LWRs) is an important tool in fisheries biology and ecology with several applications such

as converting length data into biomass, calculating the standing crop biomass, stock assessment procedures, investigation of ontogenetic changes, assessment of the population dynamics, understanding the life cycle traits (e.g. condition factor, mortality and growth) as well as comparing the growth rates and its pattern in different populations (Froese, 2006; Mouludi-Saleh et al., 2021). The study of age and growth in fish is a prerequisite to generate the information on recruitment, longevity, mortality and fluctuations in fishery caused by various year classes, all of which can contribute towards planning for a rational exploitation of these fish stocks. Such studies with proper statistical refinements are helpful in describing the present status and the past history of a fish population along with the future course of the fishery (Khan and Khan, 2014).

Accurate estimates of growth parameters are important for monitoring fish population status, as well as for assessing fisheries management decisions against external pressures (Zhu et al., 2016). The different indices based on biological aspects such as growth, reproduction, and trophic activities vary with reproductive cycles, food intake, life history, and a variety of environmental stressors (Barton et al. 2002). Condition factor (K) is used to assess well-being of fishes under different conditions, including physiological, climatic and environmental circumstances hence, it can be affected by many parameters, including nutritional quality, aquatic system (rivers or lakes) and seasonal changes (Mouludi-Saleh et al., 2021). Condition variations can be due to stages differences in ontogenetic development, and also differences in length, age, sex, gonadal development (Ricker, 1975; Sasi and Ozay, 2017).

Several studies have been carried out on the biological characteristics and growth parameters of the cyprinid fishes, including the populations of common chub and Scoranza bleak from the Ohrid-Drin-Shkoder catchment. Focusing on the growth characteristics of two species that are the object of our study, we can point out the publications of Filipi (1959), Petrovski and Sidorovski (1971), Točko (1975a; 1975b; 1985), Šorić (1982), Memia et al. (1988), Kolaneci and Kuka (2009), Dervishi et al. (2018), Milošević and Mrdak (2016), Milošević and Talevski (2016) as well as Pepa et al. (2024). In our discussion we will refer to the results of some of these studies.

Material and Methods: Taking into consideration the spatial distribution of the fishing areas in the Albanian part of Ohrid Lake, the sampling stations were: the coast of the lake in front of the city of Pogradec (40° 54' 19" N and 20° 39' 17" E); the coastal area between the villages of Lin and Piskupat (41° 03' 57" N and 20° 38' 26" E) as well as the coastal area in front of the village Udenisht (40° 57' 51" N and 20° 38' 38" E) (Figure 1.a).



Figure 1. a. The map of the Albanian part of Ohrid Lake (Google, 2023); b. Fishing of the bleak and chub using a beach trawl (<https://www.voxnews.al/english/2023/>); c. The fishing gears (gillnet and trammel net) in the coast of Ohrid lake (Halpern, Joel Martin. Ohrid lake, ca. May 1954 (FS 001)).

In the 11-month period, from June 2023 to April 2024, eight samplings were carried out for each of the two fish species included in the study: a) five samplings for the evaluation of growth indicators within the 11-month period; b) one sampling for the evaluation of the growth immediately after the reproduction (June), and c) two samplings for the evaluation of the growth within the period of active feeding (June-October). All samples were taken from the commercial catches. Their collection is carried out immediately after the end of the daily catches. All sizes present in the catches were included in the samples. Also, each sample contained individuals of both sexes.



Figure 2. Common chub (*Squalius cephalus* Linnaeus, 1758).

For morpho-gravimetric measurements, was used a scheme of the fishes of the Cyprinidae Family, according to Bilici et al. (2016). Each individual of the sample was measured for their zoological length (or total length, TL_{cm}), with an accuracy of 0.1 mm, using a digital Vernier calliper. The live weight (or total body weight W, g), was measured with an accuracy of 0.01 g, using a HC-Electronic balance. The largest number of individuals was measured at the sampling stations. The individuals that

were processed in the laboratory were transported by refrigeration in POL-EKO thermostatic boxes. The growth parameters estimated and assessed for the stocks of common chub and Scorzana bleak, were: a) The coefficients a and b in the LWRs; b) Three types of the condition coefficient (or condition factor) (K, K' and K_n).



