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special edition

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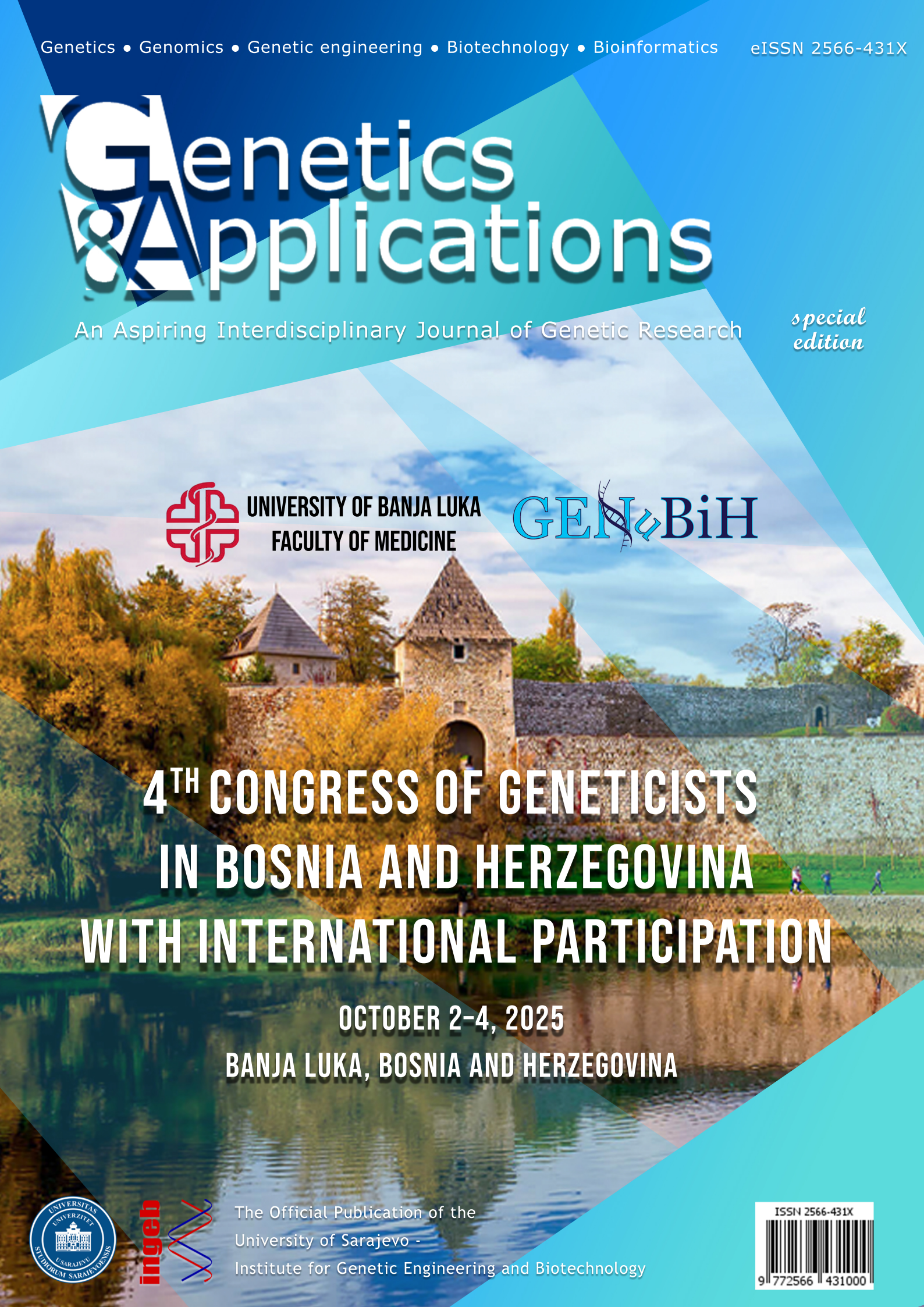

4TH CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION

OCTOBER 2-4, 2025

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4TH CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION

2ND - 4TH OCTOBER 2025, BANJA LUKA, BOSNIA AND HERZEGOVINA

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The abstracts underwent a streamlined submission process, wherein authors retained full responsibility for both the content and the language therein.

SCIENTIFIC PROGRAMME

4th Congress of Geneticists in Bosnia and Herzegovina with International Participation
Hotel Bosna, Banja Luka, Bosnia and Herzegovina, 02nd - 04th October, 2025

THURSDAY 2nd October

12:00 **Registration desk opening and poster mounting (Hotel Bosna)**

13:30 **OPENING CEREMONY: WELCOME NOTE (President of the Association, President of the Organizing Committee, Dean of the Faculty of Medicine, University of Banja Luka)**

Chairs: Marija Vuković, Dragana Šnjegota

13:45 – 14:20 **I1 Zoran Popovski** (*Ss. Cyril and Methodius University, Faculty of Agricultural Sciences and Food, Skopje, North Macedonia*): MOLECULAR AND GENETIC TOOLS IN LIFESCIENCES – AN OVERVIEW

14:20 – 14:55 **I2 Borut Peterlin** (*University Medical Center Ljubljana, Clinical Institute of Genomic Medicine, Ljubljana, Slovenia*): PATHWAYS TO GENOMIC MEDICINE IN HEALTHCARE

14:55 – 15:30 **I3 Zoran Galić** (*University of California Los Angeles, Los Angeles, United States of America*): PLURIPOTENT STEM CELLS IN HUMAN THERAPY: FROM DISCOVERY TO APPLICATION

15:30 – 16:00 **COFFEE BREAK/POSTER SESSION**

Chairs: Borut Peterlin, Vanja Vidović, Nela Maksimović

16:00 – 16:20 **O1 Jelena Pejić** (*University of Belgrade, Institute of Molecular Genetics and Genetic Engineering, Belgrade, Republic of Serbia*): ASSESSMENT OF ACUTE EXPOSURE TO ENERGY DRINKS AND THEIR MAJOR COMPOUNDS (CAFFEINE AND TAURINE) ON FUNCTIONAL CHARACTERISTICS OF NT2-DERIVED NEURONS AND ASTROCYTES

16:20 – 16:40 **O2 Jovana Krstić** (*Mother and Child Health Care Institute of Serbia "Dr Vukan Čupić", Division of Clinical Genetics, Belgrade, Republic of Serbia*): BODY COMPOSITION IN PEDIATRIC PATIENTS WITH MARFAN SYNDROME

16:40 – 17:00 **O3 Lejla Pojskić** (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): PROFESSIONAL GUIDELINES FOR THE IMPROVEMENT OF HIGHER EDUCATION PROGRAMS IN THE FIELD OF BIOTECHNOLOGY IN BOSNIA AND HERZEGOVINA

17:00 – 17:15 **S1 Juraj Hlinicky** (*CeGat, Tübingen Germany; Family Health, Belgrade, Republic of Serbia*): CeGaT – COMPREHENSIVE GENETIC SOLUTIONS

17:30 – 18:30 **Elective Assembly of the Association of Geneticists in Bosnia and Herzegovina** *(members only)*

20:00 – 22:00 **WELCOME RECEPTION** (Hotel Bosna, Kralja Petra I Karađorđevića 97)

FRIDAY 3rd October

08:00 **Registration desk opening (Hotel Bosna)**

Chairs: Ranko Škrbić, Anja Haverić

08:30 - 09:05 **I4 Bojana Žegura** *(National Institute of Biology, Department of Genetic Toxicology and Cancer Biology, Ljubljana, Slovenia; Jozef Stefan International Postgraduate School, Ljubljana, Slovenia):* FROM EXPOSURE TO EFFECT: GENOTOXICITY PROFILING OF INDOOR AIR POLLUTANTS USING ADVANCED IN VITRO 3D LIVER CELL MODELS

09:05 – 09:40 **I5 Merve GÜDÜL BACANLI** *(University of Health Sciences Turkey, Gülhane Faculty of Pharmacy, Department of Pharmaceutical Toxicology, Ankara, Türkiye*): IMMUNOTOXIC EFFECTS OF NANOPARTICLES: AN EVALUATION OF INFLUENCING FACTORS

09:40 – 10:15 **I6 Dijana Plaseska-Karanfilska** *(Macedonian Academy of Sciences and Arts, Research Centre for Genetic Engineering and Biotechnology, Skopje, North Macedonia):* UNRAVELING THE GENETIC PUZZLE OF EARLY PREGNANCY LOSS: FROM CHROMOSOMES TO RARE MONOGENIC DISORDERS

10:15 – 10:50 **I7 Miloš Brkušanin** (*University of Belgrade - Faculty of Biology, Centre for Human Molecular Genetics, Belgrade, Republic of Serbia*): NEWBORN SCREENING FOR SMA: HOW TIMELY DIAGNOSIS CHANGES LIVES

10:50 -11:20 **COFFEE BREAK/POSTER SESSION**

Chairs: Belma Kalamujić Stroil, Gaye Kandemir

11:20 – 11:55 **I8 Snežana Tomanović** (*University of Belgrade, National Institute of Republic of Serbia Group for Medical Entomology, Institute for Medical Research, Centre of Excellence for Food and Vector-borne Zoonoses, Belgrade, Republic of Serbia*): FROM THE LOCAL DIVERSITY OF TICK-BORNE PATHOGENS IN QUESTING TICKS TOWARDS TAILOR MADE APPROACHES IN MANAGEMENT OF TICK-BORNE DISEASES – PRELIMINARY RESULTS OF TALKTOTICK PROJECT

11:55 – 12:30 **I9 Belma Kalamujić Stroil** (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology Sarajevo, Bosnia and Herzegovina*): MICROSCOPIC THREATS, MACROSCOPIC IMPACT: A DECADE OF TICK RESEARCH AND PUBLIC HEALTH IMPLICATIONS

12:30 – 13:05 **I10 Gaye Kandemir** (*Forest Tree Seeds and Tree Breeding Research Institute Directorate, Ankara, Türkiye*): THE PAST AND FUTURE OF FORESTRY BASED ON BİOTECHNOLOGY

13:05 – 13:20 **S2 Weronika Gutowska-Ding** (*EuroGentest, European Society for Human Genetics; EMQN CIC, Manchester, United Kingdom):* BEYOND COMPLIANCE: EUROGENTEST INITIATIVES AND EVIDENCE FOR THE ROLE OF EXTERNAL QUALITY ASSESSMENT IN DRIVING LABORATORY IMPROVEMENT

13:20 – 14:30 **LUNCH BREAK/POSTER VIEWING**

Chairs: Bojana Žegura, Dijana Plaseska-Karanfilska

14:30 – 14:45 **O4 Merve Becit-Kizilkaya** (*Afyonkarahisar Health Sciences University, Faculty of Pharmacy, Department of Pharmaceutical Toxicology, Afyonkarahisar, Türkiye)*: CYTOTOXIC AND GENOTOXIC EFFECTS OF BERBERINE-GEMCITABINE COMBINATION IN A549 HUMAN LUNG CANCER CELLS

14:45 – 15:00 **O5 Duygu Sevim-Tatar** *(University of Health Sciences Turkey, Gülhane Faculty of Pharmacy, Department of Pharmacognosy, Ankara, Türkiye):* COMPREHENSIVE ASSESSMENT OF DNA DAMAGE, CYTOTOXICITY, APOPTOSIS, AND OXIDATIVE STRESS INDUCED BY TURKISH ROSEHIP (*Rosa canina* L.) EXTRACTS IN GLIOBLASTOMA AND MELANOMA CELLS

15:00 – 15:15 **O6 Saša Perović** *(Clinical Center of Montenegro, Center for Genomic Medicine and Immunology, Podgorica, Montenegro):* A NEW INSIGHT INTO THE IMPACT OF THE CES1 RS2244613 VARIANT ON CLOPIDOGREL THERAPY RESPONSE: POTENTIAL PROTECTIVE ROLE

15:15 – 15:35 **O7 Tea Bećirević** (*University Medical Centre Ljubljana, Clinical Institute of Genomic Medicine, Ljubljana, Slovenia*): DO GENES DRIVE KIDNEY STONES? EVIDENCE FROM SLOVENIAN PATIENTS AND POPULATION STUDIES

19:30 **CONGRESS DINNER** (Hotel Courtyard by Marriott , Prvog Krajiskog Korpusa 33)

SATURDAY 4th of October

08:00 **Registration desk opening (Hotel Bosna)**

Chairs: **Zoran Galić, Nina Marić, Marija Dušanović Pjević**

08:30 - 09:05 **I11 Bojan Ristivojević** (*University of Belgrade, Institute of Molecular Genetics and Genetic Engineering, Belgrade, Republic of Serbia*): PHARMACOGENOMICS OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA IN CHILDREN IN SERBIA

09:05 – 09:40 **I12 Marija Dušanović Pjević** *(University of Belgrade, Faculty of Medicine, Institute of Human Genetics, Belgrade, Republic of Serbia)*: PHARMACOGENETICS IN ACUTE ISCHEMIC STROKE: CURRENT PERSPECTIVES AND FUTURE DIRECTIONS

09:40 – 10:15 **I13 Milka Grk** (*University of Belgrade, Faculty of Medicine, Institute of Human Genetics, Belgrade, Republic of Serbia*): PHARMACOGENETIC APPROACHES IN THE MANAGEMENT OF RHEUMATIC DISEASES: CURRENT TRENDS AND FUTURE CHALLENGES

10:15 – 10:50 **I14 Nikola Tanić** (*University of Belgrade, National Institute of the Republic of Serbia, Institute for Biological Research "Siniša Stanković", Belgrade, Republic of Serbia*): ALTERATION OF THE EXPRESSION OF A SET OF PROTEINS THAT DEFINES A "HIGH-RISK" PROGNOSTIC PROFILE IN PATIENTS WITH TRIPLE-NEGATIVE BREAST CANCER

10:50 – 11:15 **COFFEE BREAK/POSTER SESSION**

Chairs: **Jasmina Čakar, Žana Radić-Savić**

11:15 – 11:35 **O8 Bojana Kožik** (*University of Belgrade, National Institute of the Republic of Serbia, Institute of Nuclear Sciences "Vinča", Belgrade, Republic of Serbia*): MULTI-OMICS AND DOCKING STRATEGIES REVEAL CANDIDATE PATHWAYS DRIVING VASCULAR INVASION IN RECTAL CARCINOMA

11:35 – 11:55 **O9 Amila Čatić** (*University of Sarajevo, Faculty of Health Studies, Sarajevo, Bosnia and Herzegovina*): APPLICATION OF MODERN METHODOLOGY IN GENETIC ANALYSES FOR THE MASS IDENTIFICATION OF MISSING PERSONS IN BOSNIA AND HERZEGOVINA

11:55 – 12:15 **O10 Sumejja Goharian** (*University of Sarajevo, Faculty of Health Studies, Sarajevo, Bosnia and Herzegovina*): AUTOPHAGY AS A POTENTIAL MODULATOR OF CELLULAR LONGEVITY

12:15 **CLOSING OF THE CONGRESS**

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POSTERS

Human and Medical Genetics

GRUJIČIĆ DARKO (*University of Kragujevac, Faculty of Science, Department of Biology and Ecology, Kragujevac, Republic of Serbia)*: GENETIC INSTABILITY IN PERIPHERAL BLOOD LYMPHOCYTES OF PREGNANT WOMEN WITH THREATENED SPONTANEOUS ABORTION IN THE FIRST TRIMESTER OF PREGNANCY

KUZMANOVIĆ MAJA (*Public Institution Cantonal Hospital Zenica, Department of Hospital Pharmacy, Zenica, Bosnia and Herzegovina*): MELANOMA AND GENOTOXICITY OF BIOLOGICAL THERAPY: THE IMPORTANCE OF CLINICAL PHARMACOGENETIC RISK ASSESSMENT

MAČKIĆ-ĐUROVIĆ MIRELA (*University of Sarajevo, Faculty of Medicine, Sarajevo, Bosnia and Herzegovina*): HOMOLOGOUS INVERSION OF CHROMOSOME 9 IN A MALE WITH AZOOSPERMIA: A CASE REPORT

ALIĆ LEJLA (*University of Sarajevo, Faculty of Medicine, Department of Medical Biochemistry, Sarajevo, Bosnia and Herzegovina*): ASSOCIATION OF RS1061170 AND RS6677604 POLYMORPHISMS WITH GESTATIONAL AGE AT BIRTH IN CHILDREN WITH ASTHMA

SELMA ĆUROVAC (*Genetic Association in Bosnia and Herzegovina, Sarajevo, Bosnia and Herzegovina*): INITIAL ASSESSMENT OF TELOMERE LENGTH IN THE BOSNIAN-HERZEGOVINIAN POPULATION USING REAL-TIME PCR AND FISH

LASIĆ LEJLA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): ONE HEALTH" CONCEPT IN PRACTICE: INVESTIGATION OF TICK-BORNE PATHOGENS IN HUMAN–ATTACHED TICKS IN THE FEDERATION OF BOSNIA AND HERZEGOVINA"

MENSUDA HASANHODŽIĆ (*University Clinical Center Tuzla, Center for Rare Diseases and Medical Genetics, Tuzla, Bosnia and Herzegovina*): THE FIRST CASE OF CAMURATI-ENGELMANN DISEASE ASSOCIATED WITH THE TGFB1 GENE IN BOSNIA AND HERZEGOVINA: A CASE REPORT

ĐUZIĆ NERMIN (*International Burch University, Department of Genetics and Bioengineering, Sarajevo, Bosnia and Herzegovina*): RETT SYNDROME IN BOSNIA AND HERZEGOVINA: SINGLE-CENTER STUDY

OMERČIĆ AMELA (*University Clinical Center Tuzla, Center for Rare Diseases and Medical Genetics, Tuzla, Bosnia and Herzegovina*): HEREDITARY SPASTIC PARAPLEGIA ASSOCIATED WITH SLC33A1: c.339T>A VARIANT: FAMILY CASE STUDY FROM BOSNIA AND HERZEGOVINA

IBRELIĆ LUNA (*University Clinical Center Tuzla, Clinic for Pediatric Diseases, Tuzla, Bosnia and Herzegovina*): EARLY CLINICAL AND GENETIC DIAGNOSIS OF TUBEROUS SCLEROSIS TYPE 2 IN BOSNIA AND HERZEGOVINA: CASE REPORT OF NEWBORN WITH DELETION OF TSC2 GENE

HASANHODŽIĆ MENSUDA (*University Clinical Center Tuzla, Center for Rare Diseases and Medical Genetics, Tuzla, Bosnia and Herzegovina*): THE GENETIC SPECTRUM OF NEUROFIBROMATOSIS TYPE 1 IN BOSNIA AND HERZEGOVINA

MAHMUTOVIĆ ENA (*Health Center Tešanj, Pediatric Department, Tešanj, Bosnia and Herzegovina*): LEOPARD SYNDROME IN BOSNIA AND HERZEGOVINA: FAMILY CASE CAUSED BY HETEROZYGOUS VARIANT IN PTPN11 GENE (p.TYR279CYS)

AVDIĆ ALDIJANA (*University of Tuzla, Faculty of Natural Sciences and Mathematics, Department of Biology, Bosnia and Herzegovina*): ENDOTHELIAL NITRIC OXIDE SYNTHASE (ENOS) G894T AND ANGIOTENSIN-CONVERTING ENZYME (ACE) I/D GENE POLYMORPHISMS AND THEIR ASSOCIATION WITH ANTHROPOMETRIC AND BIOCHEMICAL PARAMETERS

