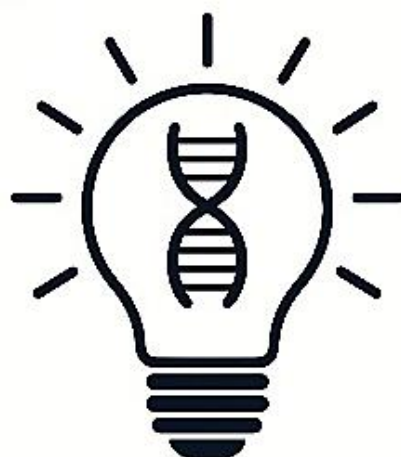

International Conference for PhD students in Quantitative and Natural Sciences “Bio Idea 6.0”

Book of Abstracts



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Abstracts

GENETIC MANIPULATION OF PHOSPHOLIPID BIOSYNTHESIS PATHWAYS ALTERS MEMBRANE COMPOSITION AND VIRULENCE IN *AGROBACTERIUM FABRUM*

Yevheniia Smirnova^{1*}, Kamil Żebracki¹, Iwona Komaniecka¹

¹*Department of Genetics and Microbiology, Faculty of Biology and Biotechnology, Institute of Biological Sciences, Maria Curie-Skłodowska University, 19 Akademicka Street, 20-033 Lublin, Poland*

**yevheniia.smirnova@mail.umcs.pl*

Agrobacterium fabrum is a Gram-negative, soil-borne phytopathogen capable of infecting numerous species of cultivated and ornamental plants. Infection relies on *vir* genes–regulated transfer of bacterial T-DNA from the tumor-inducing (Ti) plasmid into plant cells. Increasing evidence indicates that membrane integrity and phospholipid composition are critical for efficient host interaction and virulence.

To investigate the contribution of major phospholipid classes to bacterial invasiveness, we constructed a mutant defective in phosphatidylcholine (PC) biosynthesis ($\Delta pcsA$) and a double mutant impaired in phosphatidylethanolamine (PE) and PC biosynthesis ($\Delta pcsA/\Delta pssA$). The $\Delta pcsA$ mutant was generated using the allelic exchange vector pCM351. Upstream (784 bp) and downstream (720 bp) flanking regions were PCR-amplified from the wild-type genome, cloned sequentially into the vector, and introduced into the wild-type strain by biparental conjugation from *Escherichia coli* S17-1. Transconjugants resistant to gentamicin but sensitive to tetracycline and ampicillin were selected, and successful allelic replacement was confirmed by PCR. The double mutant was obtained by introducing the same construct into the $\Delta pssA$ background.

Thin-layer chromatography (TLC) of membrane lipids revealed pronounced alterations in lipid profiles in both mutants. In a carrot disc infection assay, the $\Delta pcsA$ mutant induced fewer and smaller tumors than the wild-type strain, whereas the $\Delta pcsA/\Delta pssA$ mutant induced almost no tumors.

Together, these results demonstrate that disrupting phospholipid biosynthesis significantly alters membrane lipid composition and reduces virulence in *A. fabrum*, highlighting the importance of membrane lipids in plant infection.

Keywords: *Agrobacterium fabrum*, membrane phospholipids, virulence, mutagenesis, thin-layer chromatography

THE EFFECT OF STRAIN INTERACTIONS ON THE STABILITY OF A DESIGNED BACTERIAL CONSORTIUM

Dawid Świstak¹, Willian Cleisson Lopes de Souza^{1,2}, Karolina-Jaros Tsoj^{1,3},

Jaco Vangronsveld^{1,3}, Małgorzata Wójcik¹, Jolanta Jaroszuk-Ścisiel⁴

¹ Department of Plant Physiology and Biophysics, Institute of Biological Sciences, Maria Curie-Skłodowska University, Akademicka 19, 20-033 Lublin, Poland

² Department of Agronomy, Faculty of Agricultural Sciences, Federal University of Jequitinhonha and Mucuri Valleys, Diamantina, MG 39100-000, Brazil

³ Centre for Environmental Sciences, Hasselt University, Agoralaan, building D, B-3590 Diepenbeek, Belgium

⁴ Department of Industrial and Environmental Microbiology, Institute of Biological Sciences, Maria Curie-Skłodowska University, Akademicka 19, 20-033 Lublin, Poland

*corresponding author's e-mail address: dawid.swistak@mail.umcs.pl

The increasing interest in the use of microorganisms in environmental biotechnology and sustainable agriculture highlights the need to develop stable and functionally effective bacterial consortia. Such consortia may serve as biostimulants, supporting plant growth and enhancing tolerance to heavy metals in crops cultivated on contaminated soils. The aim of this study was to evaluate the interactions among bacterial strains isolated from seeds of crambe (*Crambe abyssinica* L.) and to assess their suitability for constructing a stable consortium.

The strains were isolated from specially selected seeds obtained from Wageningen and were identified based on 16S rRNA gene sequence analysis. Inter-strain interactions were examined using inhibition zone assays on solid medium (PDA, Potato Dextrose Agar), allowing the assessment of mutual tolerance. In addition, liquid culture assays were performed to evaluate the effects of soil extract from heavy metal-contaminated soil and selected heavy metals (Cd, Zn, Pb) on bacterial growth. The results indicated predominantly neutral interactions among the tested strains, with no significant antagonistic effects observed.

A subset of strains exhibiting high mutual compatibility and stable growth in liquid media supplemented with heavy metals was identified as promising candidates for consortium development. These findings provide a basis for further optimization of consortium composition and its potential application in phytomanagement of metal-contaminated soils.

This work was supported by the European Union's Horizon Europe Programme under Grant Agreement No 101157430 (IASIS Project – www.iasis-soil.eu).

Keywords: bacterial consortium, co-culture, *Crambe abyssinica*, phytomanagement, seed endophytes

BIOLOGICAL PROPERTIES OF CALCIUM PHOSPHATES OBTAINED FROM WASTE MATERIAL

Katarzyna Gdula^{1,2}, Anna Michalicha³, Anna Belcarz-Romaniuk³ Aleksandra Szcześ¹,

¹ Department of Interfacial Phenomena, Institute of Chemical Sciences, Faculty of Chemistry, Maria Curie-Skłodowska University in Lublin, Sq. M. Curie-Skłodowska 3, 20-031 Lublin,

² Doctoral School of Quantitative and Natural Sciences, Maria Curie-Skłodowska University in Lublin, Weteranów 18, 20-040 Lublin

³ Chair and Department of Biochemistry and Biotechnology, Medical University of Lublin, Chodźki 1, 20-093 Lublin

e-mail: katarzyna.gdula@mail.umcs.pl

Calcium phosphates are widely used as biomaterials due to their bioactivity, biocompatibility, and chemical similarity to bones and teeth. They are commonly applied in bone regeneration, implantology, and dentistry. Various Ca²⁺ sources are used for their synthesis, including soluble calcium salts and calcium-rich waste materials (shells, eggshells, animal bones, and fish scales).

The aim of this study was to synthesize calcium phosphate materials using wastewater from the industrial soda ash production process (Solvay process) and to comprehensively evaluate the biological properties of the obtained materials.

The synthesis was performed using a synthetic industrial wastewater solution from Solvay process (1.1 M CaCl₂, 0.95 M NaCl) as an alternative calcium source, resulting in the formation of brushite (dicalcium phosphate dihydrate). During synthesis, partial substitution (5 mol%) with selected metal ions (Cu²⁺, Zn²⁺, Ag⁺, and Sr²⁺) was introduced to enhance biological activity.

The release of calcium and phosphate ions from undoped brushite was investigated in artificial saliva to assess its behavior under conditions relevant to the oral environment. Biological assays demonstrated that brushite substituted with Cu²⁺ and Ag⁺ ions exhibited strong antibacterial activity against *Staphylococcus aureus* and *Staphylococcus epidermidis*. In vitro cytocompatibility studies showed that materials doped with Zn²⁺, Ag⁺, and Sr²⁺ ions were biocompatible with osteoblast and fibroblast cell lines, whereas Cu²⁺-doped brushite exhibited cytotoxic effects. Hemocompatibility tests revealed hemolytic activity only for Ag⁺-doped powders, while all tested materials significantly shortened blood clot formation time, indicating their potential as antibacterial biomaterials, particularly for dental applications.

Keywords: brushite, biomaterials, Solvay process, ion doping, biological evaluation

METALLIC NANOPARTICLES-BASED COMPOSITES AS A NEW GENERATION ACTIVE SENSORS LAYERS FOR TRACE Cd(II) AND Pb(II) DETERMINATION

Damian Gorylewski*¹ and Katarzyna Tyszczyk-Rotko¹

¹Maria Curie-Skłodowska University, Institute of Chemical Sciences, Faculty of Chemistry, Department of Analytical Chemistry, M. Curie-Skłodowska Sq. 3, 20-031 Lublin, Poland.