Figure 3. Scorzana bleak (*Alburnus scoranza* Heckel and Kner, 1857).

The relationship between the total length (TL, cm) and live weight (W, g) is a power-law function: $W = aTL^b$ (Froese, 2006; Kuriakose, 2017). This power function (simple allometry) turns into a linear function after logarithmic transformation so that estimates of a and b can be computed by linear regression. The logarithmic transformation is written as follows: $\log W = \log a + b \log TL$ (Huang and Riviere, 2014). In this linear function a is the intercept and b is the allometric scaling exponent. The exponent b simply provides a means of mathematically describing the rate of change between TL and W . The W increases proportionally with TL (isometry) when b is equal to 3.0; W increases faster than TL (positive allometry) when b is larger than 3.0 and W increases slower than TL (negative allometry) when b is smaller than 3.0 (Bagenal and Tesch, 1978; Kuriakose, 2017). If the values of the exponent b results from 3.0 to 3.5, it can be affirmed that the environmental conditions optimally meet the physiological requirements of the fish population being analyzed (Ricker, 1975). The exponents of allometric scaling are not constant and have no inherent physiological meaning (Huang and Riviere, 2014). The regression and correlation analyses and the plots of the length and weight pairs were performed to calculate the values of the a and b -coefficients and the value of the determination coefficient (R^2).

Applying the following formulas we have calculated the corresponding values of three types of condition factors: a) Fulton's condition factor $K = W \cdot 100 / TL^3$ (Fulton, 1902; Froese, 2006); allometric condition factor $K' = W \cdot 100 / TL^b$ (Bagenal and Tesch, 1978) and relative condition factor $K_n = W \cdot 100 / a TL^b$ (Zorica dhe Ćikeš Keč, 2013). In this three formulas W, g and TL_{cm} respectively represent the average values of the weight and length of the fishes included in a sample, while a and b are the values of the coefficients in LWRs of this fishes (always according to each of the specie that was analyzed and according to the sampling periods).

Statistical analyses were performed with computer's program IBM SPSS Statistics 21.0 (2019) and the Microsoft Office Excel

Software version 2010 (Pepa et al.,2024).Comparison of observed means were carried out by analysis of variance (ANOVA) (Zar,2010).The degree of the correlation between the variables was computed by the determination coefficient (R^2).The Student's t -test (t_s) was used to determine whether the parameter b is significantly different from the expected or theoretical value of 3.0 (i.e. $b=3.0$; $P<0.05$) (Mouludi-Saleh et al.,2021).

Results:

The values of coefficients a and b in LWRs:

a) The stock of common chub (*S.cephalus*)

In the graph of the Figure 4 we have shown the plot and the corresponding regression for the allometric correlation between the TL ,cm and W ,g of individuals,in a stock of common chub from the Albanian fishing areas in Ohrid Lake,according to the systematic evaluations carried out within the period from June 2023 to April 2024.

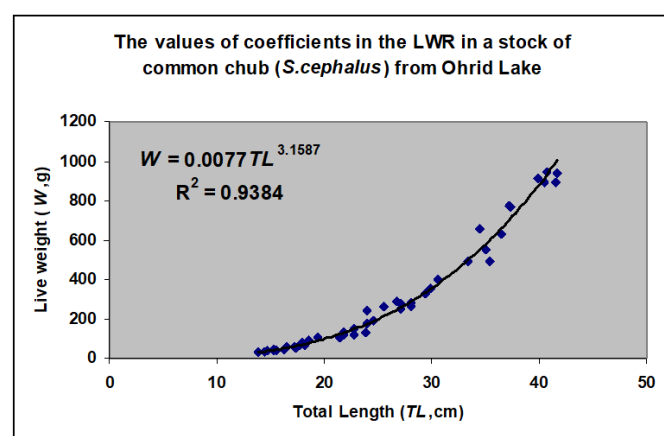


Figure 4.The allometric correlation between the total length (TL ,cm) and live weight (W ,g) in a common chub's stock,from Albanian part of Ohrid Lake,according to the evaluations of the samples taken in the period from June 2023 to April 2024 ($a=0.0077$; $b=3.169$; $r=0.968$).