BEĆAREVIĆ JELENA (*University of Banja Luka, Faculty of Medicine, Department of Human Genetics, Banja Luka, Bosnia and Herzegovina; University of Banja Luka, Faculty of Medicine, Center for Biomedical Research, Laboratory for Molecular Biology and Genetics, Banja Luka, Bosnia and Herzegovina*): THE FTO GENE VARIANT AS A POTENTIAL RISK FACTOR FOR MYOCARDIAL INFARCTION

MESELDŽIĆ NEVEN (*University of Sarajevo, Faculty of Pharmacy, Department of Pharmaceutical Biochemistry and Laboratory Diagnostics, Sarajevo, Bosnia and Herzegovina*): ASSOCIATION OF IL-1β rs16944 POLYMORPHISM WITH DISEASE SEVERITY AND BIOMARKERS IN COVID-19 PATIENTS

RAMIĆ JASMIN (*University of Sarajevo–Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): ASSESSMENT OF USE CRISPR CAS9 METHODOLOGY FOR GENE SILENCING
VUKOVIĆ MARIJA (*University Clinical Center of the Republic of Srpska, Department of Medical Genetics, Banja Luka, Bosnia and Herzegovina*): IMPACT OF INHERITED THROMBOPHILIA AND GENETIC RISK FACTORS ON THROMBOSIS IN JAK2 V617F-NEGATIVE PATIENTS
ĆELIĆ MILICA (*University of Belgrade, Faculty of Biology, Belgrade, Republic of Serbia*): THROMBOSIS IN JAK2 V617F POSITIVE ESSENTIAL THROMBOCYTHEMIA AND POLYCYTHEMIA VERA

Genetics of Natural Resources

MEMIŠEVIĆ HODŽIĆ MIRZETA (*University of Sarajevo, Faculty of Forestry, Sarajevo, Bosnia and Herzegovina*): EARLY GENETIC EVALUATION OF SESSILE OAK FOR BREEDING IN BOSNIA AND HERZEGOVINA
BALLIAN DALIBOR (*University of Sarajevo, Faculty of Forestry, Sarajevo, Bosnia and Herzegovina*): THE NEW ROLE OF FOREST WOODY FRUITS IN EUROPEAN FORESTS
HANJALIĆ KURTOVIĆ JASNA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): ADVANCING CHAROPHYCEAE RESEARCH IN BOSNIA AND HERZEGOVINA: A CALL FOR EXPANDED BARCODING EFFORTS
NOVAKOVIĆ ANDREA (*University of Belgrade, National Institute of the Republic of Serbia, Institute for Biological Research "Siniša Stanković", Belgrade, Republic of Serbia*): DEVELOPMENT OF DROPLET DIGITAL PCR ASSAYS FOR ENVIRONMENTAL DNA DETECTION OF CRITICALLY ENDANGERED STURGEON SPECIES
MIRALEM MERIMA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): CITIZEN SCIENCE IN ACTION: EARLY INSIGHTS FROM THE TICK SPOTTING PROJECT
MIRALEM MERIMA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): THE IMPACT OF SAMPLE DRYING ON DNA EXTRACTION AND MICROSATELLITE AMPLIFICATION IN NORWAY SPRUCE (*PICEA ABIES*)

Bioengineering, Biotechnology and Bioinformatics

POPOVIĆ VLADAN (*Institute of Forestry, Belgrade, Republic of Serbia*): GENETIC STRUCTURE AND CONSERVATION MEASURES FOR THE BALKAN SESSILE OAK (*QUERCUS DALECHAMPII* TEN.) IN THE DJERDAP NATIONAL PARK
KALAJDŽIĆ ABDURAHIM (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Laboratory for Bioinformatics and Biostatistics, Sarajevo, Bosnia and Herzegovina*): INTEGRATING MACHINE AND NOVEL LEARNING SIMULATIONS TO PREDICT GENE FLOW AND ITS INFLUENCE ON HUMAN POPULATION DEMOGRAPHIC STRUCTURES
HASANOVIĆ MUJO (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): SOILS ADJACENT TO HIGH-TRAFFIC AREA NEAR URBAN TRAMLINES ACCUMULATE HEAVY METALS AND INFLUENCE BACTERIAL COMMUNITIES
KOŽIK BOJANA (*University of Belgrade, National Institute of the Republic of Serbia, Institute of Nuclear Sciences "Vinča", Belgrade, Republic of Serbia*): MULTI-OMICS AND DOCKING STRATEGIES REVEAL CANDIDATE PATHWAYS DRIVING VASCULAR INVASION IN RECTAL CARCINOMA

Biomonitoring and Genetic Toxicology

GRDOVIĆ TAMARA (*University of Belgrade, National Institute of the Republic of Serbia, Institute for Biological Research "Siniša Stanković", Belgrade, Republic of Serbia*): MICROPLASTICS AS A VECTOR FOR TRIBUTYLTIN INTAKE IN ZEBRAFISH: EFFECTS ON GENOTOXICITY
JANIĆ MARIJANA (*University of Belgrade, National Institute of the Republic of Serbia, Institute of Nuclear Sciences "Vinča", Belgrade, Republic of Serbia*): GENOTOXICITY AND ANTIGENOTOXICITY OF DEEP EUTECTIC SOLVENT BASED ON CHOLINE CHLORIDE AND ASCORBIC ACID IN HUMAN PERIPHERAL BLOOD MONONUCLEAR CELLS

ŠARIĆ MEDIĆ BELMINA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): DOSE-DEPENDENT CYTOTOXICITY OF CERIUM OXIDE NANOPARTICLES IN MG-63 OSTEOSARCOMA CELLS AND THE MODULATORY ROLE OF TWEEN-80

ĆUROVAC SELMA (*Genetic Association in Bosnia and Herzegovina, Sarajevo, Bosnia and Herzegovina*): CYTOTOXIC POTENTIAL OF PM10 PARTICULATE MATTER ON HUMAN BLADDER CARCINOMA CELLS IN VITRO: A CASE STUDY FROM SARAJEVO

KOSTIĆ MILA (*University of Belgrade, National Institute of the Republic of Serbia, Institute of Nuclear Sciences "Vinča", Belgrade, Republic of Serbia*): YELLOW GENTIAN INFUSION MITIGATES ɣ-RAYS INDUCED GENOTOXIC EFFECTS BY ALTERING LEVELS OF DNA REPAIR ENZYMES

RADOŠEVIĆ KSENIJA (*University of Belgrade, National Institute of the Republic of Serbia, Institute of Nuclear Sciences "Vinča", Belgrade, Republic of Serbia*): GENOTOXICITY ASSESSMENT OF LASER-SYNTHESIZED SILVER NANOPARTICLES WITH SALVIA OFFICINALIS AQUEOUS EXTRACT

DURAKOVIĆ LAMIJA (*University of Sarajevo, Faculty of Science, Sarajevo, Bosnia and Herzegovina*): IN VITRO INSIGHTS INTO THE CYTOTOXIC AND GENOTOXIC POTENTIAL OF COMMERCIAL NEEM POWDER

DURMIŠEVIĆ IRMA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): GENOTOXIC PROFILE OF GREEN GRAPHENE QUANTUM DOTS IN A NON-INVASIVE HUMAN CELL MODEL

TOMIĆ NIKOLINA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): EFFECT OF HALOGENATED BOROXINE AND CERIUM OXIDE NANOPARTICLES ON OSTEOSARCOMA CELLS IN VITRO

PANDUREVIĆ MAJA (*University of Sarajevo, Faculty of Science, Sarajevo, Bosnia and Herzegovina*): ASSESSMENT OF DNA DAMAGE INDUCED BY ETHANOLIC EXTRACTS OF JUNIPERUS SPECIES

Forensic Genetics

ČAKAR JASMINA (*University of Sarajevo-Institute for genetic engineering and biotechnology*): DNA PHENOTYPING OF SKELETAL REMAINS FROM MEDIEVAL BOSNIA

JUSIĆ BELMA (*University of Sarajevo-Institute for Genetic Engineering and Biotechnology, Sarajevo, Bosnia and Herzegovina*): FINDINGS ON DNA METHYLATION PROFILES IN A HEALTHY COHORT: PRELIMINARY RESULTS FROM AN ONGOING STUDY

PLENARY LECTURES

Plenary lecture – Invited speaker

MOLECULAR AND GENETIC TOOLS IN LIFESCIENCES – AN OVERVIEW

Popovski Zoran T.[1], Miskoska-Milevska Elizabeta[1], Terzikj Marija[2], Nestorovski Tome[3], Saiti-Musliji Zimere[4], Porcu Koco[1], Bandjo Oreshkovikj Katerina[5], Svetozarević–Arsović Milica[6], Tanaskovski Blagica[7]

[1]*Ss. Cyril and Methodius University, Faculty of Agricultural Sciences and Food, Skopje, North Macedonia*
[2]*Macedonian Academy of Sciences and Arts, Research Center for Genetic Engineering and Biotechnology "Georgi Efremov", Skopje, North Macedonia*
[3]*University Ss. Cyril and Methodius, Faculty of Veterinary Medicine, Skopje, North Macedonia*
[4]*Mother Teresa University, Faculty of Technology, Skopje, North Macedonia*
[5]*University Ss. Cyril and Methodius, Institute of Agriculture, Skopje, North Macedonia*
[6]*University of Belgrade, Innovation Center of Faculty of Technology and Metallurgy, Belgrade, Republic of Serbia*
[7]*Institute for Reference Materials and Measurement - Joint Research Center, Geel, Belgium*

The advancement of life sciences and related applied disciplines cannot be imaged without systematic application of modern techniques in which focus are nucleic acids and proteins. In last fifty years molecular biology was developed as separate discipline leaving permanent mark to those tools to be named as molecular. The premise on which the molecular and genetic tools are based is that genetic information is a resource that can be analyzed in different ways to achieve certain goals in basic and applied sciences. In this review, the subject of analysis is the application of molecular genetic tools in life and related sciences, with the exception of medical sciences. On one side, these molecular genetic tools, mainly PCR-based techniques are used in biology, agriculture, animal science, biotechnical sciences, microbiology, proteomics, evolutionary biology. Some of the most common uses are: so called marker assisted selection (MAS), in evolutionary studies and determination of genetic distance, for expression studies; to identify and characterize animal and plant pathogens, for production of recombinant proteins and GMO analysis etc. On the other side, in the last two decades, we have witnessed an incredible development of these molecular tools in the direction of accelerating the flow of analyses, enormously increasing the capacities for analyzing the number of samples and discovering completely new and more efficient approaches in the analysis of nucleic acids and proteins. This has greatly changed the perception of the application of these techniques in the life science and related applied fields. If the problem in the past was to analyze the sample, nowadays the problem is the analysis of the data from the sample results. This has undoubtedly led to an even greater connection between biology and computer science resulting in a discipline called bioinformatics. The overview contains a numerous case studies for application of molecular-genetic tools in usage of MAS in animal science, characterization of plant viruses, using of microsatellites in evolutionary studies in domestic animals and crops, performing of expression studies based on RNA analysis, production of recombinant enzymes and immune-modulators and food control.

Keywords: PCR; techniques; application; biology; bio-technics

Correspondence: zoran_popovski@yahoo.com

Plenary lecture – Invited speaker

PATHWAYS TO GENOMIC MEDICINE IN HEALTHCARE

Peterlin Borut

University Medical Center Ljubljana, Clinical Institute of Genomic Medicine, Ljubljana, Slovenia

Genomic medicine is reshaping healthcare, yet adoption often lags as medical evidence evolves in real time. To meet this challenge, we developed and implemented the Knowledge-First genomic service model at the Clinical Institute for Genomic Medicine (Slovenia) in 2013. We have cultivated professional genomic expertise, embedded rigorous standards, anchored workflows in clinically governed pathways, and ensured secure data stewardship, while pacing capital investment to clinical need. As a result, genomics has been integrated into publicly funded care, reducing reliance on external reference laboratories and improving access, autonomy, turnaround times, and overall sustainability. In rare diseases, our programme delivers a diagnostic yield of approximately 40%, equating to more than one confirmed genetic diagnosis per day. Through the Slovenian Genome Project, we have aggregated over 12,000 genomic datasets (predominantly WES) and curated them within the national Slovenian Genome Variant Database, enabling estimation of the population burden of genetic disease, accelerating routine variant interpretation, and informing the design of public-health applications such as genomic screening. Building on the Knowledge-First model, we partner with institutions to co-deliver diagnostics and counselling while transferring expertise to establish durable local capacity—a scalable, resource-sensitive pathway that brings genomics into everyday medicine for all citizens.

Keywords: genomic medicine; healthcare; rare diseases; genetic testing; genetic services

Correspondence: borut.peterlin@kclj.si

Plenary lecture – Invited speaker

PLURIPOTENT STEM CELLS IN HUMAN THERAPY: FROM DISCOVERY TO APPLICATION

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Human pluripotent stem cells (hPSCs), encompassing both embryonic stem cells (hESCs) and induced pluripotent stem cells (iPSCs), represent one of the most transformative platforms in modern biomedical research. Over the past two decades, these cells have advanced from proof-of-concept discoveries to tangible clinical applications, offering unprecedented opportunities for regenerative medicine, disease modeling, and drug discovery. Clinical trials are now actively exploring the use of hESC- and iPSC-derived products in treating conditions such as macular degeneration, Parkinson's disease, heart failure, diabetes, and spinal cord injury. These early studies not only demonstrate feasibility and safety but also highlight the capacity of pluripotent cells to generate functional cell types that restore or replace damaged tissues. At the same time, iPSCs have revolutionized personalized medicine by enabling patient-specific disease models and paving the way for autologous therapies. Looking ahead, the therapeutic promise of hPSCs continues to expand, with advances in genome editing, organoid technology, and scalable cell manufacturing addressing many of the limitations that once hindered clinical translation. While ethical considerations, immune compatibility, and long-term safety remain challenges, the trajectory of progress suggests that pluripotent stem cells will be central to the future of regenerative medicine. This presentation will review the major milestones and current clinical trials involving hESCs and iPSCs, discuss the opportunities and hurdles that define this field today, and highlight the innovations that are likely to shape the next generation of stem cell-based therapies.

Keywords: human pluripotent stem cells

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Plenary lecture – Invited speaker

FROM EXPOSURE TO EFFECT: GENOTOXICITY PROFILING OF INDOOR AIR POLLUTANTS USING ADVANCED IN VITRO 3D LIVER CELL MODELS

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Indoor air pollution poses a significant threat to human health, with polycyclic aromatic hydrocarbons (PAHs) representing a major class of hazardous contaminants. Commonly generated by combustion processes such as heating, cooking, and smoking, PAHs like benzo[a]pyrene (B[a]P), dibenzo[a,h]anthracene (DB[a,h]A), benz[a]anthracene (BaA), benzo[b]fluoranthene (BBF), and benzo[g,h,i]perylene (BGP) are known or suspected carcinogens. Conventional *in vitro* testing using two-dimensional (2D) monolayer cultures fails to replicate the complex physiology and metabolism of human tissues, limiting their relevance for human health risk assessment. To overcome these limitations, we developed physiologically relevant three-dimensional (3D) liver models derived from human HepG2 cells, cultured under both static and dynamic conditions. These models better mimic liver tissue architecture, cellular heterogeneity, and metabolic competence, enabling more accurate assessment of xenobiotic bioactivation and cellular responses. They also allow for long-term exposures and better simulate *in vivo* microenvironment. We applied these models to evaluate the genotoxic potential of selected PAHs at non-cytotoxic concentrations, focusing on an in-depth investigation of their effects and mechanisms of action. Our results showed that the 3D cell systems, particularly those cultured under dynamic conditions, have improved sensitivity for detecting the adverse genotoxic effects induced by PAHs. The tested PAHs induced genotoxic responses and modulated the expression of genes involved in metabolic activation, oxidative stress, and DNA damage repair. These findings demonstrate the relevance of 3D hepatic cell models as a powerful tool for mechanistic toxicology and support their integration into advanced testing strategies for next-generation chemical risk assessment, particularly for complex mixtures including indoor air pollutants.

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Keywords: 3D cell model; genotoxic; indoor air pollution

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Plenary lecture – Invited speaker

IMMUNOTOXIC EFFECTS OF NANOPARTICLES: AN EVALUATION OF INFLUENCING FACTORS

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Nanoparticles, defined as particles smaller than 100 nm, are increasingly encountered in every field due to their widespread use. These particles are known to cause diverse toxic effects due to their small size and distinct physicochemical properties. In particular, decreasing particle size increases surface area, and this increased surface area, due to the abundance of functional groups on the surface, leads to increased interaction with the biological environment and the nanostructure's ability to penetrate cells and interact with organelles. These interactions can lead to toxic effects. Furthermore, the different particle shapes or the binding of specific functional groups can also alter the toxic effects of nanoparticles. While the primary toxic mechanism of nanoparticles is known to be the generation of reactive oxygen species (ROS), uncontrolled production of ROS can trigger a proinflammatory response, leading to the release of mediators such as tumor necrosis factor (TNF)-α, interleukin (IL)-1β, IL-2, and IL-6. It has been suggested that the immunotoxic effect of NP may trigger inflammatory activation and immune responses. Therefore, when assessing potential toxic effects from NP exposure, emphasis should be placed on detecting potential changes in inflammatory biomarkers. Therefore, this study will focus on the factors that influence the immunotoxic effects of nanoparticles.

Keywords: nanoparticle size; shape; inflammation; immunotoxicity

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Plenary lecture – Invited speaker

UNRAVELING THE GENETIC PUZZLE OF EARLY PREGNANCY LOSS: FROM CHROMOSOMES TO RARE MONOGENIC DISORDERS

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Pregnancy loss (PL) is among the most frequent complications of human reproduction, affecting approximately 15% of couples attempting to conceive. Early pregnancy loss (EPL), defined as loss before 12 weeks of gestation, and recurrent pregnancy loss (RPL), defined as two or more consecutive losses, present substantial clinical and emotional challenges. While chromosomal abnormalities—such as trisomies, monosomy, and polyploidy—are well-established as major contributors to EPL, nearly 50% of RPL cases remain unexplained, highlighting the need for deeper genetic investigation. This presentation will provide an overview of the genetic landscape of EPL, focusing on current diagnostic practices and testing strategies. I will present data from our study examining the incidence and spectrum of chromosomal abnormalities in EPL and their associations with clinical parameters. In addition, findings from targeted association studies in our patient cohort will be discussed, exploring the contribution of genetic variants in thrombophilia, angiogenesis, and vascularization pathways, as well as several variants recently implicated in RPL through genome-wide association studies (GWAS). A key focus will be our recent research on rare monogenic causes of EPL, identified through whole exome sequencing (WES). These include lethal alleles leading to embryonic demise as well as variants associated with rare diseases of variable severity. Our complementary proteomic analyses further illuminate the biological pathways involved and identify potential biomarkers that may enhance future diagnostics and therapeutic approaches for managing EPL and RPL.