**corresponding author's e-mail address: damian.gorylewski@mail.umcs.pl*

Due to intensive human activity, environmental pollution with heavy metal ions (HMIs) continues to increase. Exposure to HMIs such as Cd(II) and Pb(II) contributes to the development of numerous diseases and can even be fatal. Therefore, monitoring the content of these elements in the environment and food is crucial. While various analytical techniques for Cd(II) and Pb(II) determination have been documented, voltammetry has emerged as a prominent method for trace-level analysis, owing to its superior sensitivity and low-cost analysis. Numerous procedures for simultaneous determination of cadmium and lead ions at trace levels in environmental samples using Fe₃O₄, Bi₂O₃, Bi or Sb nanoparticles (NPs) are also described in the literature. Most of them allow for the detection of these elements at nanomolar (10⁻⁹ mol L⁻¹) levels, while maintaining a relatively short measurement time. Among metallic nanoparticles, magnetite gaining popularity due to its magnetic properties, ease of synthesis, simple modification, and low toxicity. Moreover, this material is susceptible to modification. The surface charge adjustment by coating with organic or inorganic stabilizing agents is one of the possible modifications of NPs. This makes it possible to introduce additional functional groups into the material, and the use of carbon material as a framework effectively improves the catalytic properties of NPS and stabilizes them. The developed procedures available in the literature are characterized by excellent analytical parameters and can be successfully used for environmental monitoring of Cd(II) and Pb(II).

Keywords: Metallic MNPs, Simultaneous Cd(II) and Pb(II) Determination, Voltammetry

THE INFLUENCE OF SURFACTANT TYPE ON THE STABILITY OF ETHOSMES

Jagoda Chudzińska-Skorupinska^{1*}, Agata Wawrzyńczak¹, Agnieszka Feliczak-Guzik¹

¹*Department of Applied Chemistry, Faculty of Chemistry, Adam Mickiewicz University in Poznań, Uniwersytetu Poznańskiego 8, 61-614 Poznań, Poland*

**corresponding author's e-mail address: jagoda.chudzinska@amu.edu.pl*

Ethosomes are spherical structures composed of phospholipids, ethanol, and water, optionally containing surfactants or glycols. They can be used as transdermal drug delivery systems. Their stability depends on zeta potential (ZP), hydrodynamic diameter (D_h), and polydispersity index (PDI).

The aim of the study was to evaluate the stability of ethosomes containing various surfactants: Tween 80, Tween 20, and the biosurfactant Mirasoft® SL L60. The samples were prepared using two methods: cold preparation with magnetic stirring (500 rpm) or high-speed homogenization (3 min; 15,000 rpm). The carriers consisted of 2.5 w/w % phospholipid, 30 w/w % ethyl alcohol, 10 w/w % ethylene glycol, and either 1.25 w/w % of a single surfactant or a 0.625 w/w % mixture of Tween 80 and Mirasoft® SL L60. Measurements of ZP, D_h , and PDI were taken immediately after preparation, after 24 hours, and after 14 days of refrigerated storage.

Among samples containing a single surfactant, Tween 80-based ethosomes showed the best results, exhibiting similar ZP (approx. -25 mV) and D_h (approx. 100 nm) values at all measurement points, while only the PDI values increased after 14 days of storage (approx. 0.400).

Samples containing a mixture of Tween 80 (60 w/w %) and Mirasoft® SL L60 (40 w/w %) showed the highest stability, allowing the total surfactant content to be reduced by half. The best result was observed for the sample prepared by high-speed homogenization ($D_h = 323.20 \text{ nm} \pm 1.32 \text{ nm}$, $ZP = -23.47 \text{ mV} \pm 0.40 \text{ mV}$, and $PDI = 0.269 \pm 0.008$).

Keywords: ethosomes, drug delivery, biosurfactant

Jagoda Chudzińska-Skorupinska is a scholarship holder of the Adam Mickiewicz University in Poznań Foundation for the 2025/2026 academic year.

FROM ECOLOGICAL STATUS OF WATER TO FORENSIC RESEARCH – THE REMARKABLE ROLES OF DIATOMS

Wanessa Lewandowicz¹, Magdalena Grabowska²

¹Doctoral School, University of Białystok, Ciołkowskiego 1K, 15-245 Białystok, Poland

²Department of Hydrobiology, University of Białystok, Ciołkowskiego 1J, 15-245 Białystok, Poland

**corresponding author's e-mail address: w.lewandowicz@uwb.edu.pl*

Microscopic, single-celled autotrophic organisms with extremely durable and ornamented siliceous frustules with beautiful ornamentation provide a brief description of diatoms. Such tiny organisms are not only an inspiration for artists, but most importantly, play important roles for environment and humans.

Diatoms are generally used as bioindicators. They are valuable indicators of water pollution and trophy. The assessment of the ecological status of waters is based on analysis of species characteristics, frustules morphology, and environmental DNA. Diatoms are also organisms frequently used in predicting anthropogenic changes. As autotrophic organisms, they participate in all services dependent on photosynthesis, which main result is production of oxygen and organic matter (their share is up to 40%). Diatomaceous earth (diatomite) is produced from diatom frustules. It has a wide range of applications, from mild abrasive in antiquity to for example pet litter or activator in blood clotting studies. In addition, diatoms are important micro-witnesses in forensic research. They can be used for example as evidence in diagnosing drownings, identifying perpetrators, the scene of the crime and even the tools used. Due to their small size, diatoms are invisible to perpetrators, making them secret but crucial witnesses. In crime diagnosis, it is necessary to do a diatom test, which involves quantitative and qualitative identification and comparison of diatoms, for example, from the deceased organs, the perpetrators' and victims' clothes, and environmental samples. To sum up, despite their microscopic size, diatoms certainly play a huge role in the environment and human life.

Keywords: diatoms, ecological status of water, primary producers, diatom test, forensic research

SYNERGISTIC ACTIVITY OF A CHK1 INHIBITOR AND DISULFIRAM IN OVARIAN CANCER: DEPLETION OF ALDH+ CELLS AND DOWNREGULATION OF β -CATENIN IN A 3D MODEL

Wiktoria Bębenek^{1,2,*}, Aneta Rogalska¹

¹ *Department of Medical Biophysics, Institute of Biophysics, Faculty of Biology and Environmental Protection, University of Lodz, 90-236 Lodz, Poland*

² *Doctoral School of Exact and Natural Sciences, University of Lodz, Jana Matejki 21/23, 90-237, Lodz, Poland*

*wiktoria.bebenek@edu.uni.lodz.pl

Ovarian cancer remains one of the most lethal gynecological malignancies, primarily due to late diagnosis and the development of treatment resistance. Increasing evidence indicates that the tumor microenvironment and the spatial organization of cancer cells significantly modulate therapeutic response. In this context, three-dimensional culture models (spheroids) provide a useful tool for studying mechanisms of resistance, as they better recapitulate *in vivo* conditions than classical two-dimensional cultures. Subpopulations of cells with enhanced adaptive capacity, including those with elevated aldehyde dehydrogenase (ALDH) activity, are thought to play a particularly important role in therapeutic resistance.

To better reflect tumor behavior, OVCAR-8 cells were cultured in 3D spheroids. Cytotoxicity was assessed using the resazurin reduction assay, and selected concentrations of MK-8776 (CHKi) (2.5 μ M) and disulfiram (ALDHi) (5 μ M) showing synergistic anti-cancer activity were used for further analysis of ALDH-positive cells and β -catenin signaling. ALDEFLUOR cytometry revealed a distinct ALDH-positive subpopulation in control spheroids. Combination therapy showed the strongest effect, nearly eliminating ALDH-positive cells. Western blot analysis demonstrated a decrease in β -catenin levels in the combination group, which was confirmed by immunohistochemistry showing near-complete loss of β -catenin signal in treated spheroids. In contrast, GLI1, a Hedgehog pathway effector, was undetectable, indicating SHH signaling does not drive OVCAR-8 resistance.

Overall, combined CHK1 and ALDH inhibition effectively targets ALDH-positive cells and suppresses Wnt/ β -catenin signaling in OVCAR-8 spheroids. These findings highlight the value of three-dimensional models for uncovering adaptive mechanisms of therapy resistance and suggest potential strategies for improving treatment efficacy in highly resistant ovarian cancer populations.

Keywords: Ovarian cancer, 3D spheroids, Disulfiram, MK-8776.

EXOSOMES AS CELL-FREE THERAPEUTICS IN REGENERATIVE MEDICINE

Magdalena Krasowska-Kunach^{1*}, Agnieszka Szuster-Ciesielska¹

¹*Department of Virology and Immunology, Faculty of Biology and Biotechnology, Maria Curie-Skłodowska University, ul. Akademicka 19, 20-033 Lublin*

**corresponding author's e-mail address: magdalena.krasowska-kunach@mail.umcs.pl*

Regenerative medicine aims to restore the function of damaged tissues and organs by stimulating repair and regeneration. Although cell-based therapies, particularly those using mesenchymal stem cells (MSCs), have shown promising results, their clinical application is limited by safety, biocompatibility, stability, and the risk of immune rejection.

In recent years, attention has increasingly focused on exosomes as key mediators of the regenerative effects previously attributed to stem cells. Exosomes are small extracellular vesicles released by various cell types, including MSCs, and play a crucial role in intercellular communication. They carry a diverse cargo of bioactive molecules, including proteins, lipids, and nucleic acids (such as miRNAs and circRNAs), enabling modulation of inflammatory processes, stimulation of angiogenesis, cell proliferation, and tissue regeneration.