According to the evaluations that were carried out only during the period of active grazing (mid-June-early November, 2023),the values of the coefficients at LWRs, were:

$$W = 0.0045 TL^{3.2709} ; R^2 = 0.849 ; r = 0.921$$

In the following,we have shown the values that were calculated for the coefficients in the TL - W relationship,immediately after the breeding season of the common chub's stock:

$$W = 0.0135 TL^{2.8266} ; R^2 = 0.856 ; r = 0.925$$

Judging by the order of the theoretical values of the exponent b ,from the three values that resulted by our calculations,in a stock of common chub,two values resulted positive allometric ($b>3.0$) and one value was negative allometric ($b<3.0$).The Student's t -test proved the existence of significant difference only between the average values of the coefficient b ,that corresponded to the period of active grazing and the period after the reproduction ($t=3.52$; $P<0.05$; $n>50$).

a) The stock of Scorzana bleak (*A.scoranza*)

Figure 5, like Figure 4,contains the same growth parameters,which belong to the evaluations in the Scorzana bleak's

stock,estimated during the period from June 2023 to April 2024.

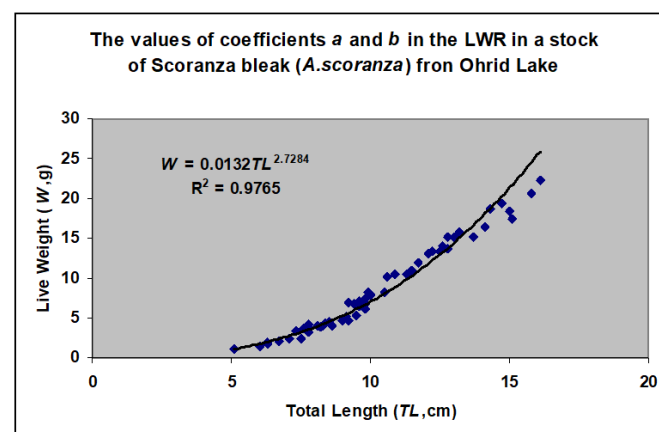


Figure 5.The allometric correlation between the total length (TL ,cm) and live weight (W ,g) in a Scorzana bleak's stock,from Albanian part of Ohrid Lake,according to the evaluations of the samples taken in the period from June 2023 to April 2024 ($a=0.0132$; $b=2.728$; $r=0.987$).

In the other two periods,the following values were estimated for the coefficients in the LWRs.

-In the annual period of the active grazing:

$$W = 0.0094 TL^{2.901} ; R^2 = 0.873 ; r = 0.934$$

-Immediately after the breeding season:

$$W = 0.0173 TL^{2.6486} ; R^2 = 0.824 ; r = 0.907$$

Calculated values of the exponent b in three intervals of the life cycle of the bleak's stock,that are distinguished by the physiological specifics of this species,were in all cases smaller than 3.0.This fact proved that,in addition to the values quite close to the isometric value ($b=3.0$), which we calculated after the analysis of the samples taken in the period of June - November,the other values calculated in the other months included in the 11-month period,proved that the growth of individuals in the analyzed stock was negative allometric ($b<3.0$).As for the stock of common chub,also for the stock of Scorzana bleak the significant difference for the average values of the exponent b was confirmed only in the comparison between the average value in the period of active grazing and the average value immediately after the reproduction ($t=2.25$; $P<0.05$; $n>50$).

The values of condition factors (K , K' , Kn):

a) The stock of common chub (*S.cephalus*)

The average values and the values of standard deviations ($M\pm SD$) of three types of condition factors (K , K' , Kn),estimated in the stock of common chub,are shown in the Figure 6.The results of our evaluations proved the existence of a general rule for the distribution of the average values of the three parameters that characterized the condition of the stock.According to this rule, the highest average values, when comparing the results of the calculations,had the three types of the condition

factors that were determined in that period of the year when the stock of common chub manifested the highest rate of food intake. On the other hand, the lowest average values were calculated for the three condition factors in fish that had recently left the breeding phase.