Keywords: early pregnancy loss; recurrent pregnancy loss; genetic causes; chromosomal aneuploidies; monogenic causes

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Plenary lecture – Invited speaker

NEWBORN SCREENING FOR SMA: HOW TIMELY DIAGNOSIS CHANGES LIVES

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Biochemical newborn screening in Serbia began in the 1980s, initially targeting phenylketonuria and congenital hypothyroidism. The program expanded in 2021 to include cystic fibrosis, marking a significant broadening of neonatal health surveillance. That same year, Serbia launched its first genetic newborn screening initiative for spinal muscular atrophy (SMA), a leading genetic cause of infant mortality that can be effectively treated if diagnosed early. This screening is centralized at the Center for Human Molecular Genetics, Faculty of Biology, University of Belgrade, which has specialized in SMA research and diagnosis since 1997. Although outside the formal healthcare system, the Government of Serbia designated this faculty as the sole national institution responsible for SMA screening. Following a 17-month pilot project screening 12,000 newborns, the national SMA newborn screening program officially commenced on September 15, 2023. The program now operates across 52 public and 6 private maternity hospitals, with dried blood spot samples analyzed at the national genetic screening laboratory in Belgrade. By August 4, 2025, Serbia has screened 112,918 newborns, identifying 19 infants with SMA. Sixteen of these infants began immediate treatment—6 with two *SMN2* gene copies, 6 with three copies, and 4 with four copies. Two infants with five *SMN2* copies remain under observation, while another case remains unresolved due to maternal neglect. This screening effort has provided Serbia's first reliable estimate of SMA incidence, approximately 1 in every 5,943 births. An Expert SMA Commission uses genetic data, clinical evaluation, and laboratory findings to ensure rapid, individualized treatment decisions. Almost all treated infants remain asymptomatic, demonstrating the critical benefits of early detection. Serbia's SMA screening program represents a successful collaboration between academia, patient organizations, the pharmaceutical industry, and the government, heralding a new era in neonatal healthcare and genetic screening nationwide.

Keywords: spinal muscular atrophy; newborn screening; genetic screening; public health

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Plenary lecture – Invited speaker

FROM THE LOCAL DIVERSITY OF TICK-BORNE PATHOGENS IN QUESTING TICKS TOWARDS TAILOR MADE APPROACHES IN MANAGEMENT OF TICK-BORNE DISEASES – PRELIMINARY RESULTS OF TALKTOTICK PROJECT

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After mosquitoes, ticks are medically the most important vectors worldwide. It is estimated that 40 anthropophilic tick species vector pathogens of up to 20 different diseases. Genetic variations in the pathogens lead to differences in virulence and thus to different clinical manifestations of the disease. In order to develop suitable concepts for the management of tick-borne diseases, an insight into the local diversity of tick-borne pathogens is essential. In our model area, five localities in and around Belgrade (Serbia) were selected to collect ticks from vegetation. Global warming and overall climate change are leading to milder winters, warm springs and summers with excessive heat and drought, which influence tick host-seeking activity. For this reason, we have extended the standard sampling practise, which is normally carried out from April to October, to include sampling every month for two consecutive years. All ticks collected are identified using standard taxonomic keys and DNA is extracted from individual ticks. Based on the previously determined prevalence, individual ticks are analysed for the presence of *Borrelia burgdorferi* sensu lato, while other pathogens such as *Borrelia miyamotoi*, *Rickettsia* spp., *Erlichia* spp., *Neoerlichia micurensis*, *Anaplasma phagocytophilusm*, *Francisella tularensis* and *Babesia* spp. are analysed using pooled samples. In case of a positive pool, the individual samples are analysed. In the first year of the project, 346 ticks were collected. The following pathogens were detected in the analysed sample with corresponding prevalence – *Borrelia burgdorferi* sensu lato (31.25%), *Rickettsia* spp. (24.57%), *Babesia* spp. (1.45%), *Anaplasma phagocytophilum* (1.16%), *Neoerlichia mikurensis* (2.31%) and *Borrelia miyamotoi* (1.16%). Sequencing revealed the presence of four species from the *Borrelia burgdorferi* sensu lato complex, with *Borrelia lusitaniae* absolutely dominating (63.8% of *Borrelia*-positive samples), followed by *Borrelia afzelii* (23.4%), *Borrelia garinii* (6.4%) and *Borrelia burgdorferi* sensu stricto (6.4%). Two *Rickettsia* species were genotyped – *Rickettsia monasensis* and *Rickettsia helvetica*.

Keywords: tick-borne diseases; *Borrelia burgdorferi* sensu lato; ticks; Serbia; diversity

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Plenary lecture – Invited speaker

MICROSCOPIC THREATS, MACROSCOPIC IMPACT: A DECADE OF TICK RESEARCH AND PUBLIC HEALTH IMPLICATIONS

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Over the past decade, a team of researchers from the University of Sarajevo – Institute for Genetic Engineering and Biotechnology has been intensively studying ticks and tick-borne pathogens, integrating field research, taxonomy, and molecular biology. In addition to surveys on free-dwelling ticks, special attention was given to the investigation of ticks collected from the patients who sought medical assistance at primary and secondary healthcare institutions across Bosnia and Herzegovina. Through detailed field collection and laboratory analysis, the diversity of ticks in Bosnia and Herzegovina has been documented, including species that parasitize bats. This work has filled a significant gap in regional fauna data and enabled better assessment of potential reservoirs of zoonotic pathogens. In parallel, methods for reliable detection of *Borrelia* spp. DNA from engorged ticks were developed and optimized, overcoming technical challenges caused by the presence of inhibitors. Using these methods, various genospecies of the *Borrelia* bacterium—*B. afzelii, B. garinii, B. burgdorferi s.s., B. bavariensis,* and *B. valaisiana*—were molecularly confirmed for the first time in *Ixodes ricinus* populations in Bosnia and Herzegovina. Bosnia and Herzegovina has been identified as one of the hotspot areas in Europe for ticks infected with *Borrelia burgdorferi*, the causative agent of Lyme disease. These findings significantly contribute to understanding the presence and distribution of Lyme borreliosis pathogens in the region, providing a foundation for more precise epidemiological monitoring and improvement of public health measures. The microscopic threats posed by ticks have a direct macroscopic impact on public health, underscoring the importance of continuous monitoring, a multidisciplinary approach, and raising awareness among the public and healthcare professionals regarding vector-borne diseases.

Keywords: tick; *Borrelia*; Lyme boreliosis; *Ixodes ricinus*; monitoring

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Plenary lecture – Invited speaker

THE PAST AND FUTURE OF FORESTRY BASED ON BİOTECHNOLOGY

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The three primary categories of biotechnologies utilized in forestry are the creation of genetically modified organisms (GMOs) or transgenic trees, the application of molecular genetic markers, and vegetative reproduction techniques. Biotechnology in forestry has developed rapidly over the last 40 years. In particular, the development of numerous molecular techniques allows tree genomes to be analyzed and gene transfer to tree genomes is being made. Biotechnology is being applied to forestry, as it is to other fields. Initially, these were used to increase wood production and improve the paper industry, but now they are used tree health protection, microbial relation, directly or indirectly related with tree physiology. Future tree improvement initiatives around the world will have exciting opportunities as a result of the advancements and integration of these sectors, which will have a significant impact in many ways and keep producing new knowledge. In fact, it is frequently regarded as one of the scientific disciplines where the fastest progress has been achieved recently.

Keywords: biotechnology; forestry; genetically modified organisms; molecular markers; vegetative reproduction

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Plenary lecture – Invited speaker

PHARMACOGENOMICS OF CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA IN CHILDREN IN SERBIA

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Personalized medicine uses modern treatment approach aiming to tailor therapy to the individual genetic and molecular characteristics of each patient. In Serbia, pharmacogenomics research has demonstrated the potential of this approach in children with acute lymphoblastic leukemia (ALL), the most common malignancy in the pediatric population. Although the cure rate for ALL is high, treatment is often accompanied by significant side effects and drug resistance, highlighting the need for further improvement of therapeutic protocols. As part of a collaborative study between the Institute of Molecular Genetics and Genetic Engineering and the University Children's Hospital in Belgrade, pharmacogenetic markers associated with the response to thiopurine drugs, glucocorticoids, vincristine, and methotrexate were analyzed in the Serbian pediatric population. Variants in candidate genes were identified using PCR and Sanger sequencing methodologies. The resulting genetic data were retrospectively correlated with clinical parameters and treatment outcomes. Additionally, a polygenic risk score (PRS)-based model was developed to predict methotrexate-induced hepatotoxicity, offering a potential tool for individualized treatment planning. The results of our study highlight the importance of tested molecular markers in determining the efficacy and safety of therapy. Also, they indicate the need for additional research to support the broader application of these findings in clinical practice in Serbia. Further recommendations emphasize the implementation of advanced methods for detecting genetic variants, such as next-generation sequencing (NGS), along with the integration of bioinformatics tools and machine learning algorithms. Additionally, the use of patient-derived induced pluripotent stem cells model system for research is proposed. These advancements will support the progress and implementation of personalized medicine in Serbia.

Keywords: childhood acute lymphoblastic leukemia; pharmacogenetic markers; polygenic risk score

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Plenary lecture – Invited speaker

PHARMACOGENETICS IN ACUTE ISCHEMIC STROKE: CURRENT PERSPECTIVES AND FUTURE DIRECTIONS

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Acute ischemic stroke (AIS) is one of the leading causes of mortality and long-term disability worldwide. The introduction of thrombolytic therapy, particularly recombinant tissue plasminogen activator (rtPA), has significantly improved functional outcomes in selected patients. However, the clinical response to rtPA remains highly variable, suggesting that additional factors, beyond clinical and imaging criteria, may influence therapeutic efficacy and safety. Among these, genetic factors are increasingly recognized as contributors to the inter-individual differences in treatment response. Pharmacogenetics, which explores how genetic variations affect drug metabolism, efficacy, and safety, holds great potential in optimizing stroke therapy. In AIS, pharmacogenetic studies aim to identify genetic variants that are associated with favorable or unfavorable outcomes, including risk of symptomatic intracerebral hemorrhage and mortality following rtPA administration. Polymorphisms involved in fibrinolytic pathways, drug metabolism, platelet function, and vascular reactivity have been proposed as potential biomarkers to guide personalized treatment strategies. Understanding these genetic determinants may allow for better stratification of patients and more informed therapeutic decisions. With the rapid development of genetic testing and wider availability of sequencing technologies, pharmacogenetics is becoming increasingly relevant in clinical practice. A more precise identification of genetic predictors of response could contribute to the optimization of treatment protocols, reduction of adverse effects, and improvement in overall outcomes. This approach represents a significant step forward in the implementation of personalized medicine in the management of AIS and highlights the need for further translational research and clinical validation of pharmacogenetic markers.

Keywords: ischemic stroke; pharmacogenetics; thrombolytic therapy; polymorphisms, personalized medicine

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Plenary lecture – Invited speaker

PHARMACOGENETIC APPROACHES IN THE MANAGEMENT OF RHEUMATIC DISEASES: CURRENT TRENDS AND FUTURE CHALLENGES

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Rheumatological diseases, such as rheumatoid arthritis, seronegative spondyloarthropathies, and systemic lupus erythematosus, require long-term and often complex pharmacotherapy, which includes the use of immunosuppressants, biologic agents, and targeted synthetic drugs. However, the therapeutic response is highly variable, and the risk of adverse reactions remains significant. Pharmacogenetics offers the possibility of more precise drug selection through the identification of genetic variants that affect the pharmacokinetics and pharmacodynamics of drugs, as well as the overall patient response to a given medication. Polymorphisms in genes such as *TPMT*, *NUDT15*, *HLA*-DRB1, and *FCGR3A* can affect the efficacy and safety of methotrexate, azathioprine, and biologics. Current trends include the introduction of genetic testing into clinical practice to predict treatment outcomes and minimise potential toxicity, which is particularly important given the benefits of initiating therapy early in the disease course. Despite progress, there are numerous challenges such as limited availability of testing, lack of standards in interpretation of results, and the need for validated clinical guidelines. With the increasing availability of next-generation sequencing (NGS) and the development of integrated biomarker panels, pharmacogenetics has the potential to become a key component of personalised medicine in rheumatology.

Keywords: rheumatology; pharmacogenetics

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Plenary lecture – Invited speaker

ALTERATION OF THE EXPRESSION OF A SET OF PROTEINS THAT DEFINES A "HIGH-RISK" PROGNOSTIC PROFILE IN PATIENTS WITH TRIPLE-NEGATIVE BREAST CANCER

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Breast cancer is the most common type of malignancy and the leading cause of cancer-related death in women worldwide. Triple negative breast cancer (TNBC) is characterized by the absence of ER, PR and HER-2 receptors and it accounts for 10-15% of all breast cancer cases. In comparison to other types of breast cancer, TNBC is more aggressive, has higher recurrence, metastasis and mortality rates. The only available therapy is cytotoxic chemotherapy, which is largely ineffective due to the development of resistance (MDR). Therefore, defining better molecular markers for better TNBC subtypes stratification and clarifying the mechanisms of drug resistance are of crucial importance for their successful therapy treatment. Numerous mechanisms lead to the development of resistance of neoplastic cells to cytotoxic drugs, including overexpression of efflux pumps, altered cellular pathways, abnormal tumor microenvironment. To that end, our first step was to analyze protein expression of the ATP-binding cassette transporters, trans-membrane proteins that utilize ATP to transport – efflux diverse compounds across cellular membranes among which are cytotoxic drugs. Second step was to analyze protein expression of one of the most frequently activated pathways in many types of cancers including breast cancer, PI3K/PTEN/AKT/mTOR pathway, which enhances drug efflux by efficiently expressing ABC transporters and reducing the response of chemotherapeutic drugs. Third step was to analyze the expression of cell membrane proteins, receptors and ligands important for breast cancer promotion and progression like AR, EGFR, PD-L1, claudins etc. Our results revealed the package of genes with altered protein expression that represent the "high risk" profile for bad outcome of TNBC patients: PI3K-high/PTEN-low/mTOR-high expression profile, followed by elevated expression of ABC transporters (ABCB1, ABCC1, ABCG2) and PD-L1-high/AR-low/EGFR-high expression profile. This complex profile is a very bad news for TNBC patients and identified marker genes should be taken in consideration for future multiple TNBC therapy.

Keywords: Triple negative breast cancer (TNBC); multidrug resistance (MDR); ABC transporters; PI3K/PTEN/AKT/mTOR pathway; trans-membrane receptors

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Plenary lecture – Sponsored

CEGAT – COMPREHENSIVE GENOMIC SOLUTIONS

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The latest update of ExomeXtra, the unique analysis that offers the most advanced solution in exome diagnostics will be covered. ExomeXtra's sequencing products uniquely integrate the benefits of both whole exome sequencing (WES) and whole genome sequencing (WGS), representing the only solution of its kind available globally. Engineered to deliver highly comprehensive sequencing data, the exome diagnostics sets a new standard for precision genetic testing with exceptional performance and features. Moreover, being aware of the importance of rare diseases today, insight in the use of different genetic panels will be shown. Equally important use of the newest accomplishments in the field of genetic testing is applied in the oncology. Oncogenetic tests for the determination of personalized targeted therapy of malignant diseases will be discussed, as well as the development of a personalized peptide tumor vaccine as a state-of-the-art approach to the treatment of malignancy based on exome testing of tumor tissue. At the end of the discussion, different possibilities for researchers such as genome sequencing, transcriptome sequencing, "single cell" RNA sequencing, spatial transcriptome sequencing, epigenomic sequencing, "long read" sequencing, microbiome sequencing (shotgun metagenomics sequencing and 16s sequencing) will be shown, followed by different case reports.

Keywords: WES; diagnosis; oncogenetic

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Plenary lecture – Sponsored

BEYOND COMPLIANCE: EUROGENTEST INITIATIVES AND EVIDENCE FOR THE ROLE OF EXTERNAL QUALITY ASSESSMENT IN DRIVING LABORATORY IMPROVEMENT

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External Quality Assessment (EQA) plays a central role in ensuring accuracy, reliability, and clinical utility in genomic testing, while also providing a mechanism for continuous improvement. Within EuroGentest, the Joint Committee on Poor Performance (JCPP) was established to address inconsistencies in how poor performance is defined and managed across Europe. Bringing together major EQA providers, including Equalis, Instand, ERNDIM, GenQA, and EMQN CIC, the JCPP is working to harmonise criteria, thresholds, and corrective action strategies to create a transparent, standardised framework for assessing underperformance. This initiative aims to reduce confusion for participating laboratories, foster comparability of data, and ultimately raise diagnostic standards across Europe. Beyond harmonisation, the committee is also exploring effective intervention strategies for persistently underperforming laboratories, including guidance for corrective action, enhanced training, and greater collaboration with regulatory bodies.Complementing this policy-level work of JCPP, a longitudinal study of EQA data from ten genomic testing schemes was performed, each with at least a decade of consistent data and participation from more than fifty laboratories per cycle. Results demonstrate measurable improvements in both genotyping and interpretation accuracy over time, with interpretation showing the most pronounced gains. Importantly, the rate of critical errors declined steadily with increased participation, indicating that sustained engagement in EQA directly supports quality enhancement rather than serving only as a compliance exercise. A small subset of laboratories displayed persistent performance fluctuations, underlining the importance of targeted support and intervention. Together, these findings highlight that EQA serves not only as an accreditation tool but also as a driver of lasting quality improvement. By combining harmonisation efforts through EuroGentest with evidence of impact from longitudinal analyses, we demonstrate the dual value of EQA in promoting excellence, comparability, and patient safety across genomic laboratories in Europe.

Keywords: EuroGentest; External Quality Assessment; genomic testing; laboratory quality improvement; patient safety

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ORAL PRESENTATIONS

Section: Human and Medical Genetics
Oral presentation

ASSESSMENT OF ACUTE EXPOSURE TO ENERGY DRINKS AND THEIR MAJOR COMPOUNDS (CAFFEINE AND TAURINE) ON FUNCTIONAL CHARACTERISTICS OF NT2-DERIVED NEURONS AND ASTROCYTES

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In recent years, energy drink consumption has notably increased among children and youth, with a growing trend of their combined use with alcohol. Studying the effects of those drinks on neural cells *in vitro* is a crucial step before considering their potential impact on the human brain. Retinoic acid-induced neural differentiation of pluripotent embryonal carcinoma NT2/D1 cells represents a valuable model of human *in vitro* neurogenesis, widely used for neurotoxicity studies on terminally differentiated NT2-derived neurons (NT2-N) and astrocytes (NT2-A). In this study, we investigated the effects of acute exposure to energy drinks and their major compounds—caffeine and taurine—with and without ethanol on the mature human neurons and astrocytes. Our results showed that NT2-N cells were more sensitive to acute treatment than NT2/A, observed as a slight reduction in cell viability following combined treatment with caffeine and taurine, as well as with an energy drink. In contrast, NT2-A viability remained unaffected by all treatments. Furthermore, all treatments led to elevated reactive oxygen species (ROS) levels in NT2-A, whereas NT2-N showed a differential response: caffeine and taurine (with and without ethanol) increased ROS production, while energy drinks (with and without ethanol) reduced ROS levels. Analysis of glutamate transporters (EAAT2 and EAAT1) expression patterns revealed that all treatments—except for energy drink combined with ethanol—significantly downregulated expression of these transporters in NT2-A. Intracellular glutamate levels remained unchanged across all treatment conditions. These findings emphasize how different types of human neural cells uniquely respond to acute exposure to energy drinks and their key compounds. Further research should focus on testing the effects of acute treatment in a co-culture system of neurons and astrocytes to better understand their responses and potential synergistic interactions.