Due to their low immunogenicity, high stability, and ability to cross biological barriers, exosomes are an attractive alternative to conventional cell-based therapies. Consequently, they have significant therapeutic potential in tissue regeneration, including wound healing, cardiovascular diseases, nervous system regeneration, and musculoskeletal disorders. Understanding the mechanisms of exosome-mediated regeneration may contribute to the development of safer, more effective therapeutic strategies in regenerative medicine.

Keywords: exosomes, regenerative medicine, immunomodulation, cell-free therapies

OBTAINING SILICA FROM AGRICULTURAL WASTE USING GREEN SYNTHESIS METHODS

Veronica Latini¹, Agata Wawrzyńczak¹, Agnieszka Feliczak-Guzik¹

¹*Department of Applied Chemistry, Faculty of Chemistry, Adam Mickiewicz University in Poznań,
Uniwersytetu Poznańskiego 8, 61-614 Poznań, Poland*

**veronica.latini@amu.edu.pl*

The production of silica using low-cost methods and environmentally friendly reagents has attracted increasing interest in recent years. One promising approach is the recovery of silica from agricultural waste. Common silica-rich residues include rice husks and straw, corn cobs, sugarcane straw and bagasse, potato residues, wheat husks, and various types of fruit waste such as coconut shells, orange peels, walnut shells, banana peels, and coffee residues.

The aim of this presentation is to outline current research methods for obtaining biosilica from plant-based resources, with particular emphasis on the green synthesis applying post-agricultural waste.

Three main methods are commonly used to produce biosilica: sol-gel, hydrothermal, and acid leaching. In all approaches, the raw material is first rinsed with distilled water and dried, followed by acid treatment to remove metallic impurities. In recent studies, environmentally friendly organic acids such as citric acid, L-cysteine hydrochloride monohydrate, and gluconic acid have increasingly replaced conventional mineral acids. In the sol-gel method, the purified material is incinerated and silica is extracted through sodium silicate formation under basic conditions, followed by neutralization with acids and drying to obtain silica gel. The hydrothermal method involves heating the plant material in an autoclave, whereas in the acid leaching method the acid-treated material is rinsed, dried, and incinerated in a muffle furnace.

Biosilica obtained by these methods can be used in agriculture to enhance nutrient and water uptake and improve plant resistance, supporting circular economy principles and sustainable development.

Keywords: Silica, Agriculture waste, Green synthesis

GENETIC DIFFERENCES IN THE O-ANTIGEN BIOSYNTHESIS CLUSTER OF *PROTEUS MIRABILIS* O78 AND THEIR IMPACT ON STRAIN IMMUNOREACTIVITY

Katarzyna Zegadło¹, Grzegorz Czerwonka¹, Dominika Drzewiecka²

¹ Zakład Mikrobiologii, Instytut Biologii, Wydział Nauk Ścisłych i Przyrodniczych, Uniwersytet Jana Kochanowskiego w Kielcach, ul. Uniwersytecka 7, 25-406 Kielce

² Katedra Biologii Bakterii, Wydział Biologii i Ochrony Środowiska, Uniwersytet Łódzki, Stefana Banacha 12/16, 90-237 Łódź

*s127045@student.ujk.edu.pl

Proteus mirabilis is an opportunistic Gram-negative pathogen frequently associated with catheter-associated urinary tract infections. Its ability to swarm, form biofilms, and evade host immunity is closely linked to the structural variability of its lipopolysaccharide O-antigen.

This study examines genomic diversity within the O-antigen biosynthesis cluster of twenty *P. mirabilis* O78 isolates, representing the most common serogroup in the Łódź region. Whole-genome sequencing, assembly, and gene annotation enabled reconstruction of complete O-antigen biosynthetic loci. Although the general cluster organization was conserved, several isolates showed clear genetic divergence within a region encoding a DUF1919 domain-containing protein of unknown function. In one strain, this divergent DUF1919 segment was preceded by a putative transposable element, suggesting recent horizontal gene movement or local genomic rearrangement.

The presence of a mobile element near the DUF1919 gene indicates possible consequences for O-antigen structure. Such variation may influence antigenic epitopes and affect strain-specific reactivity in immunoblot assays. These findings support the hypothesis that the DUF1919 protein may participate in glycosyl transfer or modification steps during O-antigen assembly. Ongoing analyses aim to determine whether affected strains incorporate ribitol or alternative sugar residues into their surface polysaccharides, which would help clarify the biochemical role of this locus.

These results demonstrate that even within the O78 serogroup, the O-antigen biosynthesis region is not genetically homogeneous. The genetic changes identified here, particularly those involving the DUF1919 domain containing protein and the adjacent mobile element, may influence how individual strains construct their O-antigen and how they react in serological assays.

Keywords: O-antigen biosynthesis, *Proteus mirabilis* O78, genetic variability, LPS structure, strain reactivity

ANTIMICROBIAL PEPTIDES DERIVED FROM PROBIOTIC STRAINS INHIBIT THE FORMATION OF *PSEUDOMONAS AERUGINOSA* PAO1 BIOFILM

Sylwia Nawrot¹, Natalia Czarnecka^{1,2}, Magdalena Jankowska², and Grzegorz Czerwonka⁽¹⁾

¹ Zakład Mikrobiologii, Instytut Biologii, Uniwersytet Jana Kochanowskiego w Kielcach, Stefana Żeromskiego 5, 25-369, Kielce, Polska,

² Regeneris Sp. z o.o., Podzamcze 45, Polska

* sylwianawrot18@gmail.com

Introduction Antimicrobial peptides (AMPs) are bioactive molecules produced by lactic acid bacteria (LAB), including *Lactocaseibacillus rhamnosus*. They are part of the secondary metabolism of these bacteria and can be detected in the cell-free culture supernatant. AMPs play an important role in microbial competition and food preservation and have gained attention for their potential applications in combating antibiotic-resistant pathogens. Although their activity is mainly directed against Gram-positive bacteria, some LAB-derived peptides also exhibit effects against Gram-negative species under specific conditions. AMP production depends on environmental factors such as pH, temperature, and nutrient availability.

Methods This study evaluated the antimicrobial and antibiofilm activity of peptides present in the cell-free culture supernatant of probiotic LAB species against *Pseudomonas aeruginosa* PAO1. Minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC), and minimum biofilm inhibitory concentration (MBIC) were determined using standard broth microdilution assays in 96-well plates with three biological replicates. MBIC was defined as the lowest concentration significantly inhibiting biofilm formation. Pyoverdine production was measured as an indicator of quorum sensing activity.

Results The analyzed supernatant reduced biofilm formation in *P. aeruginosa* PAO1. The determined values were MIC = 7.82 mg/mL, MBC = 15.63 mg/mL, and MBIC = 15.63 mg/mL. Biofilm inhibition correlated with decreased pyoverdine secretion, suggesting interference with quorum sensing mechanisms. These findings indicate that LAB-derived AMPs may act through membrane interaction or disruption of pyoverdine recycling. Further mechanistic studies are required to confirm the exact mode of action.

Keywords: peptydy antybakteryjne, probiotyk, biofilm, *Pseudomonas aeruginosa* PAO1

NH₄OH MODIFICATION OF CORNCOB BIOCHAR FOR THE REMOVAL OF SILVER IONS FROM AQUEOUS MEDIA

Desmond Kwayela Sama¹, Elis-Bright Iteke Molua¹, Katarzyna Szewczuk-Karpisz¹

¹*Institute of Agrophysics, Polish Academy of Sciences, ul. Doświadczalna 4, 20-290 Lublin, Poland*

**adres e-mail autora do korespondencji: dkwayela@ipan.lublin.pl*

The intensification of agricultural activities to meet the growing population has led to environmental hazards. One major issue is generating large amounts of waste from crop residue, as well as pollution caused by silver-based products applied in agriculture and industry. An environmentally beneficial and sustainable management technique such as biochar, can effectively remove pollutants in addition to managing waste issues. However, BC may include harmful compounds and possesses poor textural parameters that are insufficient for a certain need. Modifying corncob biochar (BC) with ammonium hydroxide (NH₄OH) and demonstrating its capacity to remove silver ions (Ag⁺) from aqueous solutions are the goals of this work. BC was produced by pyrolysis of corncob at 700 °C for 1 h. Then, it was chemically modified using the 25% NH₄OH, and the obtained product was marked as BCM. The adsorption was conducted in a batch experiment, and the concentration of Ag⁺ was measured with a selective silver electrode. The effects of ion concentration, time, adsorbent dosage, and pH were studied. After modification of BC, there was increase in S_{BET}, microporosity, basic functional groups, and total carbon content. The adsorption capacity decreased consistently with increasing adsorbent dosage. The equilibrium was achieved after 480 min. The performed modification improved adsorption efficiency of Ag⁺ from 73.5% to 90.72%. All things considered, this work shows that NH₄OH-modified corncob biochar is a sustainable and efficient adsorbent, the production of which allows the management of troublesome waste.