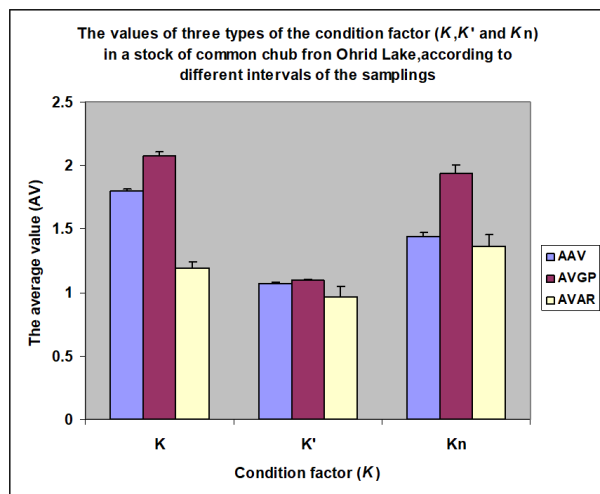


Figure 6. The average values ($M \pm SD$) of the condition factors (K -Fulton's condition factor; K' -allometric condition factor and Kn -relative condition factor), in a stock of common chub (*S.cephalus*) exploited in Albanian part of Ohrid Lake (AAV-Average annual values; AVGP-Average values in the grazing period; AVAR-Average values after reproduction).

The highest average value was found for the Fulton's condition factor ($K=2.079 \pm 0.029$) in the grazing period, while the lowest average value was calculated for the allometric condition factor ($K'=0.967 \pm 0.075$) immediately after the reproduction. Were not proved the same results regarding the significance of the differences between the average values, after pairwise comparisons made between the same factor, that was calculated in different phases of the annual life cycle of the common chub. However, significant differences were proven ($P < 0.05$) when were compared the average values of the three condition factors, calculated immediately after the reproduction with the average values of these parameters, calculated in the period of active grazing. Also, significant differences were confirmed in the comparisons for the average values of K and Kn between the values that were obtained for the 11-month period and those that were obtained in the grazing period ($P < 0.05$).

a) The stock of *Scoranza bleak* (*A.scoranza*)

The graph in the Figure 7 presents the average values ($M \pm SD$) of three types of condition factors, calculated for the stock of *Scoranza bleak*, in three time-intervals of the one-year life cycle. For the three calculated parameters, the highest average values were found in the period of active grazing. The highest average value (1.152 ± 0.058) belonged to the relative condition factor (Kn). The lowest average values were calculated for the three condition factors in the *Scoranza bleak*'s samples that were taken

immediately after the reproduction. The lowest average value resulted for the Fulton's condition factor ($K=0.683 \pm 0.032$). The values of the allometric condition factor (K') had the highest variability ($Var\%=9.97$) in the period of active grazing, while the values of the relative condition factor (Kn) showed the lowest variability ($Var\%=2.05$), measured immediately after the reproduction period.

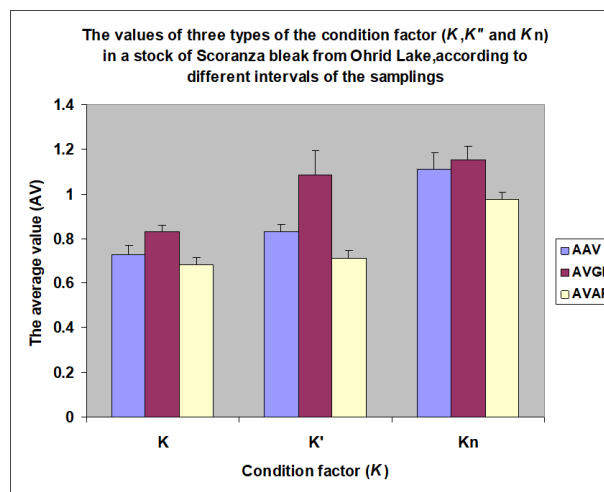


Figure 7. The average values ($M \pm SD$) of the condition factors (K -Fulton's condition factor; K' -allometric condition factor and Kn -relative condition factor), in a stock of *Scoranza bleak* (*A.scoranza*) exploited in Albanian part of Ohrid Lake (AAV-Average annual values; AVGP-Average values in the grazing period; AVAR-Average values after reproduction).