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Keywords: energy drinks; caffeine; taurine; NT2-N, NT2-A

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Section: Human and Medical Genetics
Oral presentation

BODY COMPOSITION IN PEDIATRIC PATIENTS WITH MARFAN SYNDROME

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Marfan syndrome (MFS) is a multisystem connective tissue disorder, affecting 1 in 5 000–15 000 individuals. It is caused by mutations in the *FBN1* gene, which encodes fibrillin-1 involved in the formation of microfibrils and the regulation of transforming growth factor-beta (TGF-β) signaling. Patients with MFS are well known to exhibit a tall and slender build, disproportionately long limbs and fingers, and joint hypermobility; however, body composition in this group is less studied. Few studies on body composition in MFS patients showing reduced muscle mass and strength, low BMI, as well as uneven fat distribution. Study group included ten pediatric patients (6 girls and 4 boys), with an average age of 13,5 years with confirmed MFS. The average height of the patients was 169,4 cm. Measurements included height z score, aortic dimensions at the level of the aortic bulb, with calculated Z-scores, presence of mitral valve prolapse, BMI z score, and body composition assessed by bioelectrical impedance- BIA (skeletal muscle mass - SMM and percent body fat - PBF). Aortic bulb dilatation ($Z > 2$) was found in 3/10, and mitral valve prolapse in 8/10. Body composition analysis with BIA showed reduced SMM in 6 patients, normal in 3, and increased in 1. Findings align with studies showing most MFS youth have reduced muscle mass. On the other hand, PBF was within the normal range in 6 patients, decreased in 3, and elevated in one patient. Previous studies have shown that body composition (increased PBF and decreased SMM) may have a significant impact on aortic dilatation in adult with MFS. Lifelong cardiovascular monitoring is essential for the early diagnosis and management complications. Therefore, data obtained using the BIA method could be particularly important for assessing the vascular risk of these patients, in addition to measuring the aortic diameter itself.

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Keywords: Marfan syndrome; bioelectrical impedance; body composition

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Section: Bioengineering, Biotechnology and Bioinformatics
Oral presentation

PROFESSIONAL GUIDELINES FOR THE IMPROVEMENT OF HIGHER EDUCATION PROGRAMS IN THE FIELD OF BIOTECHNOLOGY IN BOSNIA AND HERZEGOVINA

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On May 22-23, 2025, GENUBIH and its partners: Academy of Sciences and Arts of Bosnia and Herzegovina, the Institute of Genetic Engineering and Biotechnology and the Faculty of Natural Sciences and Mathematics of the University of Sarajevo and the Association of Biochemists and Molecular Biologists in Bosnia and Herzegovina organized a scientific and professional symposium*: Biotechnologists of the New Generation – Skills of Future Educators*. Guided by the fact that the global Sustainable Development Goals (SDGs), such as the goals of the 2030 Agenda (SDG 2030), impose the need to revise societal development strategies, including higher education and business, and the implementation of sustainable technologies in line with general trends. The scientific conference "Next Generation Biotechnologists: Skills of Future Educators" aimed to exchange knowledge and good practices in the application of the latest scientific knowledge in the innovation of production processes and technologies. The symposium presented an opportunity to discuss the importance of scientific and educational capacities and technologies that enable this transition, and brought together experts in the field of natural sciences, doctoral students and postdoctoral students from biotechnical, biomedical and other related fields. The target audience was also academics, researchers and civil servants engaged in research, development-planning and implementation processes, as well as young entrepreneurs and leaders in biotechnology, especially in the context of sustainable agriculture and biotechnological innovations. The focus is on creating innovative educational programs that will enable the development of highly qualified experts for the challenges of sustainable industrial development. The conference was financially supported by the Federation of European Associations of Biochemists (FEBS), the Ministry of Science, Education and Youth of the Canton of Canton, and the Ministry of Education and Science of the Federation of Bosnia and Herzegovina, and this lecture will present the main aspects of the two-day intensive work and reflection on the importance of biotechnology for the development of BiH modern society and the education of personnel for the future, as well as the research of attitudes of all levels of the academic community that preceded the mentioned event. The outcomes of the survey have been

formulated into draft guidelines for the education of future personnel in this field, which we want to introduce to the wider community of geneticists in BiH.

Keywords: SDGs; 2030 Agenda; higher education; biotechnology; curriculum; knowledge; skills

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Section: Biomonitoring and Genetics Toxicology
Oral presentation

A CYTOTOXIC AND GENOTOXIC EFFECTS OF BERBERINE-GEMCITABINE COMBINATION IN A549 HUMAN LUNG CANCER CELLS

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Lung cancer is one of the most common cancers with high mortality rates. Resistance and toxicity due to gemcitabine limit treatment effectiveness. Combined therapy with phytochemicals represents a promising approach to improve outcomes. Berberine, a compound with anticancer activity, was selected as a potential combination agent. In this *in vitro* study, the effects of gemcitabine, berberine and their combinations on cytotoxicity and genotoxicity in A549 lung cancer cells were investigated. Cytotoxicity was determined using XTT method and genotoxicity using Comet assay. Synergy was analyzed using SynergyFinder based on the Bliss-Loewe model. Statistical analyses were performed using Tukey test for cytotoxicity and Kruskal Wallis test with Bonferroni correction for genotoxicity. Both compounds demonstrated dose-dependent cytotoxic effects with IC_{50} values of 321.509 ± 6.135 μM and 42.646 ± 1.724 μM, respectively, after 48 hours. Combined treatment showed significant antiproliferative effects compared with monotherapies ($p < 0.001$), with additive interaction (Bliss-Loewe score: 0.685). Genotoxic effects were evaluated based on tail length, tail % DNA and tail density analysis. Combination treatment demonstrated synergistic effects on tail length (score: 11.937), while additive effects were observed for tail % DNA (5.038) and tail density (4.221). The highest DNA damage was observed in high-dose combinations, with gemcitabine $IC_{50}/2$ and berberine IC_{50} (160.754 and 42.646 μM) showing significantly increased tail length (64.586 ± 0.477 μm), tail % DNA (53.079 ± 0.580%), and tail density (20.596 ± 0.307) compared to controls ($p < 0.001$). These results suggest that berberine significantly enhances both cytotoxic and genotoxic effects of gemcitabine in lung cancer cells. This combination approach provides valuable insights for future preclinical investigations.

Keywords: gemcitabine; berberine; comet assay; A549 cells; synergy analysis

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Section: Biomonitoring and Genetics Toxicology
Oral presentation

COMPREHENSIVE ASSESSMENT OF DNA DAMAGE, CYTOTOXICITY, APOPTOSIS, AND OXIDATIVE STRESS INDUCED BY TURKISH ROSEHIP (*ROSA CANINA* L.) EXTRACTS IN GLIOBLASTOMA AND MELANOMA CELLS

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Rosa canina L., commonly known as rosehip, is a perennial shrub of the Rosaceae family, encompassing over 200 species globally distributed across Europe, Asia, the Middle East, Africa, and North America. It is abundantly found in Turkey. *R. canina* L. has long been used worldwide as a source of vitamins, medicinal supplements, and food for its nutritional and medicinal benefits. Rich in vitamin C, polyphenols, carotenoids, and fatty acids, it shows various pharmacological effects, including anticancer, antioxidant, antidiabetic, anti-inflammatory, hepatoprotective, neuroprotective, and antimicrobial activities. In the present study aimed to evaluate and compare the cytotoxic, genotoxic, oxidative, and apoptotic effects of hexane and hydroalcoholic extracts of *R. canina* L. fruits on human glioblastoma (U87) and melanoma (SK-MEL-30) cell lines. The results demonstrated that both extracts exhibited notable effects on U87 glioblastoma cells after short-term exposure (24 h), particularly at low concentrations, whereas their effectiveness diminished at higher concentrations. However, upon prolonged exposure (72 h), both extracts showed increased cytotoxic effects in a concentration-dependent manner. At 24 h, the hexane extract was found to induce apoptosis more prominently at low concentrations and also caused oxidative stress and genotoxicity. In SK-MEL-30 melanoma cells, both extracts reduced cell viability in a concentration-dependent manner at both 24 h and 72 h. Notably, at lower concentrations, the ethanolic extract was more effective in inducing apoptosis, oxidative stress, and genotoxicity, indicating a significant impact on melanoma cell viability. These findings indicate that *Rosa canina* L. extracts exert time- and concentration-dependent cytotoxic, apoptotic, oxidative, and genotoxic effects on glioblastoma and melanoma cells. Notably, the hexane extract was more effective at inducing apoptosis in glioblastoma cells, while the hydroalcoholic extract showed stronger genotoxic and apoptotic activity in melanoma cells. These results highlight the anticancer potential of *R. canina* L. and support further investigation into its therapeutic applications.

Keywords: rosehip extract; *Rosa canina*; genotoxicity; ethanol; hexane; U87; SK-MEL-30

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Section: Human and Medical Genetics
Oral presentation

A NEW INSIGHT INTO THE IMPACT OF THE CES1 RS2244613 VARIANT ON CLOPIDOGREL THERAPY RESPONSE: POTENTIAL PROTECTIVE ROLE

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Carboxylesterase 1 (CES1) is the most abundantly expressed hepatic enzyme in humans, a serine protease type, responsible for 80–95% of the hydrolytic activity involved in the metabolism of drugs, xenobiotics, and endogenous biomolecules. CES1 is responsible for the hydrolysis of 85% of clopidogrel prodrug into inactive metabolites. Impaired enzyme activity, due to the presence of polymorphisms in the *CES1* gene, can affect the amount of prodrug that is inactivated, and thus influence the efficacy of clopidogrel therapy, which is manifested through the occurrence of adverse cardiovascular events. Among a few well-known genetic variants, one of the less studied is rs2244613, c.1168-33A>C, located in the intronic region of the gene. This variant has previously been shown to potentially be associated with reduced drug efficacy, that is, to lead to increased CES1 enzyme activity. In our study, we aimed to investigate whether this polymorphism is indeed associated with reduced drug efficacy or if it plays a different role. We recruited 196 Montenegrin patients with acute coronary syndrome (ACS) who were on clopidogrel therapy and divided them into two groups based on their therapeutic response—effective and ineffective. Genotypic analysis was performed using the RT-PCR method with specific TaqMan probes. The results showed that the frequency of the *CES1* minor allele was higher in the group with effective therapy—19.2% compared to 8.6% (p=0.05). Additionally, the frequency of *null* genotypes was twice as high in patients with effective therapy—34% versus 17.2%, respectively (p=0.06). Although with borderline statistical significance, our results suggest that this CES1 variant may have a protective role, potentially associated with reduced CES1 enzyme activity, which could increase the amount of active drug and improve therapeutic efficacy. This study is the first to suggest a potentially protective role of the CES1 rs2244613 variant, though further confirmation is needed.

Keywords: carboxylesterase 1; clopidogrel; ACS; therapy effectiveness

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Section: Human and Medical Genetics
Oral presentation

DO GENES DRIVE KIDNEY STONES? EVIDENCE FROM SLOVENIAN PATIENTS AND POPULATION STUDIES

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Kidney stones (KS) are a common urological disorder affecting 5–9% of the population in the European Union (EU), and their incidence has increased in recent decades. KS is estimated to be over 45% heritable, yet genetic testing remains uncommon in clinical practice due to an incomplete understanding of its genetic basis. To date, approximately 46 monogenic (single-gene) causes of kidney stone disease have been identified. The aim of our study was to determine the prevalence of KS-predisposing genes in Slovenian patients with kidney stones, including those with underlying metabolic disorders in which kidney stones are a primary manifestation, and to assess the frequency of these variants in a control Slovenian population. In a cohort of 21 patients, we identified a total of 7 likely pathogenic/pathogenic (LP/P) variants across five different genes (PKHD1, CASR, AVPR2, CYP24A1, and ATP6V0A4). In the Slovenian population, comprising 12,971 analyzed exomes, we identified 156 distinct likely pathogenic/pathogenic (LP/P) variants reported in ClinVar across 47 genes. Of these, 454 individuals (3.5%) were heterozygous carriers, and two individuals (0.015%) were homozygous. We also screened for novel high-risk variants not reported in ClinVar and identified three potential candidates in high-risk KS genes. These novel variants were classified as LP/P using ACMG criteria. In conclusion, our findings underline the significance of genetic factors in kidney stone disease and encourage the utilization of genetic testing for individuals at high risk, such as those with early-onset or recurrent stones, a family history of kidney stones or related metabolic or genetic abnormalities.

Keywords: kidney stones (KS); genetic testing; high-risk variants

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Section: Bioengineering, Biotechnology and Bioinformatics
Oral presentation

MULTI-OMICS AND DOCKING STRATEGIES REVEAL CANDIDATE PATHWAYS DRIVING VASCULAR INVASION IN RECTAL CARCINOMA

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Rectal carcinoma (RC) accounts for nearly one-third of colorectal cancers and represents a clinically distinct entity. Vascular invasion (VI) is an established adverse prognostic factor, strongly associated with recurrence, metastasis, and reduced survival. However, molecular drivers underlying VI remain insufficiently characterized. In this study, we interrogated transcriptomic and epigenomic data from The Cancer Genome Atlas (TCGA) rectal carcinoma cohort (n=78 with defined VI status) to explore potential molecular modulators of VI. Among 41 pre-selected candidate genes implicated in extracellular matrix (ECM) remodeling, angiogenesis, and epithelial-mesenchymal transition, only *ADAMTS8* expression showed a significant association with VI. Protein–protein interaction analysis revealed no direct clustering of *ADAMTS8* with ECM remodeling pathways, suggesting a distinct regulatory role. To identify potential co-regulators, we integrated DepMap dependency analyses, highlighting seven *ADAMTS8*-co-dependent genes (*DNAL4, EVI2B, PPP1R35, PTGR3, RPL21, SOX4, ZNF3*). In the TCGA cohort, decreased *DNAL4* and *PTGR3* and increased *RPL21* expression were significantly linked with VI. Molecular docking of 9,684 compounds, derived from toxicogenomic and PubChem similarity screening, identified four high-affinity candidates—cyanoginosin LR, doxorubicin, benzo[a]pyrene, and dibenzo(a,e)pyrene—that exhibited stable interactions across all eight protein targets. Our findings suggest that aberrant *ADAMTS8* expression, potentially modulated by epigenetic silencing, contributes to VI in rectal carcinoma. Moreover, co-dependent gene networks and compound docking analyses reveal candidate molecules with pan-target binding properties, warranting further experimental validation. Collectively, this work provides mechanistic insights into the molecular basis of VI in rectal carcinoma and highlights ADAMTS8 and its interactome as promising avenues for prognostic stratification and therapeutic exploration.

Keywords: rectal carcinoma; vascular invasion; *ADAMTS8*; molecular docking

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Section: Forensic Genetics
Oral presentation

APPLICATION OF MODERN METHODOLOGY IN GENETIC ANALYSES FOR THE MASS IDENTIFICATION OF MISSING PERSONS IN BOSNIA AND HERZEGOVINA

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In the course of the mass identification of missing persons in Bosnia and Herzegovina, DNA analysis played a vital role, particularly when anthropological and dental techniques could not be applied. The purpose of this study is to present the procedure for the first mass DNA identification, which became the cornerstone for the development of this molecular genetic technology. The phases of laboratory preparation of the samples were described as part of an international identification program. Laboratory preparation included chemical and mechanical cleaning of bones and teeth, grinding into a powder, isolation of DNA using demineralization buffers, digestion with proteinase K, and purification using phenol-chloroform or Chelex, alongside strict measures to prevent sample impurity. After laboratory preparation, DNA was quantified and amplified using the polymerase chain reaction. Targeted markers such as autosomal short tandem repeat loci, Y chromosome short tandem repeats markers, and hypervariable regions of the mtDNA enabled robust profiling, even for degraded samples. Sanger sequencing was applied specifically for mtDNA analysis. Recovered skeletal remains were then compared to reference samples from close relatives to establish kinship and allow statistical evaluation. A major challenge in the DNA identification process was the development of an algorithm for assessing DNA matches between the skeletal remains of missing persons and their relatives. The collaboration between forensic laboratories in Bosnia and Herzegovina and the International Commission on Missing Persons reached a high level of success, even in cases involving fragmented or degraded remains. The results demonstrate that the use of forensic and genetic techniques, together with appropriate databases, is essential in resolving complex cases and providing closure to the families of victims.

Keywords: DNA analysis; skeletal remains; STR profiling; forensic genetics; Bosnia and Herzegovina

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Section: Human and Medical Genetics
Oral presentation

AUTOPHAGY AS A POTENTIAL MODULATOR OF CELLULAR LONGEVITY

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The biological process of aging is marked by a reduction in cellular and functional capacity, which lowers quality of life and increases the chance of developing various diseases. The term autophagy, which is derived from the Greek words for "self" (auto) and "eat" (phagein), ultimately refers to a highly conserved process where lysosomes break down cellular components, such as defective organelles or proteins. Since autophagy failure is linked to the emergence of many age-related illnesses, its significance in the aging process is becoming more widely acknowledged. The purpose of this research is to examine the potential role of autophagy as a modulator of cellular longevity, particularly when it's triggered by fasting patterns including calorie restriction (CR), intermittent fasting (IF), and time-restricted feeding (TRF). For the purposes of this paper, a non-experimental, qualitative approach was applied through a systematic analysis of scientific articles from relevant databases. The analyzed studies showed that intermittent fasting and targeted genetic activation of autophagy contribute to the reduction of cellular aging, preservation of mitochondrial function and amplification of key genes involved in autophagy and longevity pathways. In both human and animal models, oxidative stress is decreased, mitophagy is triggered, and cellular aging is slowed. Therefore, autophagy plays a key role in reducing cellular aging, particularly when it is triggered by nutritional stress like fasting. It's crucial to remember that the use of fasting patterns must be carefully adapted to the age and health status of the individual, as improper or prolonged use may have adverse effects. Although the results indicate a beneficial link between autophagy activation and slowed cellular aging, as well as its potential in the prevention of age-related illnesses, further research is needed to fully understand its impact on human lifespan.

Keywords: autophagy; cell aging; senescence; intermittent fasting; time restricted feeding

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POSTER PRESENTATIONS

Section: Human and Medical Genetics
Poster presentation

GENETIC INSTABILITY IN PERIPHERAL BLOOD LYMPHOCYTES OF PREGNANT WOMEN WITH THREATENED SPONTANEOUS ABORTION IN THE FIRST TRIMESTER OF PREGNANCY

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Genetic instability can be the basis of various pathological conditions in humans, including the disruption of normal physiological processes such as the course and maintenance of pregnancy. This is the reason for our determination to analyze a sample of 40 phenotypically healthy pregnant women in the first trimester of pregnancy of which 20 were pregnant women with threatened spontaneous abortion, before using supstitution therapy, average age of 25.95±5.14, and 20 control pregnant women without an indication for threatened spontaneous abortion, average age of 27.45±7.90. Assessment of chromosomal damage in peripheral blood lymphocytes of pregnant women was determined by analyzing 1000 binucleate (BN) lymphoblasts, using the cytokinesis block micronucleus (CBMN) test. The average frequency of MN in the group of pregnant women with threatened miscarriage was 13.45±7.10 MN/1000 BN, which is 2.3 times higher than the average frequency of MN in peripheral blood lymphocytes of control pregnant women (5.90±3.01 MN/1000 BN) ($t=4.76$; $p<0.001$). Analysis of the distribution of MN in BN cells showed that in pregnant women with threatened spontaneous abortion, the percentage of cells with MN increased several times (1.25% vs. 0.57%), including the percentage of cells with a higher number of MN (2MN and 3MN) compared to control pregnant women (0.08% vs. 0.03%). The obtained results indicate that the observed significant difference in the variability of the frequency of MN in peripheral blood lymphocytes of pregnant women with threatened spontaneous abortion (range 5-29 MN/1000 BN) compared to control pregnant women (range 1-12 MN/1000 BN). The results obtained indicate that physiological-genetic instability in pregnant women may be the cause of the threatened miscarriages in the first trimester of pregnancy. At the same time, these results emphasize the importance of genetic integrity in order to improve the reproductive health of human populations.