Keywords: Maize residue, metal ion, water treatment, engineered biochar

CONSERVATION OF GlcNAc AND GalNAc METABOLIC PATHWAYS IN *PROTEUS MIRABILIS*

Leon Petruńko^{1,2}, Dawid Gmitter³

¹Department of Microbiology, Institute of Biology, Jan Kochanowski University of Kielce, Uniwersytecka 7, 25-406 Kielce

²Student Scientific Society of Biotechnologists MIKROBY, Faculty of Natural Sciences, Jan Kochanowski University of Kielce, Uniwersytecka 7, 25-406 Kielce

³University of Warsaw, Faculty of Biology, Institute of Microbiology, I. Miecznikowa 1, 02-096, Warsaw

*corresponding author's e-mail address: leonpetrunko@gmail.com

ORCID numbers: Leon Petruńko 0009-0004-8346-5440; Dawid Gmitter 0000-0001-8663-129X

Proteus mirabilis is a leading causative agent of complicated urinary tract infections (UTIs), particularly among catheterized patients (CAUTIs). These infections pose a significant clinical and economic challenge due to the bacterium's persistence, versatile arsenal of virulence factors and increasing antibiotic resistance. A critical factor for *P. mirabilis* colonization and infection is its metabolic adaptation to the host urinal environment, which is exceptionally competitive.

Amino sugars, specifically N-acetylglucosamine (GlcNAc) and N-acetylgalactosamine (GalNAc), are abundant in the urinary tract as components of mucus and free metabolites in urine. They serve as essential sources of carbon and nitrogen for bacteria and are key precursors for cell wall synthesis and protein glycosylation. The catabolism of these sugars is governed by specific gene clusters: the *nag* operon, responsible for GlcNAc utilization, and the *aga* operon, involved in GalNAc metabolism.

In this study, we analysed the distribution of these pathways in *P. mirabilis* isolates from the in-house collection of the Department of Microbiology at Jan Kochanowski University of Kielce. Metabolic profiles were characterized using DRAM v1.4.6 (Distilled and Refined Annotation of Metabolism) to annotate functional gene potential. Structural modelling of key enzymatic proteins was performed using Phyre2, while phylogenetic relationships among the isolates were visualized using ANIclustermap v1.3.0.

Result indicated that the genes required for the utilization of GlcNAc and GalNAc are highly conserved across all *P. mirabilis* strains analyzed. This indicates that amino sugar metabolism constitutes a core metabolic trait of the species, likely linked to its adaptation to host-associated niches rich in mucin-derived carbohydrates.

Keywords: *Proteus mirabilis*, Bacteriology, Bioinformatics, Carbohydrate metabolism, UTI

GENOMIC CONSERVATION OF Mg^{2+} HOMEOSTASIS AND PHOPQ-REGULATED LPS MODIFICATION PATHWAYS IN *PROTEUS MIRABILIS*

Aleksandra Omelaniuk*¹ Dawid Gmitter²

¹ Department of Microbiology, Institute of Biology, Jan Kochanowski University of Kielce, Uniwersytecka 7, 25-406, Kielce

² University of Warsaw, Faculty of Biology, Institute of Microbiology, I. Miecznikowa 1, 02-096, Warsaw

*adres e-mail autora do korespondencji: aleksandra.omelaniuk@ujk.edu.pl

Proteus mirabilis is a Gram-negative and one of the most common causative agents of catheter-associated urinary tract infections, particularly in elderly patients. Gene expression in response to environmental changes is regulated by two-component systems (TCS), which also control the expression of virulence factors. In *P. mirabilis*, 16 gene sets encoding such regulatory systems have been identified. One of them is the PhoPQ system, composed of the sensor kinase PhoQ and the response regulator PhoP, which controls gene transcription. In many bacteria, the PhoPQ system regulates the cellular response to changes in magnesium (Mg^{2+}) concentration. Magnesium is one of the most abundant metals in living cells and plays essential biological roles. In bacteria, it contributes to membrane stabilization and acts as a cofactor for numerous enzymes, influencing fundamental metabolic processes.

In the context of increasing antibiotic resistance and a rapidly aging population, research on the regulatory and metabolic mechanisms of *P. mirabilis* is of significant clinical importance. A better understanding of the role of magnesium in this bacterium may contribute to the development of more effective therapeutic strategies. The aim of this study was to analyze the presence of metabolic pathways involved in magnesium homeostasis, cellular response regulation, and LPS modification in selected *P. mirabilis* strains. Bioinformatic analysis was performed using the DRAM v1.4.6 (Distilled and Refined Annotation of Metabolism) software. The analysis revealed that core Mg^{2+} transporters and PhoPQ-associated LPS modification genes are highly conserved across all examined strains, while certain regulatory or accessory components are variably distributed.

Keywords: *Proteus mirabilis*, two-component regulatory system, PhoPQ, magnesium homeostasis

EPIZOIC FUNGI – POORLY UNDERSTOOD GROUP OF FUNGI WITH EXTRAORDINARY METABOLIC AND ECOLOGICAL POTENTIAL

Anna Ratajewicz¹, Andrzej Górz²

^{1,2} Department of Zoology, Institute of Biology and Earth Sciences,

University of the Commission of National Education, Podchorążych Street 2, 30-084 Kraków

**author's e-mail address for correspondence: d751478@doktorant.uken.krakow.pl*

According to modern systematics, fungi are classified as a separate kingdom of eukaryotic organisms, characterized by extraordinary diversity both in terms of morphology and metabolic activity. Their ubiquity means that they perform many important functions in the environment for example, in decomposition of organic matter, circulation of bioelements or the reduction of parasitic insects, thus supporting the preservation of ecological balance of terrestrial ecosystems.

Saprophytic fungi are particularly noteworthy due to their association with nutrient-rich dung and bedding. Their biodiversity around the world is estimated at several hundred species, most of which have been recorded in warm climate zones with high relative air humidity. Furthermore, the interesting fact is that the group of fungi mentioned above is characterized by the ability to synthesize a wide range of secondary metabolites, including antiseptic and enzymatic compounds used in many branches of processing and biotechnology industries. In addition, according to the literature, it is also assumed that some species show metabolic activity towards mutagenic and cytotoxic compounds, enabling their use in the process of environmental reclamation. Moreover, research conducted in the Polish part of the Carpathians suggests that some species may be seasonally colonized the exoskeletons of coprophagous beetles from the Scarabaeoidea superfamily – epizoic mycobiota, the spores of which could be naturally transmitted in the local environment as a result of the behavior and high mobility of the mentioned insects. Analysis in this area will therefore fill the existing research gap and contribute to deepening knowledge about the ecological role of epizoic fungi.

Keywords: coprophilous fungi, dung, secondary metabolites

A COMPARATIVE STUDY OF PARTICULATE MATTER AND TRACE ELEMENT WASH-OFF FROM URBAN VEGETATION UNDER NATURAL AND SIMULATED RAINFALL

Mariia Pismanik¹, Arkadiusz Przybysz¹, Hanna Moniuszko¹, Bingjie Zhang², Chunyang Zhu²

¹*Centre for Climate Research SGGW, Warsaw University of Life Sciences—SGGW (WULS—SGGW), Nowoursynowska 166, 02-787 Warsaw, Poland*

²*College of Horticulture and Forestry, Huazhong Agricultural University, No. 1 Shizishan Street Hongshan District, Wuhan, Hubei, 430070, China*

*adres e-mail autora do korespondencji: mariia_pismanik@sggw.edu.pl

The role of urban vegetation in mitigating air pollution is significant; it captures pollutants such as particulate matter (PM) and trace elements (TEs). Nevertheless, the retention is only temporary because precipitation can wash off the deposited pollutants. The long-term impact of vegetation on air pollution mitigation requires an accurate understanding of the rainfall's capability to wash off pollutants. Due to the variability of natural rainfall, many studies use simulated rain to evaluate wash-off processes, although the comparability of these methods remains unclear. The goal of this study is to analyze the capability of natural and simulated rainfall in washing off PM and TE from the foliage of 17 plant species (trees, shrubs, and herbaceous plants) in an urban park in Wuhan, China. In most plant groups, simulated rainfall was more effective in washing off PM and TEs. However, natural rainfall was more effective in some cases, particularly for evergreen trees. Notably, natural rain resulted in increased concentrations of Cu and Zn. Leaf morphological traits, such as texture, waxiness, and surface structure, were key factors influencing wash-off efficiency, especially under natural conditions. The findings highlight that simulated rain does not fully replicate real-world wash-off processes and that natural rainfall involves complex interactions influenced by environmental and plant-specific factors. This underscores the importance of incorporating natural variability when evaluating the role of urban greenery in air pollution mitigation.

Keywords: air phytoremediation, leaf morphology, precipitation, natural rain, simulated rain

EFFECT OF Zr INCORPORATION ON THE STRUCTURAL AND PHYSICOCHEMICAL PROPERTIES OF CeO₂ SUPPORTS

Joanna Lupa^{1*}, Grzegorz Słowik², Andrzej Wójtowicz³, Gabriela Grzybek³, Agnieszka Kierys²

¹ *Chemical Sciences, Doctoral School of Quantitative and Natural Sciences, Maria Curie-Skłodowska University, Weteranów St. 18, 20-400 Lublin*

² *Faculty of Chemistry, Institute of Chemical Sciences, Maria Curie-Skłodowska University, M. Curie-Skłodowska Sq. 3, 20-031 Lublin*

³ *Faculty of Chemistry, Department of Environmental Chemistry, Jagiellonian University, Gronostajowa 2 Str., 30-387 Kraków*

**Joanna.lupa@mail.umcs.pl*

Cerium oxide is widely used as a support for the active phase in various catalytic processes, including ethanol steam reforming, primarily due to its high lattice oxygen mobility and its ability to reversibly form oxygen vacancies associated with the Ce⁴⁺/Ce³⁺ redox transition. However, at high temperatures, cerium oxide exhibits limited structural stability, leading to morphological changes and a decrease in specific surface area, which restricts its overall application as a catalytic support. One strategy to enhance its thermal stability involves lattice modification by incorporating cations with different ionic radii. The incorporation of Zr⁴⁺ ions, which have a smaller ionic radius than Ce⁴⁺, modifies the lattice parameters and oxygen defect concentration and, depending on synthesis conditions, may either promote the formation of a Ce–Zr solid solution (generally desirable) or lead to segregation of separate CeO₂ and ZrO₂ oxide phases. One way to obtain various oxides with the desired properties is the one-step hard template method, using a porous polymer template such as Amberlite XAD7HP™.