It seems that compared to the stock of common chub, in the stock of *Scoranza bleak*, the differences between the average values for the three parameters of the condition that were estimated, according to the three annual intervals, were more emphasized. On the other hand, the values calculated for the variance ($Var\%$) in each of the three condition indicators, were higher. For these reasons, despite the similarity between the stocks of the two fish species that were evaluated, the distribution of the average values of K , K' and Kn in the *bleak*'s stock, according to the variants of the study, had its own specifics. This statement was supported by the results of the Student's t -test analysis. The pairwise comparison of the average values of the three condition factors resulted in the confirmation of two significant differences for the values of K ($t=3.61$; $t=2.29$; $P < 0.05$), three significant differences for the values of K' ($t=3.68$; $t=2.23$; $t=3.58$; $P < 0.05$) and one for the values of Kn ($t=2.81$; $P < 0.05$).

Discussion

At the beginning of the discussion, we can note two basic features of the methodology of this study, as well as some characteristics of the variables that were included in the calculation of the parameters.

First, all the protocols performed in the calculations were based on the results of the measurement of the individuals included in the fish samples for two characters, one morphometric (total

length TL , cm) and one gravimetric (live weight or total weight W , g).

Second, it is important to quantify the differences for the range of year-round variability that characterizes the values of TL and W , in dependence of the periodic realization of different biological life story elements of fish species that were analyzed, taking into account the fact that we are dealing with poikilothermic animals. This intervention is necessary to find out the rates of reduction of the body condition or its improvement in specific phases of the one-year life cycle.

The first point justifies the relatively similar annual rhythm of the evaluated parameters. In fact, both the average values of the exponent b and the average values of the three types of condition factors (K , K' and Kn), in the two fish species that were included in our analysis, were higher in that period of the year when these cyprinids actively grazed, lowest in the period following the reproduction and almost intermediate when the evaluations included all sampling data of the 11-month period. Regarding the second point, we should mention the well-known fact that the annual rhythms of life activities in poikilothermic animals, including the rhythms of body mass growth, are depending on the environmental conditions, especially the water temperature. On the other hand, it is important to take into account the differences between the degree of variability of growth in length compared to growth in weight. As a general rule, if annual data were analyzed, the variability of the weight turns out to be more pronounced compared to that manifested by the length of the animal. After the analysis of the data from the measurement of the individuals in the 11-month samplings, we found that in the Scorzana bleak aged from 1+ to 4+, the variability of live weight, estimated by the biometric parameter $Var\%$, was 2.54 times higher compared to the variability of total length. This value in common chub aged from 2+ to 7+ was 2.87.

In the period of active grazing, which starts immediately after the reproduction, the highest values calculated for the exponent b ($b=3.271$ for common chub and $b=2.901$ for Scorzana bleak), as well as the corresponding values of the three condition factors, are the results of the stimulation of the assimilation process, favored by the optimal values of the water temperature, the reduction of the differences for the growth rate according to weight and to length, the reduction of the variability of the increase in weight and the increase in the frequency of fed individuals (with high values of the gut or stomach fullness). It is argued that b may change during different time periods illustrating the fullness of stomach, general condition of appetite and gonads stages (Zaher et al., 2015). The increase in weight also causes a specific modification of the body shape, a fact that generates changes for the values of the exponent b in LWRs, generally in the direction of the isometric or positive allometric values. It must be noted that LWRs differ among fish species depending on the inherited body shape and the physiological factors such as maturity and spawning (Schneider et al., 2000). The body form and shape strongly affect the LWRs (Karachle and Stergiou, 2012).

Using the data on the total length and live weight of the individuals, which were sampled after the end of the breeding season, our calculations for the values of the exponent (b) in LWRs as well as the values of the three condition factors (K , K' and Kn), in the stocks of the two fish species, that were included in the study, resulted in the smallest values of these parameters. It is known that fish usually decrease their feeding activity and use their lipid reserves during spawning, which results in a decrease in condition (Lizama and Ambrósio, 2002). Our measurements, which were performed for Scorzana bleak immediately after the end of the breeding, showed very small changes in the length of the mature fish, while their weight was reduced from 7.8 to 19.2%. In the reproductive period of the one-year life cycle, the spawners not only use a part of the reserve deposited during the period of active grazing, for the maturation of the gametes, but also manifest weight loss after the emission of the gametes.