Keywords: cytokinesis block micronucleus (CBMN) test; first trimester of pregnancy; pregnant women, physiological-genetic instability; threatened spontaneous abortion

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Section: Human and Medical Genetics
Poster presentation

MELANOMA AND GENOTOXICITY OF BIOLOGICAL THERAPY: THE IMPORTANCE OF CLINICAL PHARMACOGENETIC RISK ASSESSMENT

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Targeted therapies, particularly BRAF and MEK inhibitors, have transformed treatment outcomes for advanced melanoma with BRAF V600 mutations. These agents improve both progression-free and overall survival. However, increasing evidence highlights their potential to induce genotoxic effects and secondary malignancies. Understanding these risks and implementing pharmaceutical surveillance is critical for long-term patient safety. A narrative review of peer-reviewed literature published between 2018 and 2024 was conducted. Clinical studies investigating genotoxic effects of BRAF inhibitors (vemurafenib, dabrafenib) and MEK inhibitors (trametinib, cobimetinib) were analyzed. Mechanisms of DNA damage, mutation induction, and reported clinical outcomes were synthesized. Implications for oncology pharmacy practice, particularly the role of clinical pharmacists in monitoring and prevention, were emphasized. BRAF inhibitors have been associated with oxidative stress, mitotic dysregulation, and paradoxical MAPK pathway activation in wild-type cells, contributing to genomic instability. Clinically, increased incidences of cutaneous squamous cell carcinoma and de novo melanomas have been reported, especially during BRAF inhibitor monotherapy. While MEK inhibitor co-administration mitigates some risks, genotoxic potential remains. Despite this, structured integration of clinical pharmacists into safety monitoring programs is inconsistent. Evidence suggests that their involvement enhances adverse event identification, promotes early intervention, and supports informed therapeutic decisions. Genetic toxicology is a crucial component in the comprehensive safety evaluation of targeted cancer therapies. Proactive involvement of clinical pharmacists in multidisciplinary oncology teams can improve the detection, communication, and management of genotoxic risks. Expanding their role enhances pharmacovigilance and supports personalized therapy in patients receiving BRAF/MEK inhibitors for advanced melanoma.

Keywords: melanoma; genotoxicity; BRAF inhibitors; MEK inhibitors; clinical pharmacy

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Section: Human and Medical Genetics
Poster presentation

HOMOLOGOUS INVERSION OF CHROMOSOME 9 IN A MALE WITH AZOOSPERMIA: A CASE REPORT

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Chromosome 9 inversion (inv[9]) is among the most frequently observed structurally balanced chromosomal variations. Pericentric inversions, especially inv(9)(p11q12) and inv(9)(p11q13), are commonly identified. Although historically regarded as a benign variant, growing evidence suggests potential associations with clinical conditions such as infertility. A rare case of homozygous inversion involving both homologous chromosome 9 segments was identified in a male individual with a karyotype of 46, XY, inv(9) (p11q13). Chromosomal aberration was detected through GTG-banding during cytogenetic testing, which was prompted by the presence of azoospermia observed in the patient's semen analysis. Following the diagnosis, genetic counselling was initiated. To date, only three prenatal and seven adult cases of homozygous inv(9) have been documented in the literature. Although a definitive link between inv(9) and azoospermia has not been established, this case contributes valuable insight to the ongoing investigation of chromosomal abnormalities in male infertility.This case underscores the importance of comprehensive genetic evaluation in cases of male infertility and illustrates the clinical relevance of rare chromosomal variants, such as homozygous inv(9). Cytogenetic analysis remains essential in uncovering genetic factors within reproductive diagnostics.

Keywords: homozygous inversion; chromosome 9; azoospermia; cytogenetic analysis

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Section: Human and Medical Genetics
Poster presentation

ASSOCIATION OF RS1061170 AND RS6677604 POLYMORPHISMS WITH GESTATIONAL AGE AT BIRTH IN CHILDREN WITH ASTHMA

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Asthma is a complex, multifactorial disease influenced by both genetic and environmental factors. Low gestational age at birth can have a long-term impact on the maturation of the respiratory system, increasing susceptibility to developing asthma. Specific complement system proteins, such as complement factor H (FH), have been identified as factors contributing to preterm birth. The aim of this study was to examine the association of polymorphisms rs1061170 and rs6677604 within the FH gene with gestational age at birth in children with asthma.The study included a total of 117 children with a diagnosis of asthma, divided into two groups: children born preterm (n=60) and children born at term (n=57). Genotyping was performed for the rs1061170 and rs6677604 polymorphisms using real-time PCR. Statistical analysis was conducted using Fisher's exact test (FET) and binomial logistic regression with Jamovi software version 2.6.44. For rs1061170, the homozygous genotype for the minor allele (CC) was more present in preterm children (20%) compared to children born at term (10,5%). Still, there was no statistically significant difference in the frequency of genotypes for this polymorphism between the two groups (FET p=0,333). For rs6677604, the homozygous genotype for the minor allele (AA) was rare in both groups (1,7% in preterm children, 3,5% in children born at term), and there was no statistically significant difference in the frequency of genotypes for this polymorphism between the groups (FET p=0,536). The results of the binomial logistic regression did not show a statistically significant association between rs1061170 and rs6677604, and the risk of preterm birth (p=0,292 and p=0,613, respectively). In conclusion, results from our study did not show a significant association between the analyzed polymorphisms and gestational age in children with asthma. Further research with a larger number of subjects is needed to more thoroughly investigate the potential genetic predisposition for the development of asthma in the context of gestational age at birth.

Keywords: Complement factor H; Preterm birth; Gestational age; Childhood asthma; Genetic predisposition

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Section: Human and Medical Genetics
Poster presentation

INITIAL ASSESSMENT OF TELOMERE LENGTH IN THE BOSNIAN-HERZEGOVINIAN POPULATION USING REAL-TIME PCR AND FISH

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Telomere length analysis is increasingly used in the assessment of biological age, risk of disease development and general health status, where it represents a reliable biological marker that reflects the functional state of the organism. In the study, conducted on 22 peripheral blood samples and buccal swabs from healthy volunteers (aged 22–73 years; 55% women and 45% men), the Real-time PCR method was used to quantify relative telomere length (RTL). As a complementary cytogenetic method, telomeric FISH (Fluorescent In Situ Hybridization) was applied to two representative samples – with the longest and shortest measured RTL values in both types of samples. As part of the FISH analysis, peripheral blood lymphocytes and oral leukocytes were previously isolated and cultured, and telomeric DNA sequences were detected on metaphase chromosomes. The results of Real-time PCR showed variability in relative telomere length among the subjects, with no statistically significant association between telomere length and age, gender, or lifestyle habits. The results of FISH analysis on selected samples in our study were consistent with the results of Real-time PCR analysis, which is reflected in the differences in fluorescence intensity for the sample with the highest and lowest relative telomere length. In conclusion, although no statistically significant association of the analyzed factors with telomere length was found, this study, the first of its kind on a sample of healthy Bosnian and Herzegovinian population, provides important preliminary insights into the application of molecular genetic and cytogenetic methods for assessing relative telomere length. This opens the door for future, more extensive research on a larger number of subjects, which could contribute to a better understanding of the role of telomeres as a biological marker in assessing the health status of individuals and populations, both in our region and beyond.

Keywords: telomeres; telomere length; biological age; PCR; telomeric FISH

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Section: Human and Medical Genetics
Poster presentation

"ONE HEALTH" CONCEPT IN PRACTICE: INVESTIGATION OF TICK-BORNE PATHOGENS IN HUMAN-ATTACHED TICKS IN THE FEDERATION OF BOSNIA AND HERZEGOVINA"

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Tick-borne diseases (TBDs) represent an increasing public health concern, influenced by ecological, climatic, and socio-behavioral factors. The country's diverse landscapes and favorable climate support the spread of ticks and a wide range of zoonotic pathogens, including Borrelia, Anaplasma, and Rickettsia. Despite the rising incidence of TBDs, systematic research and continuous monitoring in the Federation of Bosnia and Herzegovina (FBiH) remain limited. Preliminary results from a public opinion survey indicate that 93.7% of respondents frequently spend time in nature, and 84.8% have previously encountered ticks. Notably, 51.9% reported finding a tick on themselves, with 35.7% experiencing a single tick encounter, 47.6% two to five times, and 16.7% more than five times. Among those bitten, 46.5% experienced local symptoms such as redness or itching, and 2.3% reported systemic symptoms like fever. However, 79.1% did not seek medical attention following the tick bite. These findings highlight a pressing need to raise public awareness and establish integrated tick and pathogen surveillance systems. By combining molecular diagnostics with real-world data on human-tick interactions, the aim is to strengthen public health alertness. The development of hotspot maps showing the prevalence and spatial distribution of ticks removed directly from humans, along with identified pathogens, will support accurate epidemiological assessments. Ultimately, the results will inform targeted prevention strategies and enhance communication with both the general public and healthcare professionals. This integrated approach directly contributes to the "One Health" framework, which emphasizes the interconnection between human, animal, and environmental health.

Keywords: One health; TBDs; Federation of Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

THE FIRST CASE OF CAMURATI-ENGELMANN DISEASE ASSOCIATED WITH THE TGFB1 GENE IN BOSNIA AND HERZEGOVINA: A CASE REPORT

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Camurati-Engelmann disease (CED), or progressive diaphyseal dysplasia, is a rare autosomal dominant, clinically variable bone disorder characterized by bone pain and hyperostosis of the skull, long bones, and pelvis. The average prevalence is estimated to be less than 1:1.000.000, with approximately 300 cases reported worldwide. CED is predominantly caused by pathogenic variants of the TGFB1 gene, encodes the transforming growth factor beta-1 protein. TGFB1 is associated with autosomal dominant Camurati-Engelmann disease, autosomal recessive inflammatory bowel disease, immunodeficiency, and encephalopathy. We present a first genetically confirmed case of CED in Bosnia and Herzegovina. At the time of diagnosis, the subject was a 11-year-old girl with feeling fatigue, headache, lack of appetite, bone pain, and fractures in a history. The proximal muscle weakness with hypotrophy, knee and hips contractures, thoracolumbar scoliosis, facial dysmorphy with bulging eyes, emotional hypersensitivity, asthenia, anemia, and vitamin D deficiency were clinically confirmed. We used a skeletal scintigraphy and radiography to identify diaphyseal dysplasia, and comprehensive skeletal disorder gene panel (320 genes), in a foreign laboratory, to confirme the diagnosis. It was identified a heterozygous pathogenic missense variant c.652C>T (p.Arg218Cys) in TGFB1 gene. This variant had previously been described in multiple individuals with CED. The litteratures sugested this variant impair the secretion of latent TGF-β1. Other detected variants of uncertain significance (COMP, EVC2, INPPL1, LRRK1, MMP14, RMRP, SULF1, TUBGCP6 and XYLT1 genes) could have an unknown impact on the patient's phenotype. Although our patient has a negative family history, and the variant probably arose de novo, that has not been proven, as the parents have refused their genetic testing. The accurate and timely clinical and genetic diagnosis allowed for focused clinical 5 years follow-up and treatment of the patient with CED with satisfaing resuts, and also illustrates the value of NGS panels in confirmation of rare skeletal pathology.

Keywords: CED; progressive diaphyseal dysplasia; first case; genetics; Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

RETT SYNDROME IN BOSNIA AND HERZEGOVINA: SINGLE-CENTER RETROSPECTIVE STUDY

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Rett syndrome (RTT) is a rare, X-linked disorder that primarily affects girls and causes regression of motor and speech skills, stereotypy, microcephaly, scoliosis, seizures and sleeping problem. The condition affects about 1 in 8.500 females. RTT is most commonly caused by pathogenic variants in the MECP2 gene, while early-onset atypical forms include pathogenic variants in the FOXG1 or CDKL5 genes. In our study, we included data on 10 girls from Bosnia and Herzegovina, using reports of genetic analyses performed during routine diagnostics. The girls had a clinical phenotype consistent with typical or atypical RTT. Two different laboratories tested the genomic DNA. Multiplex ligation-dependent amplification probe (MLPA) served as an initial screening method for MECP2 deletions/duplications (7/10). If the results were negative, they proceeded to targeted sequencing of the MECP2 gene (5/10). Whole exome sequencing (WES) was performed in MECP2-negative or atypical presentations of RTT (3/10). Genetic testing revealed six pathogenic variants of the MECP2 gene in 9 patients and one pathogenic variant in the FOXG1 gene (patient with atypical symptoms). Four nonsense variants, c.502C>T, c.880C>T, c. 808C>T, c.916C>T, and one missense variant, c.397C>T, were detected in the MECP2 gene. The c.502C>T and c.808C>T variants each occurred twice in 4 unrelated patients. Additionally, a deletion of the entire MECP2 gene was identified in two twin sisters. To our knowledge, this is the first comprehensive study of RTT in Bosnia and Herzegovina. These data support a 3-line diagnostic strategy, an MLPA + MECP2 sequencing + WES or WGS analysis (for previously negative results). Further studies, patient registries and lists of causal gene variants will help make future strategies for rare diseases, as well as introducing early diagnostic and planning the financial resources for inclusion of innovative drugs in the management of RTT and other rare diseases in Bosnia and Herzegovina.

Keywords: Rett syndrome; MECP2; FOXG1; MLPA; WES; trofinetid, Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

HEREDITARY SPASTIC PARAPLEGIA ASSOCIATED WITH SLC33A1: C.339T>A VARIANT: FAMILY CASE STUDY FROM BOSNIA AND HERZEGOVINA

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Hereditary spastic paraplegia (HSP) is a group of neuromuscular diseases associated with over 70 genes. The global prevalence of HSP is estimated at 3.6:100,000. The pure form of slowly progressive HSP is autosomal dominant (AD) spastic paraplegia (SGP) 42, onset from childhood to adulthood, characterized by spastic gait, increased tendon reflexes, weakness and atrophy of lower limbs, extensor plantar response, and pes cavus. SLC33A1 is the causative gene for SGP42. We present first comprehensive study of the family with HSP from Bosnia and Herzegovina. The proband was a patient (III3) with symptoms of HSP. His family had 14 members, nine with same symptoms (3 male, 6 female) and five asymptomatic (2 boys, 3 girls). Pedigree analysis showed an AD inheritance. Three older patient (I1, II1 and II2) died before testing, while patients III1 and III2 did not consent to testing. We tested five family members (III3, III4, IV2, IV3, IV4) used WES and variant analysis. The remaining asymptomatic members (IV1 and the youngest IV5, IV6, IV7) not yet tested. Genetic analysis revealed a same heterozygous missense variant SLC33A1: c.339T>A (p.Ser113Arg) of unknown significance in all member with symptoms (4/5). This variant is absent in gnomAD, ClinVar, LOVD data base, and had not yet been reported in the medical literature. The computational tool indicates this variant may be disease associated. Functional studies for previously reported heterozygous SLC33A1 variants revealed that knock-in mice and zebra fish displayed motor and sensory deficits and degeneration of the central and peripheral nervous system, associated with clinical features of SGP42. The segregation analyses of the family in our study confirmed AD inheritance with significant penetrance, and genetic analysis of family members confirmed SLC33A1: c.339T>A (p.Ser113Arg) as variant associated with HSP phenotype. This variant previously classified as VUS, we classified as pathogenic associated with AD inherited SGP42.

Keywords: Hereditary spastic paraplegia; Segregation analysis; Variant classification

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Section: Human and Medical Genetics
Poster presentation

EARLY CLINICAL AND GENETIC DIAGNOSIS OF TUBEROUS SCLEROSIS TYPE 2 IN BOSNIA AND HERZEGOVINA: CASE REPORT OF NEWBORN WITH DELETION OF TSC2 GENE

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Tuberous sclerosis complex (TSC) is a rare neurocutaneous genetic disorder that includes development tumors of multiple organs. TSC occurs with an incidence of 1:6,000 newborns. It is caused by pathogenic variants of the TSC1 (type 1) or TSC2 (type 2) genes. One-third of patients inherit the disease in an autosomal dominant manner from their parents, while in others it occurs de novo. Symptoms of TSC are variable and progressive, appearing by 6 months of age and include cardiac rhabdomyomas (50%), hypomelanotic skin macules, brain, lung, kidney tumors (80%), ocular hamartomas, and refractory seizures (85%). Genetic diagnosis is necessary before starting treatment. We present a case report of male newborn delivered via cesarean section in private hospital by 34 years old mother who was treated for arterial hypertension. A newborn was admitted on the 10th day of life to University Clinical Center Tuzla because of significant bradycardia. He had seizures on admission. Echocardiography revealed multiple rhabdomyoma-like cardiac tumors, foramen ovale, as well as second-degree atroventricular block, and Wolf-Parkinson-White syndrome on electrocardiography. Brain ultrasound and CT scan showed intracranial hemorrhage, and lesions of unclear etiology. 3billion whole exome sequencing analysis identified a de novo pathogenic variant in TSC2:c.4842_4844del (p.Ile1614del), with a deletion predicted to alter the length of the protein and disrupt its normal function. This variant has previously been reported in ClinVar as pathogenic, associated with autosomal dominant TSC type 2, but there are only a few reports of infants with neonatal-onset TSC symptoms. Genetic diagnosis has guided treatment to pacemaker implantation without tumor surgery, anticonvulsant therapy, and rapamycin, a drug that inhibits the mTOR protein, a central regulator of cell growth, proliferation, and immune function. Early clinical and genetic diagnosis of TSC is very important, and it involves timely monitoring of patients by a multidisciplinary team.

Keywords: newborn; tuberous sclerosis; TSC2 gene; Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

GENETIC SPECTRUM OF NEUROFIBROMATOSIS TYPE 1 IN BOSNIA AND HERZEGOVINA

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Neurofibromatosis type 1 (NF1) is a rare autosomal dominant disease, with a variable phenotype, caused by pathogenic variants in the NF1 gene. The prevalence ranges from approximately one in 3,000 to 4,000 individuals worldwide. In a retrospective study, we investigated the medical records of 81 patients from Bosnia and Herzegovina, 54 female (65%) and 27 male (35%), who presented clinical symptoms of NF1 observed between 2010 and 2025. Sixty-three percent of them reported a positive family history. The patients met globally accepted NF1 criteria, including six hyperpigmented spots >1 cm (89.9%), axillary and inguinal freckles (45.6%), two neurofibromas (34.2%) or one plexiform neurofibroma (5%), optic glioma (15.5%), and iris Lisch nodules. The study analysed genetic reports of 41 tested patients. It had used PCR, WES or NGS testing methods. We identified 22 different NF1 variants among 33 positive findings; 16 were familial. Five patients had a missense variant c.1466A>G, four had nonsense c.574C>T and three had c.6256_6258del. The missense c.4859T>C and c.5546G>A variants were found in two patients each. The remainder of the study cohort had one of the following variants: nonsense c.1094C>G, c.6792C>G, c.1318C>T, c.2953C>T, or 6751C>T (previously known as c.6652C>T), missense c.647T>C, c.1642G>C, c.1748A>G; or c.3251C>G, splicing c.2850+1G>A or c.6819+1G>A, frameshift duplication c.4809dupA. The variant c.7100_7101delTT was reported once as the cause of cardiovascular disease. In-frame deletion c.601_606del, and intronic c.61-11050A>G are identified in the same patient. Five variants (c.6256_6258del, c.7100_7101delTT, c.4531G>T, c.601_606del, and intronic c.61-11050A>G) have not been previously described in any consulted database associated with NF1. To our knowledge, this is the first comprehensive study of NF1 in Bosnia and Herzegovina. The wide allelic heterogeneity and genotype-phenotype correlation highlight the requirement for new studies in the future, as well as for establishing diagnostic pathway, genetic counseling and clinical guidelines for long-term follow-up of patients with NF1.