This work investigates the feasibility of synthesising a Ce-Zr solid solution, specifically zirconium-doped ceria, *via* this method, and evaluates its structural and physicochemical properties. For the mixed oxides, cerium and zirconium salts were mixed in molar ratios of Ce:Zr = 0.8:0.2 and 0.5:0.5, respectively. CeO₂ synthesised by the same method served as a reference material. The materials were characterised by X-ray diffraction (XRD), Raman spectroscopy, low-temperature nitrogen adsorption/desorption analysis, and transmission electron microscopy (TEM).

Keywords: Ce-Zr mixed oxides, zirconium doping, lattice modification, hard-template synthesis, structural modification

LACTOBIONIC ACID SYNTHESIS: WHY DOES THE FUTURE BELONG TO BIOLOGICAL METHODS?

Wiktoria Piątek-Golda¹, Justyna Sulej¹, Monika Osińska-Jaroszuk¹

¹Department of Biochemistry and Biotechnology, Institute of Biological Sciences Maria Curie-Skłodowska University, Akademicka 19, 20-033 Lublin, Poland

**adres e-mail autora do korespondencji: wiktoria.piatek.golda@gmail.com*

Lactobionic acid (LBA) is a compound with a wide range of applications, from advanced medicine and pharmacy, through cosmetology, to the food industry. For years, the main method of obtaining it was chemical synthesis based on lactose oxidation. However, this process has some limitations, such as the need for expensive catalysts and the formation of toxic by-products. Nowadays, more and more research teams are focusing on the biological synthesis of LBA. These approaches, which use specific enzymes and microorganisms, are highly selective and allow the process to be carried out under mild environmental conditions. By reducing toxic waste, biological technologies are not only in line with the principles of green chemistry, but also pave the way for the use of waste raw materials. The use of immobilization techniques for biocatalysts allows the development of stable and efficient systems that, in the long term, exceed chemical methods in terms of economic and environmental benefits. The aim of this review is to make a critical assessment of the current state of knowledge on methods of lactobionic acid synthesis and explain why biotechnological solutions are the most promising way to develop LBA production.

Keywords: lactobionic acid, sustainable production, biocatalysis, biological and chemical synthesis

MOLECULAR CHARACTERIZATION OF BIOTIN UPTAKE AND ITS ROLE IN TARGETED TRANSPORT IN LIVER CANCER MODEL

Magdalena Twardowska¹, Łukasz Uram¹, Magdalena Dąbrowska², Tomasz Ruman¹,
Aneta Płaza-Altamer¹

¹*Department of Inorganic and Analytical Chemistry, Rzeszow University of Technology, Rzeszow, Poland,* ²*Laboratory of Molecular Bases of Ageing, Nencki Institute of Experimental Biology, Polish Academy of Sciences, 3 Pasteur Street, 02-093 Warszawa, Poland*

**magdalenatwardowska5@gmail.com*

Cancer remains a major global health burden. It is responsible for approximately 10 million deaths annually, and its incidence is expected to rise to 20 – 30 million new cases per year due to factors such as population aging, smoking, and unhealthy lifestyles. Surgical resection and chemotherapy remain the first-line treatment options. Gold-standard chemotherapeutics include pembrolizumab, paclitaxel, doxorubicin, and cisplatin. However, their effectiveness is often insufficient, and many patients fail to achieve satisfactory therapeutic outcomes.

To improve treatment efficacy, researchers are developing drug-delivery systems based on targeted cancer therapy. One promising strategy involves vitamin-decorated nanosystems. Because cancer cells proliferate rapidly, their demand for nutrients is high, creating an opportunity to exploit nutrient-uptake pathways for targeted delivery. Among the vitamins proposed for this purpose, B-group vitamins are the most widely used. Biotin (vitamin B7) is particularly attractive due to its ability to enhance cellular uptake of drugs and nanocarriers. Nevertheless, the mechanisms underlying biotin and biotin-decorated nanoparticle internalization remain unclear, limiting the broader application of this approach.

In this study, we investigated the uptake of biotin and biotin-decorated PAMAM G4 dendrimers in a liver cancer model (HepG2 cells), which overexpress proteins responsible for biotin transport. Biotin uptake and intracellular levels were quantified using mass spectrometry after treatment with 100 nM biotin for 1 hour. Expression of biotin-transport proteins was analyzed by Western blot, and uptake of biotinylated nanoparticles was assessed in parallel. Our results revealed increased biotin accumulation in HepG2 cells and confirmed its involvement in enhanced nanoparticle uptake.

Keywords: targeted therapy, cancer, uptake, biotin

THE ROLE OF NEWLY DEVELOPED HYDROGEL COMPOSITES FROM *HERMETIA ILLUCENS* RESIDUES IN ENHANCING SOIL QUALITY

Elis-Bright Iteke Molua¹, Olena Siryk¹, Katarzyna Szewczuk-Karpisz¹

¹*Institute of Agrophysics, Polish Academy of Sciences, ul. Doswiadczalna 4, 20-290 Lublin, Poland*

Globally, drought and heavy metal contamination are among the major problems affecting the health and quality of soil, leading to its degradation. The use of innovative technologies transforming waste generated from Black Soldier Fly (*Hermetia illucens*) into chitosan hydrogel (HG), can be applied to limit these phenomena. Novel soil conditioners will positively impact the soil by reducing the negative effects of drought and increasing the efficacy of remediation for degraded soil. Despite the benefits of polysaccharide-based hydrogels, they have some limitations, such as weak mechanical strength and rapid degradation in the soil. Given these limitations, the fillers such as biochar (BC), hydrochar (HC), activated carbon (AC), and frass are introduced into chitosan hydrogels to increase their life span by slowing degradation, improving structure, and making them resistant to heat.

Most research has focused on using BC as a carbon-rich filler in hydrogel structures, reporting increased swelling and sorption capacities for water and nutrients in the soil. Additionally, several researchers used both natural and synthetic chemicals simultaneously to create hydrogels loaded with BC, such as polysaccharides and acrylic acid. These materials improved the soil's water retention and heavy metal sorption ability. However, very few studies have examined the nutrient release characteristics of these hydrogel/BC composites, their effects on plant growth, or the properties and functions of soil. As a result, the combination of HG with carbon-rich materials such as BC, HC, and AC to create HG composite will seem to be a promising and innovative way of improving the stability and effects of HG on soil physiochemical and biological properties.

Keywords: Black soldier fly, hydrogel composites, soil degradation, soil remediation.

BIOTECHNOLOGICAL VALORIZATION OF TEXTILE WASTE USING ASPERGILLUS JAPONICUS

Michał Jędrych¹, Małgorzata Brzezińska-Rodak¹

¹*Department of Biochemistry, Molecular Biology and Biotechnology, Faculty of Chemistry,
Wrocław University of Science and Technology, Wybrzeże Stanisława Wyspiańskiego 27, 50-
370, Wrocław, Poland*

*michal.jedrych@pwr.edu.pl

In the face of the growing challenge posed by excessive textile waste, especially blended fabrics such as cotton-polyester materials, it is essential to develop environmentally friendly and efficient recycling strategies. Biotechnological approach focused on the application of cellulolytic enzymes offers a selective, sustainable, and eco-friendly alternative for processing such waste streams. The aim of this work was the evaluation of the potential usage of textile waste as a feedstock for cellulase production via both solid-state and submerged fermentation by a selected microorganism - *Aspergillus japonicus* DSM 104286. Various material pretreatment methods for cotton fibers softening, including autoclaving and alkaline treatment, were applied to three types of textiles with different cotton-to-polyester ratios. Different nutrient media were tested to support optimal fungal production of cellulolytic enzymes. The cellulase produced by the fungus was subsequently extracted and used for enzymatic hydrolysis of blended textile waste. This approach enables the efficient conversion of cellulose into simple sugars, which can then serve as substrates for further processes such as fermentation. At the same time, it allows for the recovery of polyester fibers in a form suitable for reuse contributing to the circular economy.