Using some of the scientific publications, where aspects of the growth characteristics were analyzed for the populations of Scorzana bleak and common chub in the Oher-Drin-Shkodër aquatic basin, we will make the comparisons for the values of some growth parameters, with the aim of pointing out the factors that promote possible differences. Maric and Burzanovic (2021) had carried out assessments for a stock of Scorzana bleak in Shkodra Lake. In contrast to our evaluations for the stock of this fish in Ohrid Lake, in which none of the variants analyzed had proven the positive allometry for the growth, in the evaluations of the mentioned authors, for a stock of this species in the Shkodra Lake, were confirmed the three types growth characteristics. We think that the differences in sampling protocols may be the factor that had caused the differences in the assessment results. According to Maric and Burzanovic (2021) length groups of a smaller size (juveniles) had positive allometric growth as compared to larger specimens (adult stages) that shows negative allometric growth. In our study, the data from the measurements of TL and W were taken from the samples that contained all the ages present in the catches.

The impact of the structure of the sample, according to length-classes, on the values that result after the calculation of the exponent b , was also noted by Dervishi et al. (2018). These authors had calculated for the stock of Scorzana bleak from Shkodra Lake the value of $b=2.57$, confirming, as in our study, the negative allometric growth of this fish. Also, for the stock of Scorzana bleak from Shkodra Lake, Milošević and Mrdak (2015) had calculated the value of $b=2.936$, proving almost isometric growth, as we also tried for the samples taken in the Spring and Summer seasons, in the stock of this fish from Ohrid Lake. Milošević and Talevski (2016) had published the value of $b=2.884$ for the stock of Scorzana bleak, according to the samples taken in the North-Macedonian part of Ohrid Lake. This value, which confirms the negative allometry of the growth, turned out to be within the range of the values that we had found for this fish, in the 11-month study period, including the period of active grazing.

We did not provide the data from the literature, about the as-

assessments on the growth characteristics, based on the calculations of growth parameters in LWRs and condition factors, for the stocks of common chub from the Ohrid-Drin-Shkoder water system. Some comparisons can be made with the results of the assessments carried out in the “sister” species as well as the stocks of *S.cephalus* from the lentic and lotic basins of other countries in the Balkan Peninsula. According to the evaluations of Milošević and Talevski (2016), *Squalius prespensis* in Prespa Lake manifests positive allometric growth. Also Milošević and Mrdak (2015) found the value of $b=3.027$ in a stock of *Squalius platycephus* from Shkodra Lake, proving the isometric growth for this species. Sasi and Ozay (2017) had evaluated a rheophilic population of *Squalius cephalus* in Turkey and, after measuring the fishes in the mixed samples according to the two sexes, they had calculated the value of $b=2.733$ (negative allometry of the growth). On the other hand, the value of the Fulton’s condition factor was from $K=1.32$ to $K=1.37$. Muntean et al. (2021), in Romania, had calculated the values of the exponent b in LWRs and had found the value of $b=3.258$ (positive allometric growth) in a rheophilic population of *S.cephalus* and the value of $b=2.952$ (almost isometric growth) in a limnophilic population of this species. These authors had pointed out that the differences for the growth and condition parameters were caused by the adaptation of the two populations to the specific living conditions that distinguished the river from the lake.

Most of the authors who have made assessments on the growth characteristics of the populations and fish stocks, based on the weight and length data of the individuals, are referred mostly to Bagenal and Tesch (1978) as well as Froese (2006). These authors had argued that the differences in LWRs of fishes may be attributed to several factors, such as number and length range of the sampled specimens, gonad maturity, sex, diet, stomach fullness, and growth phase. However, agreeing with this argumentation, we consider that the scientific support related to the differences in the values of the growth parameters, calculated using the TL and W data, from the individuals included in the samples, is difficult if special assessments are not carried out according to the specific impacting factors. Therefore, we agree with the statement made by Tsoumani et al (2006), according to which: “While we cannot conclusively explain the agreements and disagreements with published literature, it might be due to the condition of the species itself, its phenotype and its specific geographic location and hence its environment as several researchers have observed”.

Conclusion: Following the studies that were carried out before for the populations of Scorzana bleak and common chub in Ohrid Lake, our study is a modest contribution in the knowing of the growth characteristics of these species. Given that the model of the growth reflect not only the recuperation potential of stocks and the quality of the living environments, but also the pressure of the exploitation from the fishing activity, the results of the evaluations on the growth parameters can be used as indicators in the programs for the responsible exploitation and conservation of the fish species that stand out for their dual, faunal and economic values.

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