Keywords: neurofibromatosis type 1; genetic spectrum; fenotype; Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

LEOPARD SYNDROME IN BOSNIA AND HERZEGOVINA: FAMILY CASE CAUSED BY HETEROZYGOUS VARIANT IN PTPN11 GENE (P.TYR279CYS)

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Leopard syndrome is a rare, autosomal dominant, multisystem genetic disorder with an estimated prevalence of less than 1:1,000,000. The condition is caused by heterozygous pathogenic variants in the PTPN11 (85%) and RAF1 (10%) genes. We report the family case of Leopard syndrome in Bosnia and Herzegovina. The proband is boy born in 2011 years. At the age of six, he had a few lentiginous, and no other severe sing of the disease. Few years after, he was examined again, and presented dysmorphic facial features (midline facial prominence, hypertelorism, and high nasal root), multiple lentiginous and nevus, cardiac abnormalities (interventricular septal hypertrophy, subvalvular aortic stenosis, and first-degree atrioventricular block), ocular disorders (exophoria, hyperopia, and amblyopia), chest deformity (pectus excavatum), and joint laxity. His stature was on the 27th percentile, with normal intelligence but specific learning difficulties. The pedigree confirmed that several members from his family on the maternal side had clinical diagnosis of Leopard syndrome. The inheritance was consistent with an autosomal dominant pattern. The whole exome sequencing analysis identified a heterozygous pathogenic missense variant c.836A>G (p.Tyr279Cys) in the PTPN11 gene. This variant is known and it was also reported in a first family study on Leopard syndrome from Bosnia and Herzegovina (2014). In contrast to this study and other presented data in the literature, in our study, all affected family members except proband, had a history of cancer in adulthood. The grandfather had a prostate cancer, mother had rectal cancer, and uncle had a cancer of unknown origin. Patients with Leopard develop of multiple granular cell tumors of the skin and subcutaneous tissues during adolescence, but there is no data of cancer risk for other organs in adulthood. Our study highlights an importance of early recognition of clinical manifestations, and early molecular confirmation, especially in asymptomatic cases.

Keywords: Leopard syndrome; PTPN11 variant; cancer; Bosnia and Herzegovina

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Section: Human and Medical Genetics
Poster presentation

ENDOTHELIAL NITRIC OXIDE SYNTHASE (ENOS) G894T AND ANGIOTENSIN-CONVERTING ENZYME (ACE) I/D GENE POLYMORPHISMS AND THEIR ASSOCIATION WITH ANTHROPOMETRIC AND BIOCHEMICAL PARAMETERS

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The primary objective of this study was to analyze the frequency of alleles and genotypes of the G894T polymorphism of the endothelial nitric oxide synthase (eNOS) gene and the insertion-deletion (I/D) polymorphism of the angiotensin-converting enzyme (ACE) gene, in correlation with body mass index (BMI) and biochemical parameters. The distribution of genotypes and alleles in relation to smoking - non-smoking status was also analyzed, in order to examine the possible correlation between genetic predispositions and lifestyle factors. The frequency of genotypes in correlation with hypertension was also analyzed. The study included a total of 64 subjects. By analyzing the genotypes distribution of the eNOS gene G894T polymorphism in relation to BMI, in the group of subjects with BMI ≤24.9, the GT+TT genotype was determined in 11 subjects, and in the in 25 subjects from the group with BMI ≥ 25. For the ACE I/D polymorphism in the group of subjects with BMI ≤ 24.9, the ID+DD genotype was determined in 10 subjects, and in 36 subjects from the group with BMI ≥ 25. However, no statistically significant difference in the frequency of alleles and genotypes was determined between the analyzed groups of subjects (≤ 24.9; ≥ 25; ≥ 30) in relation to BMI for any of the polymorphisms ($p > 0.05$). The analysis showed that the GT+TT (eNOS G894T) genotypes were more frequently present in subjects with elevated levels of glucose, total cholesterol and triglycerides compared to the GG genotype. Also, in subjects with values of these parameters above the reference limits, the ID+DD (ACE I/D) genotypes occurred more frequently than genotype II. The main limitation of this study is a relatively small sample, and the results of this study should be considered preliminary and cannot be used for generalization without confirmation in studies with a larger and more homogeneous sample.

Keywords: endothelial nitric oxide synthase; ACE; BMI; biochemical parameters

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Section: Human and Medical Genetics
Poster presentation

THE FTO GENE VARIANT AS A POTENTIAL RISK FACTOR FOR MYOCARDIAL INFARCTION

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The fat mass and obesity-associated gene (FTO) encodes an enzyme that is involved in regulating energy balance and appetite, with the highest expression in the hypothalamus. The rs9939609 polymorphism in FTO has been associated with obesity, type 2 diabetes, and increased lipid levels, all of which are established risk factors for cardiovascular disease. Because of its role in metabolic regulation, the FTO gene has been suggested as a candidate for affecting cardiometabolic risk and susceptibility to myocardial infarction. This study aimed to examine the possible association of the FTO rs9939609 variant with myocardial infarction and related cardiometabolic risk factors. It included 93 patients with myocardial infarction who were not receiving lipid-lowering therapy and 93 healthy individuals matched by age and sex. Blood samples were collected at the Cardiology Clinic of the University Clinical Centre of the Republic of Srpska in Banja Luka, Bosnia and Herzegovina. Genotyping of the rs9939609 polymorphism was performed using quantitative polymerase chain reaction. The results showed that patients with myocardial infarction carrying the AA genotype had significantly higher body mass index compared to controls ($p=0.046$). Overall, body mass index was also higher in patients with myocardial infarction than in healthy individuals ($p<0.01$), supporting the link between elevated body mass index and coronary artery disease risk. Additionally, the rs9939609 variant was significantly associated with low-density lipoprotein cholesterol levels ($p=0.049$), with AA carriers showing higher mean low-density lipoprotein values compared to TT and TA genotypes. These results suggest that the FTO rs9939609 variant may be a potential risk factor for myocardial infarction. Future studies with larger numbers of participants are needed to confirm these findings.

Keywords: FTO; rs9939609; polymorphism; myocardial infarction; cholesterol

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Section: Human and Medical Genetics
Poster presentation

ASSOCIATION OF P16INK4A METHYLATION WITH METASTATIC POTENTIAL OF RECTAL CANCER

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Metastatic risk in rectal cancer (RC) is driven mainly by stage (T/N), imaging-detected venous invasion, and pathological features (lymphovascular invasion, poor differentiation, tumor budding). p16INK4a promoter hypermethylation is a common, variable epigenetic alteration in rectal/colorectal tumors that can reduce p16 expression and contribute to tumorigenesis, immune suppression, and worse outcomes. Clinically, p16INK4a methylation has been associated with adverse features in many studies, but its independent prognostic value across colorectal cancer (including rectal cancer) is inconsistent. The aim of our study was to evaluate the prognostic role of the p16INK4a methylation status in RC patients. This preliminary study was conducted on 35 RC patients who underwent curative resection from 2016 to 2018 at the Oncology Institute of Vojvodina. Genomic DNA was isolated from postoperative tumor FFPE samples, while methylation-specific PCR (MSP) was used to examine methylation status of p16INK4a gene. Our findings showed that p16INK4a methylation was more commonly detected in tumor tissues from the lower and mid-rectum compared to the upper rectum (71.4% and 62.5% vs. 20%, p=0.019). Additionally, we observed a higher prevalence of p16INK4a methylation in patients with high-grade tumors and lymphovascular invasion, although these results were not statistically significant (p=0.108 and p=0.163, respectively). Regarding disease outcomes, p16INK4a methylation was more frequent in patients who developed metastases (66.7% vs. 30.8%), approaching statistical significance (p=0.058). Moreover, the metastasis-free period appeared to be shorter for patients with detected p16INK4a methylation compared to those without it (48.96 ± 7.26 vs. 60.90 ± 4.86 months, p=0.081). These findings suggest a potential prognostic role for the assessment of p16INK4a methylation in the clinical setting for rectal cancer (RC) patients. However, further validation is needed with a larger cohort of RC patients, with particular emphasis on the methylation status of this gene in different tumor locations within the rectal tissue.

Keywords: rectal cancer; p16INK4a methylation; prognostic role

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Section: Human and Medical Genetics
Poster presentation

ASSOCIATION OF IL-1B RS16944 POLYMORPHISM WITH DISEASE SEVERITY AND BIOMARKERS IN COVID-19 PATIENTS

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Genetic polymorphisms in cytokine genes may influence immune responses and clinical outcomes in COVID-19. The IL-1β rs16944 (G>A) variant has been associated with altered cytokine expression, potentially affecting inflammatory, coagulation, and respiratory pathways. In this study, we investigated the association of IL-1β rs16944 with disease severity and laboratory biomarkers in 750 PCR-confirmed COVID-19 patients from the Bosnian population. Genotyping was performed using commercial assays, while biochemical, hematological, coagulation, and acid–base status parameters were measured according to IFCC standards. Logistic regression analysis revealed significant associations between rs16944 genotypes and selected biomarkers. Carriers of the AA genotype (28.00 [26.00–32.00]) exhibited prolonged activated partial thromboplastin time (aPTT) compared with GG (28.0 [25.00–30.00]) and GA carriers (28.0 [25.0–31.0]; p=0.003), suggesting an effect on coagulation pathways. For partial pressure of carbon dioxide (pCO_2), values differed among genotypes, with AA carriers (30.80 [25.80–34.00]) showing slightly lower medians compared to GG (31.70 [28.50–34.98]) and GA (30.90 [27.55–34.85]) carriers (p=0.019). Although statistically significant, these results indicate a modest and variable effect rather than a consistent directional change, reflecting the complexity of acid–base balance in COVID-19. Overall, genotype-dependent alterations in coagulation and respiratory markers parallel known features of severe disease, where dysregulated inflammation, coagulopathy, and impaired gas exchange are key mechanisms. These findings suggest that IL-1β rs16944 contributes to interindividual variability in biomarker profiles, supporting its potential role as a prognostic genetic factor and underscoring the importance of host genetics in shaping COVID-19 outcomes.

Keywords: COVID-19; IL-1β; rs16944; biomarkers; disease severity

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Section: Human and Medical Genetics
Poster presentation

ASSESSMENT OF USE CRISPR CAS9 METHODOLOGY FOR GENE SILENCING

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This work provides both the application and methodological, economic, and capacity assessment of the CRISPR Cas9 method for the "silence" (Knock-out) of a selected gene of interest in human HEK 239 cells. In our project, the PD-L1 gene was selected, which encodes an immune inhibitory receptor ligand that is expressed in hematopoietic and non-hematopoietic cells, such as T cells and B cells of lymphocytes and various types of tumor cells. The expression of this gene in tumor cells is considered prognostic for many types of human malignancies, including colon cancer and renal cell carcinoma. We used CRISPR Cas9 technology, which is based on the use of gRNA (guided RNA) to find a specific DNA sequence on the target gene and its alteration, which results in the non-recognition of the altered sequence of the gene of interest by the transcriptional mechanisms, which further leads to a decrease or complete cessation of gene expression of the gene of interest. We used Origene's kit for PD-L1 gene knock out using two different guided RNA sequences, introduced using two plasmid vectors.The project resulted in mastering the CRISPR Cas9 technique, under the conditions available at INGEB with the possibility of further development and application of this technology. Additionally, we obtained a HEK 239 cell line with more or less reduced expression (depending on the vector used). of the PD-L1 gene that can be used for additional research.

Acknowledgements: The project was founded by Ministry of Education, Science and Culture of Kanton Sarajevo.

Keywords: gene silencing; CRISPR CAS; HEK 293; transfection

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Section: Human and Medical Genetics
Poster presentation

IMPACT OF INHERITED THROMBOPHILIA AND GENETIC RISK FACTORS ON THROMBOSIS IN JAK2 V617F-NEGATIVE PATIENTS

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Inherited thrombophilia, primarily due to Factor V Leiden (FVL) and Factor II (FII) G20210A mutations, represents a major genetic risk factor for unprovoked thrombotic events. Other variants, such as MTHFR C677T and PAI-1 4G/5G, have been suggested as potential contributors to thrombotic risk, particularly in combination with classical thrombophilia mutations. We retrospectively analyzed 50 patients tested at the Department of Medical Genetics, University Clinical Center of the Republic of Srpska (2022–2025). All patients were negative for the JAK2 V617F mutation and had normal platelet and erythrocyte counts. Genetic testing included FVL, FII G20210A, MTHFR C677T, and PAI-1 4G/5G polymorphism. Clinical records were reviewed for thrombotic events. Thrombotic events occurred in 82% of patients: deep vein thrombosis (30%), ischemic stroke (20%), pulmonary embolism (22%), myocardial infarction (2%), and other ischemic events (8%). FVL was detected in 8% of patients, all of whom experienced thrombosis (DVT, PE, or ischemia), often in combination with MTHFR and/or PAI-1 variants. The FII G20210A mutation was present in 4%; both carriers developed thrombotic events (DVT or PE). The PAI-1 4G/5G genotype was found in 18%; 16% of these patients had thrombotic complications, most commonly ischemic stroke and pulmonary embolism. Heterozygous MTHFR C677T combined with 4G/5G or 4G/4G PAI-1 genotypes was associated with thrombosis in 30% of cases, while 12% remained without events. Homozygous MTHFR C677T combined with unfavorable PAI-1 genotypes was detected in 8%, and all such patients experienced thrombotic complications (4% pulmonary embolism, 4% other ischemia). In this cohort, FVL and FII G20210A mutations were the main causes of thrombosis. However, unfavorable MTHFR and PAI-1 genotypes appeared to contribute significantly to thromboembolic risk, especially when combined with classical thrombophilia mutations. These findings highlight the potential role of extended genetic profiling in patients with unexplained thrombotic events.

Keywords: inherited thrombophilia; Factor V Leiden; Prothrombin G20210A; MTHFR; PAI-1; thrombosis

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Section: Human and Medical Genetics
Poster presentation

THROMBOSIS IN JAK2 V617F POSITIVE ESSENTIAL THROMBOCYTHEMIA AND POLYCYTHEMIA VERA

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The JAK2 V617F mutation is the most frequent genetic alteration in myeloproliferative neoplasms (MPNs), including polycythemia vera (PV) and essential thrombocythemia (ET). This mutation causes constitutive activation of the JAK2 signaling pathway, leading to excessive proliferation of hematopoietic cells and a significantly increased thrombotic risk. Thromboembolic events are the leading cause of morbidity and mortality in MPNs, making precise risk stratification a clinical priority. At the Department of Medical Genetics, University Clinical Center of the Republic of Srpska, 81 patients diagnosed with MPN were positive for the JAK2 V617F mutation. ET was confirmed in 46 patients (23 males, 23 females), while 35 were classified as PRV (23 males, 12 females). Median age at ET diagnosis was 60.82 years in men and 63.65 years in women, with median platelet counts of 684.9 $\times 10^9$/L and 665.6 $\times 10^9$/L, respectively. Thromboembolic complications occurred in 45.6% of ET patients: myocardial infarction (10.8%), stroke (4.4%), deep vein thrombosis (8.7%), pulmonary embolism (8.7%), and other ischemic events (13%). Hypertension was present in 23.9% of ET patients, while 32% had no thromboembolic events. Among PV patients, the median age was 67.56 years for males and 68.17 years for females. Median red blood cell count was 5.71 $\times 10^{12}$/L in men and 5.26 $\times 10^{12}$/L in women. Thromboembolic events occurred in 40%: myocardial infarction (5.7%), stroke (17%), deep vein thrombosis (8.6%), pulmonary embolism (2.9%), and other ischemic events (8.6%). Hypertension was present in 31.4% of patients, while 28.6% were without thrombosis. These findings confirm that the JAK2 V617F mutation represents a significant risk factor for thrombosis in MPNs. However, other genetic and acquired risk factors contribute to thrombotic risk. Expanded screening, including factor V, factor II, MTHFR, and PAI-1 variants, may provide more refined stratification and enable tailored interventions, which are essential for reducing morbidity and mortality in this high-risk population.

Keywords: JAK2 V617F mutation; myeloproliferative neoplasms; essential thrombocythemia,; polycythemia vera; thromboembolic events; genetic risk factors

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Section: Genetics of Natural Resources
Poster presentation

EARLY GENETIC EVALUATION OF SESSILE OAK FOR BREEDING IN BOSNIA AND HERZEGOVINA

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Sessile oak (*Quercus petraea* (Matt.) Liebl.) is one of the most important deciduous forest tree species in Bosnia and Herzegovina. Sixty-six percent of all forests containing sessile oak are coppice forests, reflecting the species' former economic significance and current degradation due to overexploitation. This study aimed to assess the heritability and potential for genetic improvement of sessile oak based on a progeny test of 20 families. Heights and root collar diameters of 3-year-old seedlings originated from two populations, Goražde and Konjic Bradina, were measured. Each population included progeny from 10 mother trees, sown in three replications. Statistical analyses included normality tests, descriptive statistics, and the Kruskal-Wallis test (SPSS 20.0). Broad-sense heritability was assessed using analysis of variance. Selection differentials were calculated for the five mother trees whose offspring had the highest average growth traits. Genetic gain was estimated using offspring from both the top five and the single best-performing tree. Offspring from the Konjic Bradina population had higher average heights and root collar diameter than those from Goražde. However, Goražde showed higher heritability values: broad-sense heritability for height was 0.86 (vs. 0.45 in Konjic Bradina), and root collar diameter, 0.78 (vs. 0.32). The potential genetic gain in height for Goražde was 6.4% using the top five trees and 10.7% using the best tree; for root collar diameter, gains were 5.2% and 9.6%, respectively. In Konjic Bradina, gains for height were 1.8% and 3.3%, and for root collar diameter, 1.2% and 2.8%. The results indicated potential for genetic improvement in both populations. However, as the seedlings were only three years old, continued evaluation through long-term progeny testing is recommended.