Keywords: textile waste, cellulase, filamentous fungi, circular economy

PHYTOCHEMICAL PROFILING AND SKIN-TARGETED BIOACTIVITY OF ALCHEMILLA MOLLIS (BUSER) ROTHM. EXTRACTS

Sebastian Kanak¹, Michał P. Dybowski², Rafał Typek², Katarzyna Dos Santos Szewczyk³

¹Doctoral School of the Medical University of Lublin, ul. Witolda Chodźki 7, 20-093 Lublin, Poland;

²Department of Chromatography, Faculty of Chemistry, Institute of Chemical Sciences, Maria Curie-Skłodowska University, plac Marii Skłodowskiej-Curie 2, 20-031 Lublin, Poland; ³Department of Pharmaceutical Botany, Faculty of Pharmacy, Medical University of Lublin, ul. Chodźki 1, 20-093 Lublin, Poland

*e-mail: sebastian.kanak@umlub.edu.pl

The growing demand for evidence-based, plant-derived bioactive ingredients has intensified research into multifunctional botanical extracts for dermatological and dermocosmetic applications. *Alchemilla mollis* (Rosaceae), traditionally used in skin-related disorders, represents a promising yet insufficiently characterized source of bioactive compounds. This study aimed to integrate advanced phytochemical profiling with functional *in vitro* assays to evaluate the biological potential of *A. mollis* extracts as active ingredients for skin-targeted formulations.

The chemical composition of the extracts was analyzed using LC-ESI-MS/MS and GC-MS methods. Biological activity was assessed *in vitro* by examining the inhibition of lipoxygenase (LOX), tyrosinase, elastase, and collagenase. The antioxidant potential was determined using DPPH • and ABTS •⁺ assays.

Chromatographic analysis allowed for the identification of numerous polyphenols and volatile compounds. Enzymatic studies demonstrated the multi-directional activity of the plant material. The methanol-acetone-water (MAW) extract most strongly inhibited LOX (80.5% at 5 mg/mL) and showed a significant effect on elastase and collagenase activity, suggesting its potential to protect skin structure from degradation. Tyrosinase inhibitory activity was also observed. These results correlate with high antioxidant activity, particularly for the MAW extract, which achieved 108.04 mg T/g e in the DPPH test and 852.37 mg T/g e in the ABTS assay.

The obtained data indicate that *A. mollis* is a valuable source of compounds with dermatoprotective effects. The ability to simultaneously inhibit inflammatory and proteolytic enzymes makes this species a promising raw material for the production of modern dermatological and anti-aging dermocosmetic formulations.

Keywords: *Alchemilla mollis*, elastase, collagenase, GC-MS, tyrosinase

EFFECTS OF NON-THERMAL PLASMA ON FUNGAL AND MYCOTOXIN CONTAMINATION IN FOOD

Karina Lenard^{1*} Magda Caban² Angelika Nowak¹ Pawel Pohl¹ Magdalena Klimek-Ochab³
Piotr Jamroz¹ Malgorzata Brzezinska-Rodak³ Ewa Zymanczyk-Duda³ Anna Dzimitrowicz¹

¹ Department of Analytical Chemistry and Chemical Metallurgy, Faculty of Chemistry, Wrocław University of Science and Technology, 27 Wybrzeże St. Wyspińskiego, 50-370 Wrocław, Poland

² Department of Environmental Analysis, Faculty of Chemistry, University of Gdańsk, 63 Wita Stwosza, 80-308 Gdańsk, Poland

³ Department of Biochemistry, Molecular Biology and Biotechnology, Faculty of Chemistry, Wrocław University of Science and Technology, 27 Wybrzeże St. Wyspińskiego, 50-370 Wrocław, Poland

*adres e-mail autora do korespondencji: karina.lenard@pwr.edu.pl

Fungi and mycotoxins presence in food might pose a threat to food quality and safety. Overall, fungal mycotoxins are produced by selected fungal species and are challenging to eliminate using conventional removal methods. Processing of fungal-infected fruits or vegetables can lead to contamination of products with mycotoxins such as aflatoxins, patulin, ochratoxin A, and *Alternaria* toxins. Therefore, it is crucial to remove such impurities from food to ensure consumer safety. Having this in mind, a novel approach based on a non-thermal plasma (NTP) is proposed for application in food processing, such as the treatment of fruit juices ^[1]. NTP is an ionized gas generated by applying a high voltage under atmospheric conditions. The reactive oxygen and nitrogen species (RONS) formed during this process can affect the fungal growth and development as well as degrading of organic impurities, such as mycotoxins that contaminate juices. More specifically, NTP treatment has been shown to be effective against fungal strains including *Fusarium culmorum* and *Botrytis cinerae* by inhibiting conidia germination and thereby limiting mycelial growth in the fruit juice matrix. It has also demonstrated significant potential for the removal of mycotoxins. NTP treatment of fruit juices also lead to improvement of its nutritional properties such as total polyphenolic compounds concentration. Moreover, this approach also allows the preservation of other key nutritional juices properties, including ascorbic acid and total soluble solids concentrations. For this reason, the proposed NTP method is promising for the fungal inactivation and lowering mycotoxin concentration in food such as fruit juices, which demonstrates potential for further implementation in the food industry.

^[1] Lenard, K., et al. (2026) Cold Atmospheric Pressure Plasma for Blueberry Juice Processing: Implementation, Multivariate Optimization, Validation, Quality Estimation along with Fungi and Mycotoxin Decontamination, *Food Control*, Manuscript under review.

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Keywords: cold atmospheric pressure plasma, food processing, fungal toxins

ANTICANCER ACTIVITY OF *CENTAUREA* SPP. EXTRACTS IN LUNG, PROSTATE, AND GLIOMA CANCER MODELS – A CONTEMPORARY REVIEW

Joanna Kubik ^{1*}, Magdalena Iwan ², Agnieszka Korga-Plewko²

¹ *Doctoral School, Medical University of Lublin, 20-093 Lublin, Poland*

² *Independent Medical Biology Unit, Faculty of Pharmacy, Medical University of Lublin, 8b, Jaczewski Street, 20-093 Lublin, Poland*

[*joanna.kubik@umlub.edu.pl](mailto:joanna.kubik@umlub.edu.pl)

Natural plant extracts represent an important source of compounds with potential anticancer activity and offer promising opportunities for the development of novel therapeutic strategies with reduced toxicity compared to conventional treatments. Plants of the genus *Centaurea* spp. exhibit a broad spectrum of biological activity, including the ability to inhibit proliferation and induce cytotoxicity in cancer cells. This review includes studies from the last ten years on the cytotoxicity of *Centaurea* spp. extracts and their mechanisms of action in models of lung, prostate, and glioblastoma cancer.

In vitro studies have shown that *Centaurea solstitialis* extract reduced the viability of lung cancer cells (A549) by inducing apoptosis and modulating the cell cycle. Similarly, *Centaurea pichleri* extract exhibited cytotoxic effects against prostate cancer cells (PC 3, DU145), although the potency of this effect and the underlying mechanisms varied depending on the solvent and experimental conditions. *Centaurea castriferrei* extracts exhibited dose-dependent cytotoxicity in glioblastoma cells (LN229), with less effect on control cells, confirming the broad range of antiproliferative activity of these plants.

The mechanisms of action of the extracts include induction of apoptosis, modulation of the cell cycle, and alteration of the expression of genes related to cell survival. Studies indicate that anticancer activity depends on the species, type of extract, and cell line tested.

Keywords: *Centaurea* spp., anticancer activity, lung cancer, prostate cancer, glioma

SCALE-DEPENDENT CHALLENGES IN PLANT DISTRIBUTION MODELLING: INSIGHTS FROM PINE-FOREST SPECIALISTS

Inez Masiarek*^{1,2}, Marcin Kiedrzyński¹

¹Department of Biogeography, Paleoecology and Nature Conservation, Institute of Ecology and Environmental Protection, Faculty of Biology and Environmental Protection, Banacha 1/3 St., 90-237 Łódź.

²BioMedChem Doctoral School of the University of Lodz and Lodz Institutes of the Polish Academy of Sciences, Matejki 21/23 St., 90-237 Łódź.

**Corresponding author: inez.masiarek@edu.uni.lodz.pl*

Plant vulnerability to climate change is commonly assessed using broad-scale niche models, yet plant responses to environmental stress are strongly scale-dependent and may differ substantially across global, regional, and local conditions. Macroclimatic projections capture broad spatial trends, but they do not adequately represent the microclimatic and habitat conditions experienced by populations. As a result, models based only on macroclimatic averages may fail to identify suitable areas at regional and local scales – even though such sites may be critical for conservation planning. In this context, strong performance at broad scales does not necessarily translate into ecologically meaningful inference, which is the most relevant to population persistence and management.

The poster presents ongoing research on selected forest ground-layer plants associated with Scots pine forests in a region of the Polish Uplands and surrounding areas. The study addresses spatial-scale mismatch by combining biogeographic niche and distribution modelling with local microclimate observations. The question is particularly relevant because pine forests in Central Europe are projected to face increasingly negative climate-related scenarios, including declining vitality and increasing drought stress, with likely consequences for associated plants. Current work includes building an occurrence database for selected species, compiling an environmental predictor database integrating climatic, topographic, and habitat-related variables, and deploying microclimate loggers to quantify fine-scale temperature and humidity variability relevant to assessing the refugial capacity of forest complexes.