Keywords: sessile oak; heritability; phenotypic traits; genetic improvement

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Section: Genetics of Natural Resources
Poster presentation

THE NEW ROLE OF FOREST WOODY FRUITS IN EUROPEAN FORESTS

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Crop wild relatives (CWR) are wild plant taxa closely related to a crop. They represent an important source of genetic diversity for the improvement of agronomic traits and they are still available as tree species within the European forests. In the context of the One Health Initiative, temperate fruit trees are essential for human nutrition and health, yet CWR resources have hitherto been underused. Moreover, fruit tree long lifespan and a current production dominated by a few cultivars make them particularly vulnerable to the effects of global changes. To address this challenge, the FRUITDIV project will monitor, characterize, use, and conserve the diversity of emblematic fruit tree CWR, with a particular emphasis on Malus, Pyrus and Prunus, by linking horticulturists, forestry officers and citizens. To better characterize the genetic and phenotypic diversity of CWR fruit trees and identify favourable traits for future introgression into cultivars, FRUITDIV will use a combination of floristic, ethnogeography and population genomics on genebanks and historical European hotspots of diversity. We will then develop new multiomics-based breeding strategies that combine marker assisted introgression for traits of interest (e.g. resilience, resistance to pests and diseases, fruit quality) with pangenomic prediction and a reduction of CWR-associated genetic load. In addition to breeding programs, FRUITDIV will also work with networks of farmers and associations to help characterize CWR progeny in various pedo-climatic conditions in Europe. An European-wide online platform that provides genotyping and phenotyping data for free will be implemented to promote the use of CWR genitors by breeders and farmers and help disseminate plant material of interest for various usages and cultivation systems. Overall, the FRUITDIV multi-actor approach involving geneticists, forestry officers, germplasm curators, farmers and citizens, will foster the in- and ex-situ conservation of Fruit tree CWR and promote sustainable agricultural and forestry practices across Europe. FRUITDIV is by essence inter-disciplinary, gathering experts in horticulture, forestry, ecology, genetics and population genetics, genomics, bioinformatics, mathematics and social sciences. It is made of 27 partners from 10 EU countries and 4 non-EU countries.

Keywords: genetic diversity; fruit tree; european hotspots; breeding programs

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Section: Genetics of Natural Resources
Poster presentation

ADVANCING CHAROPHYCEAE RESEARCH IN BOSNIA AND HERZEGOVINA: A CALL FOR EXPANDED BARCODING EFFORTS

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Genetic research on macroalgae has significantly progressed over the past two decades, yet it remains less developed compared to studies on microalgae, vascular plants, and terrestrial crops. Among macroalgal groups, representatives from the class Charophyceae have received relatively less research attention than red and brown algae. DNA barcoding has contributed to the understanding of Charophycean algae, particularly in species identification, cryptic diversity, taxonomy, and phylogeny. The need for further analysis is underscored by the BOLD database, which currently contains 549 published records covering 99 taxa. Of these, 333 entries represent 42 taxa from the genus *Chara*, while 152 entries cover 46 taxa of *Nitella*. It is important to note that research on the diversity, taxonomy, and ecology of algae from the class Charophyceae in B&H remains scarce, with most records dating back to the early 20th century. Based on available published data, 15 taxa including 9 from the genus *Chara* and 6 from *Nitella* have been recorded in the country. However, no DNA barcoding analyses have been conducted on samples from the Balkan Peninsula to date. The BOLD database includes 115 published records for these species, with the majority originating from Norway (26.47%), the United Kingdom (24.50%), and Germany (11.76%). Notably, two species *Chara gymnophylla* (A.Braun) A.Braun and *Nitella syncarpa* (Thuilleier) Chevallier lack published genetic data, while *Chara hispida* Linnaeus holds the highest number of entries (20). The most commonly used molecular markers in Charophyceae barcoding are *rbcL* (56.83%), *matK* (23.50%), and *ITS* (19.67%). Despite progress, significant challenges remain, including limited reference sequences, cryptic species, and morphological plasticity. Expanding DNA barcoding efforts and integrating genomic tools, environmental DNA (eDNA) studies, and next-generation sequencing (NGS) technologies will improve species identification and phylogenetic resolution. A multi-gene approach, in combination with traditional morphological analysis and public database contributions, is essential for advancing Charophyceae research

Keywords: biodiversity; DNA barcoding; BOLD database; macroalgae; conservation biology

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Section: Genetics of Natural Resources
Poster presentation

DEVELOPMENT OF DROPLET DIGITAL PCR ASSAYS FOR ENVIRONMENTAL DNA DETECTION OF CRITICALLY ENDANGERED STURGEON SPECIES

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Aquatic organisms release DNA traces into the environment, enabling the molecular identification of specific species or entire communities from a single water sample. In recent years, environmental DNA (eDNA) methods have significantly enhanced freshwater biodiversity assessments and complemented traditional monitoring approaches. Environmental DNA target screening using species-specific primers and diagnostic endpoint droplet digital PCR (ddPCR) has proven to be highly specific and sensitive, demonstrating its value in aquatic biomonitoring for detecting rare and endangered species that are difficult to monitor with conventional methods. In this study, we developed the first ddPCR assays targeting two native and critically endangered Danube sturgeon species — Stellate sturgeon (*Acipenser stellatus*) and Russian sturgeon (*Acipenser gueldenstaedtii*). Currently, five out of six native Danube sturgeons species are listed as critically endangered on the IUCN Red list, with their natural habitat severely impacted by the construction of dams, pollution and overfishing. However, a defined conservation and management plan for these species still does not exist. The main reason for this is the lack of appropriate methodology to accurately assess the status of its remaining populations in the Danube, which is essential for the implementation of legal and protective measures. The established ddPCR assays provide a ready-to-use tool for the targeted and sensitive detection of presence, as well as the estimation of population abundance of *Acipenser stellatus* and *Acipenser gueldenstaedtii* in the Danube river, supporting ongoing and future regular monitoring and conservation efforts.

Keywords: eDNA; ddPCR; Danube; sturgeons

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Section: Genetics of Natural Resources
Poster presentation

CITIZEN SCIENCE IN ACTION: EARLY INSIGHTS FROM THE TICK SPOTTING PROJECT

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Citizen science is a flexible concept that allows the public to take an active role in research projects. From data collection to the dissemination of findings, citizen scientists can engage in various stages of the scientific process. The aim of the Tick Spotting project, financed by the Ministry of Civil Affairs of Bosnia and Herzegovina, is to map hotspots for the development of vector-borne diseases in Bosnia and Herzegovina. This is done by applying the DAMA protocol (Document, Assess, Monitor, Act) with citizen science as a core methodological approach. To explore public interest in participating in this research, an online survey was conducted. The results showed that young people (aged 18–25) were the most interested in participating in this type of research. Although most respondents had not heard of the term citizen science, they reported having seen ticks and were aware of the time of year when ticks are most active. While most participants knew the correct method for tick removal, only a minority were aware of the pathogens that ticks can transmit. To promote project activities, explain how citizen scientists can contribute, and educate the audience about the importance of timely and proper tick removal, an online workshop was held, and a dedicated web page with relevant information was created. This approach increased access to field research - over the course of two months, approximately 50 ticks were collected from various regions, allowing for broader geographic coverage within the same time frame. Collected ticks will be analyzed using morphological and/or molecular methods. Simultaneously, a wider audience was reached, and important information was shared as part of a broader strategy to prevent infectious diseases caused by tick-borne pathogens.

Keywords: vector-borne diseases; DAMA protocol; tick-borne pathogens

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Section: Genetics of Natural Resources
Poster presentation

THE IMPACT OF SAMPLE DRYING ON DNA EXTRACTION AND MICROSATELLITE AMPLIFICATION IN NORWAY SPRUCE (*PICEA ABIES*)

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Efficient DNA extraction is a crucial step for the successful molecular characterization of plant species. However, this process is often hindered in plants by the presence of secondary metabolites, polysaccharides, and proteins that co-precipitate with DNA and act as potent inhibitors of enzymatic reactions such as PCR, thereby reducing both DNA yield and quality. This issue is particularly pronounced in coniferous species such as Norway spruce (*Picea abies*), whose needles contain high levels of phenolic compounds, polysaccharides, tannins, and lignin. These compounds can bind to nucleic acids and contaminate DNA samples, impeding downstream applications such as PCR amplification. To evaluate the impact of tissue preservation methods on DNA quality and amplification success, freshly collected Norway spruce needles from protected areas in Kanton Sarajevo were divided into two groups upon arrival at the laboratory. One group was immediately frozen at -80 °C, while the other was air-dried at 37 °C for 10 days. Approximately 20 mg of each sample was ground and homogenized, and DNA was extracted using the CTAB Soltis protocol. Fluorescently labeled nuclear microsatellite markers WS0022.B15 and WS0092.M15 were amplified via PCR. Fragment analysis was conducted on an ABI 3500 Series Genetic Analyzer, and allele sizes were determined using GeneMapper software. PCR amplification was successful only for DNA extracted from frozen samples, while no amplification was observed in any of the air-dried specimens. The most likely explanation for this outcome is that the drying treatment caused DNA degradation, reducing the amount and integrity of amplifiable DNA in the tissue. These findings underscore the importance of sample preservation strategies in molecular studies, especially when working with coniferous species and sensitive genetic markers. Selecting appropriate tissue handling methods prior to DNA extraction is essential for ensuring the reliability of downstream applications such as genotyping, biodiversity assessments, and conservation genetics.

Keywords: sample preservation; DNA quality; genotyping

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Section: Bioengineering, Biotechnology and Bioinformatics
Poster presentation

GENETIC STRUCTURE AND CONSERVATION MEASURES FOR THE BALKAN SESSILE OAK (*QUERCUS DALECHAMPII* TEN.) IN THE DJERDAP NATIONAL PARK

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The Balkan sessile oak (*Quercus dalechampii* Ten.) is a valuable native forest tree species that plays an important ecological and genetic role within mixed oak forests in across parts of southern and southeastern Europe. Despite its significance, the genetic resources of this taxon have not been sufficiently studied, which represents a major challenge for the development of effective conservation and sustainable forest management strategies. The aim of this research was to assess the current state of the genetic diversity and structure of Balkan sessile oak populations within the Djerdap National Park and to propose practical measures for their conservation. Molecular characterization of 27 genotypes was conducted using seven highly informative SSR (Simple Sequence Repeat) markers. DNA was extracted from fresh leaf tissue and analyzed following standardized PCR protocols. The results revealed a high degree of polymorphism across all loci (mean PIC = 0.899) and an overall expected heterozygosity (He) of 0.907, indicating a substantial level of genetic variability within the studied population. The presence of significant inbreeding coefficients (F = 0.810) and deviation from Hardy-Weinberg equilibrium suggest complex population dynamics and gene flow patterns. Cluster analysis confirmed moderate genetic differentiation and highlighted the importance of preserving intra-population variability. These findings emphasize the necessity of integrating both In situ and Ex situ conservation measures. Establishing conservation units, preserving natural regeneration stands, and developing seed banks are recommended to maintain the adaptive potential of these forest genetic resources. This will ensure the long-term sustainability and resilience of Balkan sessile oak forests in the face of ongoing environmental and climatic challenges.

Keywords: forest genetic resources; genetic diversity; conservation strategies; inbreeding; gene flow

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Section: Bioengineering, Biotechnology and Bioinformatics
Poster presentation

INTEGRATING MACHINE AND NOVEL LEARNING SIMULATIONS TO PREDICT GENE FLOW AND ITS INFLUENCE ON HUMAN POPULATION DEMOGRAPHIC STRUCTURES

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This study integrates machine and novel learning simulations to predict gene flow dynamics and their influence on human demographic structures across historical periods. Population sizes for three chronopopulations, prehistoric (75,000), medieval (250,000), and contemporary (3,500,000) were estimated using historical records and expert input. Genetic drift was modeled across 3,000 years (150 generations) using two simulation methods: drift function and a Monte Carlo adaptation of Kimura's model. A dataset of 29,795 SNPs was used, with 10% randomly sampled due to computational limitations. Simulations revealed that after 32 generations, 62% of SNPs exhibited allele frequency changes, while most low-frequency SNPs from prehistoric populations were lost over time. These results contrast with their persistence in contemporary populations, indicating that modeled demographic events alone do not fully account for observed genetic variation. Regression analyses demonstrated high predictive accuracy (R^2 = 0.891–0.999), confirming the validity of both simulation approaches. Monte Carlo simulations showed strong correlations with observed data. Genomic analyses confirmed that prehistoric, medieval, and modern populations largely share a common gene pool. However, the most significant demographic impacts on allele frequencies occurred within the last 15 generations. A deep learning method has also been applied in predicting population dynamics based on genomic variations, whose results indirectly confirm the results of other mentioned simulation models. The findings suggest that unrecorded migration events, population admixture, and mutation rates must be considered alongside known demographic transitions to fully explain genetic shifts. Although mtDNA and Y-chromosome haplogroup data were not included, their future analysis could provide further insight into maternal and paternal lineages.

Keywords: learning simulations; AI, prediction; gene flow; demographic structure

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Section: Bioengineering, Biotechnology and Bioinformatics
Poster presentation

SOILS ADJACENT TO HIGH-TRAFFIC AREA NEAR URBAN TRAMLINES ACCUMULATE HEAVY METALS AND INFLUENCE BACTERIAL COMMUNITIES

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Urban tramlines in city centres with heavy vehicle traffic can contribute to heavy metal contamination in soils, exerting selective pressure on microbial communities. We collected a sample from the highly urban area of Pofalići, Sarajevo with the intent to examine soil metal load and isolate heavy metal–resistant bacteria with siderophore-producing potential. About 100 g of soil was collected from the A-horizon in an undisturbed plot. Coarse and fine particles were combined and processed as a single sample. After extraction of heavy metals and macroelements, flame atomic absorption spectroscopy (FAAS) was performed using an AA-7000 spectrophotometer. Soil bacteria were isolated from soil sample using sterile 0.85% NaCl solution. For initial screening, serial dilutions (100–200 µl) were inoculated onto yeast mannitol agar plates and incubated at 22–25°C for 24–48 h. Morphologically distinct, single cell colonies were transferred to tryptone yeast (TY) agar to establish pure cultures. A total of 25 isolates were further tested for Cu, Ni, and Co resistance and for siderophore production. Siderophore producing activity was quantified using Fe-free succinate medium and CAS reagent in a 96-well microtiter plate with absorbance reading at 630 nm. Soil analysis revealed a pH of 7.51 with Ni and Pb above and Cu nearing the acceptable treashold. All 25 isolates exhibited resistance to 100 mg/L Cu, while 7 of 25 grew at 100 mg/L Co. No isolates were able to grow in the presence of 200 mg/L Ni or Cu. Siderophore production was generally low, with a few exceptions, ranging from 10–20%, suggesting that it is not a primary bacterial strategy for coping with heavy metals. Overall, the results indicate low levels of bacterial resistance and emphasize the need for further research on urban ecosystems and the effects of long-term heavy metal accumulation in soils.

Keywords: soil bacteria; heavy metals; siderophores; tram railroad; urban contamination

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Section: Bioengineering, Biotechnology and Bioinformatics
Poster presentation

MULTI-OMICS AND DOCKING STRATEGIES REVEAL CANDIDATE PATHWAYS DRIVING VASCULAR INVASION IN RECTAL CARCINOMA

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Rectal carcinoma (RC) accounts for nearly one-third of colorectal cancers and represents a clinically distinct entity. Vascular invasion (VI) is an established adverse prognostic factor, strongly associated with recurrence, metastasis, and reduced survival. However, molecular drivers underlying VI remain insufficiently characterized. In this study, we interrogated transcriptomic and epigenomic data from The Cancer Genome Atlas (TCGA) rectal carcinoma cohort (n=78 with defined VI status) to explore potential molecular modulators of VI. Among 41 pre-selected candidate genes implicated in extracellular matrix (ECM) remodeling, angiogenesis, and epithelial-mesenchymal transition, only ADAMTS8 expression showed a significant association with VI. Protein–protein interaction analysis revealed no direct clustering of ADAMTS8 with ECM remodeling pathways, suggesting a distinct regulatory role. To identify potential co-regulators, we integrated DepMap dependency analyses, highlighting seven ADAMTS8-co-dependent genes (DNAL4, EVI2B, PPP1R35, PTGR3, RPL21, SOX4, ZNF3). In the TCGA cohort, decreased DNAL4 and PTGR3 and increased RPL21 expression were significantly linked with VI. Molecular docking of 9,684 compounds, derived from toxicogenomic and PubChem similarity screening, identified four high-affinity candidates—cyanoginosin LR, doxorubicin, benzo[a]pyrene, and dibenzo(a,e)pyrene—that exhibited stable interactions across all eight protein targets. Our findings suggest that aberrant ADAMTS8 expression, potentially modulated by epigenetic silencing, contributes to VI in rectal carcinoma. Moreover, co-dependent gene networks and compound docking analyses reveal candidate molecules with pan-target binding properties, warranting further experimental validation. Collectively, this work provides mechanistic insights into the molecular basis of VI in rectal carcinoma and highlights ADAMTS8 and its interactome as promising avenues for prognostic stratification and therapeutic exploration.

Keywords: rectal carcinoma; vascular invasion; ADAMTS8; molecular docking

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

MICROPLASTICS AS A VECTOR FOR TRIBUTYLTIN INTAKE IN ZEBRAFISH: EFFECTS ON GENOTOXICITY

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Tributyltin (TBT) is a widespread contaminant in both marine and freshwater ecosystems, mainly due to its use in boat antifouling paints. TBT is highly toxic and has both endocrine disrupting and genotoxic effects. Due to its hydrophobic nature, like many other environmental pollutants, it has a strong affinity to adhere to microplastics (MP). MP particles are widely distributed in the environment and have numerous harmful effects on organisms, including direct and indirect genotoxic effects. Although the genotoxic effects of both pollutants are well described, their combined effects have only been studied to a limited extent. The aim of this study was to investigate whether simultaneous exposure to TBT and MP affects genotoxicity in zebrafish (*Danio rerio*). The experimental setup consisted of twelve aquaria divided into four groups with three aquaria per group. Each aquarium contained fifteen fish. The fish were exposed to four different food treatments: (CTRL) a control diet without additives; (MP) microplastic-enriched diet; (TBT) TBT-enriched diet alone; and (TBT+MP) diet with TBT-adsorbed microplastics. Alkaline single cell gel electrophoresis (comet assay) was performed to evaluate the genotoxic effects. Tail intensity was used as the primary parameter to compare the extent of DNA damage among the four experimental groups. The results showed a statistically significant difference in the MP group compared to the CTRL group and in the TBT group compared to the CTRL group. In contrast, no statistically significant difference was found between the TBT+MP group and the CTRL group. In addition, the statistical analysis revealed a significant difference between the TBT and TBT+MP groups, while no significant difference was found between the MP and TBT+MP groups. These results suggest that when fish are exposed to a diet containing TBT-adsorbed microplastics, the genotoxic effects of TBT are attenuated while the effects of microplastics predominate.

Keywords: tributyltin (TBT); microplastics (MP); genotoxicity; zebrafish; comet assay

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

GENOTOXICITY AND ANTIGENOTOXICITY OF DEEP EUTECTIC SOLVENT BASED ON CHOLINE CHLORIDE AND ASCORBIC ACID IN HUMAN PERIPHERAL BLOOD MONONUCLEAR CELLS

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Natural deep eutectic solvents (NADES) represent a novel class of green solvents with promising biomedical applications, due to their good biocompatibility and biodegradability. They are formed by the interaction of hydrogen bond donors (HBDs) and acceptors (HBAs), usually choline chloride, at a specific molar ratio, to obtain high thermal and chemical stability. Choline chloride:ascorbic acid (ChCl:AA) NADES have been demonstrated to possess strong radical-scavenging activity, while maintaining a low cytotoxic profile; however, its effects on DNA damage have not been reported. In this study, we aimed to investigate the ChCl:AA effects (concentration range 50-500 μg/mL) on micronuclei incidence (MN) in human peripheral blood mononuclear cells (PBMCs) upon 24-hour treatment by employing cytokinesis-block micronucleus assay. Genoprotective potential of non-genotoxic ChCl:AA concentrations against hydroxyurea (HU, 100 μM), a chemotherapeutic agent that can induce genotoxicity mediated by oxidative stress, was also evaluated. ChCl:AA was synthesized by combining ChCl and AA in a 2:1 molar ratio, and physico-chemical characterization confirmed NADES formation. The results showed that ChCl:AA, at all tested concentrations, slightly, albeit insignificantly, reduced MN frequency without affecting the proliferation index of PBMCs. In contrast, HU treatment decreased proliferation index of PBMCs and increased MN frequency by approximately 88%, while 24-hour pretreatment with ChCl:AA at all tested concentrations led to a statistically significant reduction in MN frequency, without effects on the proliferation index. The lowest MN frequency was detected upon 300 μg/mL ChCl:AA pretreatment, decreasing it below the levels of untreated control. The obtained results indicate that ChCl:AA doesn't induce genotoxic effects up to a concentration of 500 μg/mL. On the contrary, the tested concentrations exhibit genoprotective effects against HU-induced DNA damage, likely mediated by their high antioxidative capacity. These findings provide insight into the potential therapeutic efficacy and safety of ChCl:AA.