Keywords: plant niche modelling, pine forests, forest ground-flora, microclimate, climate change

WHISPERS FROM THE FROST: UNCOVERING THE POTENTIAL OF ARCTIC PSYCHROTOLERANT MICROORGANISMS AS A SOURCE OF NOVEL COLD-ACTIVE ENZYMES FOR COMPOSTING

Filip Romaniuk¹, Karol Piekarski², Michał Stanowski², Anna-Karina Kaczorowska¹, Przemysław Decewicz², Łukasz Dziewit², Takao Ishikawa², Tadeusz Kaczorowski¹

¹*Laboratory of Extremophile Biology, Faculty of Biology, Department of Microbiology, University of Gdansk, Wita Stwosza 59, 80-308 Gdansk, Poland*

²*Institute Of Bioengineering, Faculty of Biology, University of Warsaw, Miecznikowa 1, 02-089, Warsaw, Poland;*

Presenting author email: filip.romaniuk@phdstud.ug.edu.pl

The global shift toward sustainable, circular bioeconomies has positioned biological waste valorization at the forefront of environmental policy. Metagenomic studies of Arctic ecosystems have uncovered a rich diversity of genes encoding cold-active enzymes with significant biotechnological relevance. One such application is composting, where enzymes that degrade complex polysaccharides – including cellulases, pectinases and amylases offer a means to significantly improve efficiency of the process. This project develops a novel biotechnological framework to optimize composting by leveraging the metabolic capabilities of psychrotolerant microorganisms. The study involves screening a library of Arctic bacterial isolates at 15, 20, and 30°C using both plate-based and liquid culture assays to identify polysaccharide-degrading capabilities and other vital traits. Following taxonomic identification via 16S rRNA sequencing, Oxford Nanopore technology is employed for whole-genome sequencing, followed by functional annotation and biosafety assessments. Preliminary results show that a significant majority of isolates possess at least one target trait, with several exhibiting multi-functional, temperature-dependent activities. The results demonstrate that polar culture collections contain diverse, temperature-tuned activities with potential relevance in the field. A key innovation of the project lies in the implementation of a droplet microfluidics-based ultrahigh-throughput screening platform for the rapid functional selection of enzyme-producing bacteria. Selected enzymes and microbial strains will be validated in a series of composting experiments, beginning with controlled laboratory-scale microcosms and advancing to mesocosm-scale trials simulating real-world composting conditions. These experiments will assess the efficiency of the biological preparations in degrading agricultural residues - during all seasons.

Fundings by the National Science Centre, Poland. Project title: “Discovery and exploitation of psychrotolerant bacteria and novel cold-adapted enzymes in regenerative agriculture”; Contract number: UMO-2023/51/NZ9/02910.

Keywords: Psychrozymes, bioprospecting, polar regions

SYNTHESIS AND MORPHOLOGICAL INFLUENCE OF TITANIUM DIOXIDE NANOSTRUCTURES ON PHOTOCATALYTIC ACTIVITY

Nasir Shakeel*^{1,2}, Ireneusz Piwoński*¹

1 University of Lodz, Faculty of Chemistry, Department of Materials Technology and Chemistry, Pomorska 163, 90-236 Lodz, Poland.

2 University of Lodz, Doctoral School of Exact and Natural Sciences, Jana Matejki 21/23, 90-237 Lodz, Poland

** E-mail: nasir.shakeel@edu.uni.lodz.pl, ireneusz.piwonski@chemia.uni.lodz.pl*

Titanium dioxide (TiO₂) nanostructures, including nanofibers (TNFs), nanorods (TNRs), and nanograss (TNGs), were synthesised. Synthetic methodologies significantly influenced the resultant morphology and phase. Nanomaterials were synthesised at neutral environments using ethylene glycol for TNFs, whereas those produced under highly basic conditions during the recrystallisation of TiO₂ powder had the morphology of TNRs. Both materials, TNFs and TNRs, displayed the anatase phase. Conversely, at highly acidic conditions with toluene, TNGs were generated that crystallised in the rutile phase. The specific exposed planes are directly correlated with the crystal shape. XRD measurements indicated that anatase nanomaterials (TNFs, TNRs) exhibited exposure of the {101} facet, whereas rutile nanomaterials (TNGs 1 and 2) displayed exposure of the {110} facet. The interaction among morphology, the most stable facets, and silver modification significantly influenced the photocatalytic capabilities. Anatase nanomaterials, particularly those with low crystallinity (TNFs), demonstrated superior photoactivity in the breakdown of rhodamine B (RhB), whereas highly crystalline rutile crystals shown inadequate photocatalytic performance under both UV and simulated solar light (SSL). The photoactive performance of most materials could be improved through surface modification with metallic silver and the establishment of a Schottky barrier.

Keywords: TiO₂, morphology, crystal facets, photocatalysis

TOXICOLOGICAL ASSESSMENT OF CHEMICAL WARFARE AGENTS IN FISH: PHYSIOLOGICAL, CHEMICAL, MOLECULAR, AND MICROBIOME-AWARE

Wojciech Wilczyński^{1,2,3}, Tomasz Brzeziński², Michał Czub³, Jacek Beldowski³,
Jakub Nawała⁴, Daniel Dziedzic⁴, Stanisław Popiel⁴, and Monika Radlińska¹

¹*Institute of Bioengineering, Faculty of Biology, University of Warsaw, I. Miecznikowa 1, 02-096
Warsaw.*

²*Department of Hydrobiology, Institute of Ecology, Faculty of Biology, University of Warsaw, Żwirki i
Wigury 101, 02-089, Warsaw.*

³*Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot.*

⁴*Faculty of Advanced Technologies and Chemistry, Military University of Technology, Warsaw,
Sylwestra Kaliskiego 2, 00-908, Warsaw.*

*adres e-mail autora do korespondencji: wk.wilczynski@uw.edu.pl

During the 20th century, more than one million tons of chemical weapons were dumped into seas and oceans. As corrosion progresses, chemical warfare agents (CWAs) are being released from submerged munitions at an increasingly rapid rate. This issue has so far been underestimated, resulting in a significant gap in ecotoxicological data. To comprehensively assess the risks associated with dumped chemical weapons, it is necessary to analyse the toxicity of CWAs to aquatic organisms, including fish.

The aim of the study was to evaluate the acute and chronic toxicity of selected CWAs to fish. Standardized tests (No. 236 and 215) from the OECD guidelines were used, along with the model organism *Danio rerio*. A multi-biomarker approach was applied, including the assessment of basic toxicity parameters (mortality, growth rate), toxicity thresholds (LC₅₀, EC₁₀, EC₂₀, EC₃₀), bioaccumulation of CWAs, expression levels and activity of molecular markers of oxidative stress, as well as effects on the intestinal microbiota of fish.

The study determined the acute toxicity profile for eight organoarsenic and eight organosulfur CWAs, as well as the chronic toxicity profile for two organoarsenic CWAs. The results provide valuable data on the potential ecological risks associated with CWAs and contribute to a better understanding of their short- and long-term environmental effects. The research was funded by grant no. 2020/37/N/NZ8/04099 from the National Science Centre (Poland), as well as by grant No. C056 BSR INTERREG, Marine Munition Remediation Roadmap (MUNIMAP).

Keywords: marine-dumped chemical weapons, zebrafish, ecotoxicity

BIOMIMETIC APPROACHES IN DESIGNING EFFECTIVE MATERIALS FOR ELECTROCHEMICAL CO₂ REDUCTION

Patrycja Kolbusz¹

¹ Department of Semiconductors, Photophysics and Electrochemistry, Academic Centre for Materials and Nanotechnology, AGH University of Krakow, al. Adama Mickiewicza 30, 30-059 Kraków, Poland

**corresponding author's e-mail address: pkolbusz@agh.edu.pl*

The growing demand for sustainable energy solutions makes electrochemical CO₂ conversion an essential component of low-carbon technologies. One of the main challenges in this field is the development of catalytic materials that combine high activity, selectivity, and long-term stability under realistic electrochemical operating conditions. Valuable inspiration comes from processes observed in nature, where numerous enzymes convert CO₂ under mild energetic requirements by utilizing precisely shaped metal centers and well-organized reaction environments.

This work outlines approaches that translate these natural mechanisms into modern biomimetic material design. The discussion highlights the importance of metal coordination environments, functional groups capable of stabilizing intermediate CO₂ species, and material architectures that support efficient electron and proton transfer. Attention is also given to hybrid systems that integrate organic and inorganic components to achieve greater durability than enzymatic structures while maintaining high reaction selectivity.

The presented perspectives demonstrate that biomimicry offers a promising route toward creating more efficient and resilient catalysts for next-generation CO₂ conversion technologies, supporting the development of future low-emission energy systems.

Keywords: biomimetic materials; CO₂ reduction; electrocatalysis; hybrid systems

ENGINEERING CONTROLLABLE RIBOSOME-INACTIVATING PROTEINS

Fatima Bibi¹, Jakub Czapinski¹, Krystian Łopucki², Marek Tchórzewski², Przemysław Grela²,
Adolfo Rivero-Müller¹

¹*Department of Biochemistry and Molecular Biology, Faculty of Medical Sciences, Medical University of Lublin,* ²*Department of Molecular Biology, Faculty of Biology and Biotechnology, Institute of Biological Sciences, Maria Curie-Skłodowska University, Lublin.*

65796@umlub.edu.pl

Ribosome-inactivating proteins (RIPs), are highly potent RNA N-glycosidases that inhibit protein synthesis by depurinating the 28S rRNA sarcin–ricin loop, triggering translational arrest and cell death. Their remarkable cytotoxicity has attracted attention in biomedical research and made them promising candidates for targeted anti-cancer therapies. However, despite many years of research, their therapeutic application is limited by uncontrolled basal activity, leaky intracellular expression, and incomplete understanding of the molecular mechanisms underlying their cytotoxicity.