Acknowledgments: This work was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Grant no. 451-03-136/2025-03/200017 and 451-03-3627/2025-03/3456).

Keywords: genotoxicity; hydroxyurea; natural deep eutectic solvent; DNA damage; peripheral blood mononuclear cells

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

DOSE-DEPENDENT CYTOTOXICITY OF CERIUM OXIDE NANOPARTICLES IN MG-63 OSTEOSARCOMA CELLS AND THE MODULATORY ROLE OF TWEEN-80

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Osteosarcoma, the most common malignant bone tumor in children and adolescents, often exhibits resistance to conventional therapies. Cerium oxide nanoparticles (CeO_2 NPs) have shown potential anticancer effects, including oxidative stress modulation and inhibition of tumor cell proliferation, making them a promising candidate for osteosarcoma treatment. The aim of this study was to investigate the cytotoxic effects of CeO_2 NPs dissolved with and without use of a surfactant, on MG-63 osteosarcoma cells. CeO_2 NPs were synthesized using a precipitation method with concentrated ammonia. The powdered nanoparticles were dissolved in deionized water with or without 2% Tween-80, then applied to MG-63 cells in culture medium at final concentrations of 10, 25, 50, and 100 µg/mL. Cytotoxic activity was assessed using the MTT assay. CeO_2 NPs exhibited a significant, dose-dependent cytotoxic effect, with Tween-80 enhancing this effect except at the lowest concentration, where it was slightly reduced. These findings indicate that CeO_2 NPs have notable cytotoxic potential against MG-63 osteosarcoma cells, and that Tween-80 can modulate their activity. Given that Tween-80 showed some impact, although not statistically significant, its use should be studied in more detail.

Keywords: nanoparticles; surfactant; cytotoxicity; osteosarcoma

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

CYTOTOXIC POTENTIAL OF PM_{10} PARTICULATE MATTER ON HUMAN BLADDER CARCINOMA CELLS IN VITRO: A CASE STUDY FROM SARAJEVO

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Air pollution is one of the most significant public health concerns of the modern era, directly associated with increased morbidity and mortality rates. It is particularly prominent in Bosnia and Herzegovina, where, in the capital city, Sarajevo, levels of PM_{10} frequently exceed recommended limits and rank among the highest in the world. This study analyzed the cytotoxic effects of the PM_{10} fraction of particulate matter on the human bladder carcinoma cell line 5637 (ATCC HTB-9). Samples were collected using a medium volume sampler (MVS6) at an urban location in Sarajevo and processed by ultrasonic extraction, after which the samples were used to treat the cell culture. Cytotoxicity was assessed using a colorimetric assay based on Alamar Blue reduction. Separate cell cultures were treated with the same volume of different concentrations of PM_{10} particles 18.61 μg/m³, 77.08 μg/m³, 102.29 μg/m³, 14.07 μg/m³. A cell culture treated with the same volume of destilled water was used as a negative control. Results showed inhibition of cell proliferation after exposure to PM_{10} samples. Although no significant differences were found between treatment groups, a positive correlation was observed between PM_{10} concentration and inhibition of cell proliferation, indicating a cytotoxic potential that should not be overlooked. These findings emphasize the need for further research, including chemical composition analysis of PM_{10} samples and the use of additional assays, and cell lines to provide a comprehensive and accurate assessment of their cytotoxicity. Continuous monitoring of the air pollution and the effects of PM_{10} on cells and genetic material is essential in order to protect the health of residents, particularly in urban environments and among vulnerable populations.

Keywords: air pollution; PM_{10} particulate matter; cytotoxicity

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

YELLOW GENTIAN INFUSION MITIGATES ɣ-RAYS INDUCED GENOTOXIC EFFECTS BY ALTERING LEVELS OF DNA REPAIR ENZYMES

Kostić Mila, Filipović Tričković Jelena, Radošević Ksenija, Janić Marijana, Kolić Ivana, Jovanović Ivan, Valenta Šobot Ana

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Ionizing radiation from natural and artificial sources causes DNA damage, directly and indirectly, inducing strand breaks and generating reactive oxygen species, leading to oxidative stress and biomolecular alterations. Yellow gentian (*Gentiana lutea)* root infusion has shown genoprotective potential by activating antioxidative defense and promoting DNA repair of radiation-induced cellular damage. This study aimed to elucidate the pre-treatment effect of 0.25, 0.5, 1, and 2 mg/mL of yellow gentian root infusion on genomic damage in peripheral blood mononuclear cells exposed to 0.5 and 2 Gy of gamma radiation (source ^{60}Co). Micronucleus frequency, proliferation index, and DNA fragmentation were assessed, along with expression of DNA repair genes 8-oxoguanine glycosylase-1 (OGG1), Poly(ADP-ribose) polymerase1 (PARP1), and X-ray repair cross-complementing-1 (XRCC1), via real-time PCR. Pretreatment with 0.25 and 0.5 mg/mL infusion significantly reduced micronucleus formation and DNA fragmentation in irradiated cells at 2 Gy, indicating protection against radiation-induced genetic damage. The results showed a decrease in proliferation index at 0.5 Gy, suggesting that treatments inhibited cell proliferation after exposure to the lower radiation doses. XRCC1 expression was significantly upregulated with 2 Gy at all treatment concentrations, indicating enhanced base excision repair activity. PARP expression increased significantly at all treatments' concentrations following 0.5 Gy irradiation, and at 2 Gy, induction occurred only at 0.5 and 1 mg/mL, reflecting dose-dependent modulation of PARP-mediated repair. OGG1 expression remained unchanged under all tested conditions. The results demonstrate that yellow gentian root infusion activates the base excision DNA repair pathway and may serve as a promising agent for mitigating radiation-induced damage in developing effective radiation protection strategies.

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Keywords: *Gentiana lutea***;** radioprotection; ionizing radiation; DNA fragmentation; peripheral blood mononuclear cells

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

GENOTOXICITY ASSESSMENT OF LASER-SYNTHESIZED SILVER NANOPARTICLES WITH *SALVIA OFFICINALIS* AQUEOUS EXTRACT

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In recent years, silver nanoparticles (AgNPs) have gained considerable attention due to their potent antimicrobial, anti-inflammatory, and wound healing properties. However, despite their therapeutic potential, the biosafety profile of AgNPs remains a concern, as these nanoparticles can penetrate cellular membranes and potentially induce cytotoxic or genotoxic effects. Laser "green" synthesis is based on a process of laser ablation of metal target immersed in liquid (PLAL), and represents one of the cleanest synthesis methods for AgNPs, as it eliminates the need for toxic reducing agents. The use of natural compounds could enhance synthesis by enabling nanoparticle stabilization and mitigating their toxicity. Among them, *Salvia officinalis* (sage) could be of specific importance, as it possesses anti-inflammatory, radical-scavenging, and antigenotoxic properties. In this study, we evaluated the genotoxic potential of laser-synthesized AgNPs prepared in sage aqueous leaf extract (Sage-AgNPs) versus those synthesized via pulsed laser ablation in deionized water (Dw-AgNPs). AgNPs synthesis was performed by picosecond laser system Nd:YAG EKSPLA SL 212/SH/FH, and their physico-chemical characterization was performed. The cytokinesis-block micronucleus assay was used to assess micronuclei (MN) frequency and proliferation index (CBPI) in human peripheral blood mononuclear cells upon 24-hour treatment with both AgNPs, at the concentrations of 2.5, 5 and 10 μg/mL. The results showed that Dw-AgNPs induced concentration-dependent MN increase, statistically significant at the concentrations of 5 and 10 μg/mL, while simultaneously decreasing CBPI. In contrast, MN frequency after treatment with Sage-AgNPs was in the range of the untreated control for concentrations of 2.5 and 5 μg/mL, without affecting CBPI. The highest tested concentration led to a minor, albeit insignificant MN frequency increase and significantly reduced proliferation. These findings suggest that laser-synthesized AgNPs with sage aqueous extract reduce genotoxic effects, highlighting the potential of sage extract in PLAL synthesis as a safe alternative for AgNPs synthesis for biomedical applications.

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Keywords: genotoxicity; silver nanoparticles; *Salvia officinalis* aqueous extract; biosafety

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

IN VITRO INSIGHTS INTO THE CYTOTOXIC AND GENOTOXIC POTENTIAL OF COMMERCIAL NEEM POWDER

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Azadirachta indica A. Juss. (neem) has long been used in the traditional medicine of India and Africa for its diverse therapeutic properties, including antimicrobial, antioxidant, anti-inflammatory, anticancer, antidiabetic, and immunomodulatory effects. Key bioactive compounds, such as azadirachtin, nimbin, and quercetin, influence various biological processes. However, potential toxic effects, particularly at higher doses or with chronic exposure, remain insufficiently explored. This study aimed to evaluate the effects of commercially available neem (BIOfan) powder in final concentrations of 2.5 – 100 µg/ml diluted in medium, on the cell viability of human peripheral blood mononuclear cells (PBMCs) and genetic integrity in whole blood samples. Cytotoxicity was evaluated using the MTT assay 24 hours after treatment, while genotoxicity was assessed 3 hours post-treatment using the alkaline comet assay. The MTT assay results showed no significant inhibition of cell growth at any of the tested concentrations compared to the positive control (5-FU 200 µg/ml). In contrast, the comet assay parameter % tail DNA (tail intensity, TI) revealed significant DNA damage at concentrations of 80 µg/ml and 100 µg/ml ($p < 0.001$). Similar results were obtained for the tail moment (TM), whereas for the tail length (TL), concentration of 80 µg/ml exhibited a statistically significant the highest TL value. In conclusion, while the PBMCs cells remained metabolically active and viable after treatment, higher doses caused DNA damage in whole blood samples, suggesting a possible genotoxic risk even in the absence of cytotoxicity.

Keywords: *Azadirachta indica;* MTT assay; alkaline comet assay; lymphocytes

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

GENOTOXIC PROFILE OF GREEN GRAPHENE QUANTUM DOTS IN A NON-INVASIVE HUMAN CELL MODEL

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Graphene quantum dots (GQDs) are a novel class of carbon-based nanomaterials with unique properties arising from their nanoscale size, tunable bandgap, and quantum confinement effects. Typically smaller than 10 nm and composed of a few atomic layers, GQDs exhibit excellent photoluminescence, water solubility, biocompatibility, and low toxicity. These features make them attractive for biomedical applications such as bioimaging, biosensing, drug delivery, and tumor therapy. Beyond medicine, GQDs are also applied in optoelectronics, energy storage, and environmental monitoring. Their versatile surface chemistry enables functionalization and the creation of nanocomposites with improved performance. With this combination of stability, safety, and multifunctionality, GQDs are regarded as promising materials for next-generation technologies in life sciences and engineering. The genotoxic potential of green fluorescing graphene quantum dots (G-GQDs) was investigated using the comet assay in human salivary leukocytes, a non-invasive and physiologically relevant model for evaluating DNA damage after oral exposure to nanomaterials. Salivary leukocytes were isolated from six healthy volunteers, pooled, and subsequently exposed to G-GQDs at concentrations of 2.5, 5, and 10 μg/mL for 3 hours. DNA strand breaks were evaluated by analyzing comet assay parameters, including tail length (TL), tail intensity (TI), and tail moment (TM). Measurements were performed using CometAssay IV image analysis software (Instem, Belgium), with a total of 200 cells scored per sample. The results for all three analyzed parameters revealed no statistically significant differences compared to the negative control, except for TM where a significant increase was observed at the highest tested concentration (10 μg/mL). In conclusion, G-GQDs can be considered relatively safe, as significant DNA damage was detected only at this highest dose. However, factors such as exposure duration and model-specific characteristics may affect the biological response, and should be taken into account in future safety evaluations.

Keywords: salivary leukocytes; genotoxicity; DNA damage; comet assay; nanomaterials

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

EFFECT OF HALOGENATED BOROXINE AND CERIUM OXIDE NANOPARTICLES ON OSTEOSARCOMA CELLS *IN VITRO*

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Effectiveness of available osteosarcoma chemotherapy is restricted due to side effects and the emergence of drug resistance. Combination therapies have been proven to be the most effective treatment approach. In this study, we aimed to examine efficacy of the combinatorial treatment of halogenated boroxine (HB) and dextran coated cerium oxide nanoparticles (Dex-CeNPS) on MG-63 osteosarcoma cell line. The IC_{50} values obtained from single-drug cell viability/cytotoxicity assays were used to design subsequent drug combination experiments. Following co-treatment ratios were defined: 0.8, 0.6, 0.5, 0.4, 0.2-fold of HB IC_{50} with 0.2, 0.4, 0.5, 0.6, 0.8-fold of nanoceria IC_{50} respectively. Additionally, in the same experiment, individual agents at IC_{50} concentrations were also tested. Cytotoxicity was measured using WST-1 assay and was evaluated 24h and 72h after treatment. Co-treatment with HB and Dex-CeNPS significantly reduced MG-63 cell viability at both 24 and 72 hours. At 24h, combinations of 80% HB + 20% Dex-CeNPS and 60% HB + 40% Dex-CeNPS showed weaker effects than HB alone and did not reach statistical significance. Conversely, the 20% HB + 80% Dex-CeNPS combination significantly decreased viability, indicating a potentiated effect of Dex-CeNPS. Cytotoxicity was generally more pronounced at 72 hours, with all combinations causing significant inhibition of cell viability. These results demonstrate that combined treatment with HB and Dex-CeNPs exerts enhanced cytotoxic effects on MG-63 osteosarcoma cells over time, suggesting potential for improved therapeutic strategies. Further studies are warranted to optimize dosing ratios and explore underlying mechanisms.

Keywords: halogenated boroxine; nanoparticles; cerium oxide; osteosarcoma

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Section: Biomonitoring and Genetic Toxicology
Poster presentation

ASSESSMENT OF DNA DAMAGE INDUCED BY ETHANOLIC EXTRACTS OF *JUNIPERUS* SPECIES

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Species of the genus *Juniperus* are widely recognized for their rich chemical composition and medicinal potential, making them a frequent subject of phytochemical, pharmacological, and biological studies. Traditionally, they have been applied as diuretics, antiseptics, and remedies for infections, fever, and various inflammatory conditions, with *Juniperus communis* L. and *Juniperus oxycedrus* L. being particularly significant. Their therapeutic value is linked to secondary metabolites such as essential oils, flavonoids, terpenes, and polyphenols, which exhibit antioxidant, antimicrobial, antiviral, and antiproliferative activities. These properties highlight the genus *Juniperus* as an important natural source for traditional practices and modern pharmaceutical applications. Despite their medicinal potential, data regarding the genotoxic effects and safety of *Juniperus* species remain incomplete. The aim of this study was to evaluate the genotoxic potential of galbuli from two species, *J. communis* and *J. oxycedrus*. A total of four samples of ripe galbuli were collected from different locations in Bosnia and Herzegovina (Konjic, Trebević, Fortica) and Montenegro (Kotor). Genotoxicity was assessed using the alkaline comet assay on whole blood samples treated with ethanolic extracts of the galbuli. Results showed that extracts of *J. oxycedrus* induced significantly higher DNA damage compared to *J. communis*, with increased values of tail length (TL), tail intensity (TI), and tail moment (TM). Within *J. communis*, extracts from Trebević caused stronger DNA damage than those from Konjic, while extracts of *J. oxycedrus* from both Kotor and Fortica showed consistently elevated genotoxic effects. These findings indicate clear species- and locality-related differences in the genotoxic potential of *Juniperus* galbuli and provide new insights relevant to their safe medicinal or dietary use.

Keywords: *Juniperus communis; Juniperus oxycedrus;* galbuli; comet assay; genotoxicity

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Section: Forensic Genetics
Poster presentation

DNA PHENOTYPING OF SKELETAL REMAINS FROM MEDIEVAL BOSNIA

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Visualizing our ancestors provides a unique way to connect with the past. While facial reconstruction relies heavily on artistic interpretation, DNA phenotyping offers objective insights into genetic determinants of physical appearance, such as hair, skin, and eye color. In this study, DNA was extracted from ten skeletal remains recovered from three medieval necropolises in Bosnia and Herzegovina, as well as from five contemporary volunteers who served as controls. Phenotypic prediction was performed by analyzing 40 SNP loci associated with pigmentation traits using the validated HIrisPlex-S system (Illumina DesignStudio, Illumina Inc.). Results were expressed as statistical prediction values. For the volunteers, phenotypic traits were accurately determined, strengthening the reliability of the results obtained from ancient samples. Among the skeletal remains, four individuals were predicted to have blue eyes and six to have brown eyes. Hair color predictions indicated five individuals with brown hair, two with dark brown, and three with light brown hair. Skin color analysis revealed that eight individuals had intermediate pigmentation, while two exhibited pale skin. This represents the first study investigating phenotypic characteristics of medieval individuals from Bosnia and Herzegovina, contributing valuable insight into the appearance of its past populations.

Keywords: DNA phenotyping; Medieval Bosnia; skeletal remains; HIrisPlex-S; pigmentation traits

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Section: Forensic Genetics
Poster presentation

FINDINGS ON DNA METHYLATION PROFILES IN A HEALTHY COHORT: PRELIMINARY RESULTS FROM AN ONGOING STUDY

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DNA-based age prediction methods has gained increasing prominence within human aging and health sciences. Reliable aging biomarkers, such as telomere length and epigenetic modifications, have received significant research attention. DNA methylation, a crucial epigenetic modification, was initially understood for repressing gene expression but is now also recognized for its role in gene activation. This dual capacity is fundamental to vital biological processes, and its dysregulation is consistently linked to numerous diseases. In this preliminary study, we aimed to analyze relative DNA methylation levels in a cohort of 23 healthy individuals, focusing on optimizing our methodological approach. For comparative purposes, analyses were performed on both blood and buccal cell samples, with participants categorized by sex and age (under 35, over 35 years). To assess DNA methylation levels, DNA samples underwent bisulfite conversion and subsequent quantification via Real-Time PCR using ELOVL2 (converted DNA) and ALU (genomic DNA) primers. Subsequently, Shapiro-Wilk test indicated an abnormal data distribution, likely due to the small sample size. A Mann-Whitney U test revealed no statistically significant differences in DNA methylation levels within blood or buccal cell samples when examined against demographic factors. However, blood samples exhibited significantly higher average DNA methylation levels than buccal cell samples (10.5119 vs. 2.8809, $p < 0.05$). Spearman's Rank correlation showed no linear relationship between sample type and demographic factors. Given our limited cohort size, future research with a substantially larger sample is essential for stronger statistical power and deeper insights into correlations between demographics and DNA methylation patterns in healthy populations.

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Keywords: DNA methylation; aging biomarkers; epigenetics; bisulfite conversion

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