To overcome these challenges, we developed a genetically encoded system for conditional activation of RIPs that enables precise temporal and spatial control of their activity in living cells. In one approach, a RIP is split into two inactive fragments that reconstitute functional activity via split-intein rejoining mechanism. In a parallel strategy, full-length RIP variants are designed to remain inactive until activated by a specific protease.

This platform integrates state-of-the-art transcriptional and post-translational regulation tools, including inducible or cell type-specific promoters, epitope tagging, and spatiotemporal regulation, allowing precise modulation of RIPs expression levels, subcellular localization, and catalytic activity. By enabling quantitative analysis of ribosomal depurination and downstream cytotoxic signaling, this system provides mechanistic insight into RIP-mediated cell death. Overall, this approach establishes a robust framework for engineering safer and targetable RIP-based therapeutics, offering both a versatile research tool and a potential avenue for next-generation targeted anti-cancer strategies.

Source of financing: *Polish National Science Centre grant no.2022/45/B/NZ3/02353 (OPUS 23).*

Keywords: ribosome, translation inhibition, rips, ribosomal depurination, toxins

SPECIALIZED RIBOSOMES IN HEALTH AND DISEASE

Volodymyr Shynkivskiy¹; Eliza Molestak²; Barbara Michalec-Wawiórka²; Marek Tchórzewski²;
Adolfo Rivero-Müller¹

¹ *Faculty of Medical Sciences, Department of Biochemistry and Molecular Biology,
Medical University of Lublin, Witolda Chodźki 1, Lublin*

² *Department of molecular Biology, University of Maria Curie-Skłodowska in Lublin, Akademicka 19,
Lublin*

62734@umlub.edu.pl

Ribosomes are the main players of the translational machinery. Protein expression level and cell proteome composition are thus influenced by the abundance and availability of ribosomes, ribosomal composition, translational efficiency, as well as stress conditions. In cancer cells, extensive alterations of protein expression levels can be detected, which influence their growth and proliferation rate. The main goal of our research is to identify the role of ribosomal protein isoforms/paralogs on translation and/or their non-ribosomal functions in the cell.

We have found that an isoform of ribosomal protein RPLP0 (uL10), named uL10 β , may accumulate in the nucleus and tend to relocalize to the vicinity of mitochondria upon ER stress conditions. Initially, to determine whether uL10 α and uL10 β forms are overrepresented in different cancer types, bioinformatic analysis of available RNA-seq data was performed. Data pointed toward that hematopoietic stem and progenitor cells display the highest ratio of uL10 β when mutation of P53 is present. To further experimentally analyse the behavior of uL10 β , especially whether it can become a part of the ribosome, a genetic construct was prepared to express fusion protein uL10 β -GFP in cell lines to test the behavior of the ribosome protein in *cellulo* as well as its integration into the ribosomal particles.

(Finance source: DS 717; UMO-2022/45/B/NZ3/02353)

Keywords: Ribosomal proteins, splicing, protein isoforms, ribosome heterogeneity

TERPYRIDINE-THIOSEMICARBAZONE HYBRID CHELATORS TARGET IRON-DRIVEN REDOX VULNERABILITIES IN GLIOBLASTOMA MODELS

Kajetan Reguła^{1*}, Patryk Ziola¹, Jacek Mularski², Katarzyna Malarz¹, Piotr Bartczak²,
Patrycja Rawicka¹, Robert Gawecki¹, Barbara Broł², Robert Musioł²,
Anna Mrozek-Wilczkiewicz^{1,3}

¹A. Chełkowski Institute of Physics, University of Silesia in Katowice, 75 Pułku Piechoty 1a, 41-500 Chorzów, Poland

²Institute of Chemistry, University of Silesia in Katowice, 75 Pułku Piechoty 1a, 41-500 Chorzów, Poland

³Department of Systems Biology and Engineering, Silesian University of Technology, Akademicka 16, 44-100 Gliwice, Poland

*adres e-mail autora do korespondencji: Kajetan.regula@us.edu.pl

Glioblastoma multiforme (GBM) remains the most common and highly aggressive primary brain tumour in adults and is characterised by rapid infiltration, pronounced molecular heterogeneity, and early emergence of therapy resistance. Current standard-of-care (surgery followed by radio- and chemotherapy) provides only limited survival benefit, underscoring the need for strategies that exploit vulnerabilities shared across GBM subtypes. One such vulnerability is iron dependence: GBM cells exhibit elevated demand for bioavailable iron to sustain proliferation and metabolism, yet iron also amplifies reactive oxygen species (ROS) chemistry, creating a tractable “need–danger” axis for therapeutic intervention.

Here, we present a library of terpyridine–thiosemicarbazone (TST) compounds designed as “hybrid chelators” by combining two metal-binding motifs to enhance metal complexation and disrupt iron-linked redox homeostasis. Antiproliferative activity was assessed in a panel of established GBM cell lines in 2D monolayers and then examined in 3D spheroids to better capture tumour-like microenvironmental constraints and resistance mechanisms.

Spectroscopic analyses support iron binding consistent with terpyridine-associated complex formation. Mechanistic readouts in 3D GBM spheroids indicate increased oxidative stress accompanied by engagement of antioxidant defences (e.g., elevated glutathione/GPX4 and changes in iron-transport/redox-associated proteins), while lipid peroxidation is not increased, arguing against ferroptosis as the dominant death route. Collectively, these findings position TST hybrids as a promising platform to probe and therapeutically target iron–redox biology in GBM.

Keywords: iron chelation, GBM, terpyridine, cancer treatment

COMPARISON OF CHEMICAL COMPOSITION OF SCOTS PINE WOOD AND KENAF BIOMASS AFTER ACID HYDROLYSIS PRETREATMENT

Ghita Firsty Virginia^{1*}, Andrzej Antczak¹, Monika Marchwicka¹, Jin Hyung Lee²,
Soo-Jeong Shin³

¹*Institute of Wood Sciences and Furniture, Warsaw University of Life Sciences-SGGW, 159
Nowoursynowska St., 02-776 Warsaw, Poland*

²*Korea Institute of Ceramic Engineering and Technology, Cheongju 28160, Republic of Korea*

³*Department of Wood & Paper Science, Chungbuk National University, Cheongju 28644, Republic of
Korea*

**corresponding author's e-mail address: ghita_virginia@sggw.edu.pl*

Acid hydrolysis (AH) is widely used as a pretreatment for biomass to obtain cellulose, which can be processed into glucose. The chemical composition of biomass is varied. It is known that the lignin content in softwood, such as pine, is high compared to hardwood or crops, which, on the contrary, have a high hemicelluloses content. This study compared sulfuric acid treatment of Scots pine wood and kenaf core fiber to test the ability of AH as a pretreatment to isolate cellulose and will serve as the starting point for determining optimal pretreatment conditions. Sulfuric acid was used as pretreatment agent at a 1:10 w/w solid/liquid ratio. Scots pine wood was treated with 3% of H₂SO₄ in 3h, while kenaf biomass was treated with 2.5% of H₂SO₄ in 2 h at 120 °C, and its chemical compositions were determined. Significant results showed that the solid recovery from kenaf core was only 51.5%, while Scots pine wood had a higher recovery (80.0%), even though the acid concentration was higher and the pretreatment duration longer. As a result, lignin in kenaf was reduced to only 10% after pretreatment, while Scots pine retained a high lignin content (32.6%), reducing it by only about 9.1%. In the interim, cellulose content from the kenaf core was lower(49.5%) than that from Scots pine wood (53%). After AH pretreatment the hemicelluloses contents were 0.9 % and 1.5% for Scots pine wood and kenaf core, respectively. The studies conducted concern an important issue related to bioethanol production technology.

Keywords: acid hydrolysis pretreatment, lignin removal, cellulose and hemicelluloses content

FASTING INDUCED CHANGES IN SERUM KYNURENINES DOES NOT ALWAYS REFLECT THEIR URINARY EXCRETION

Zuzanna Margas¹, Andżelika Borkowska¹, Anna Pilis², Jędrzej Antosiewicz¹

¹*Division of Bioenergetics and Physiology of Exercise, Medical University of Gdańsk*

²*Department of Health Sciences and Physiotherapy, Jan Długosz University in Częstochowa*

* zuzanna.margas@gumed.edu.pl

Background: The effects of fasting on serum kynurenines (KYNs) have been reported; however, no data are available on whether fasting also modifies their urinary excretion. Kidney organic anion transporters are involved in KYNs excretion, suggesting that changes in serum levels may result from altered urinary elimination. Considering the important role of KYNs in regulating various physiological processes, it is crucial to understand the factors that determine their blood concentrations. The present study aimed to determine the effect of an 8-day fasting period on the concentrations of KYNs in both serum and urine.

Methods: Thirteen participants underwent an 8-day fast. The exercise test was performed at baseline after an overnight fast and after 8 days of fasting.

Results: Fasting increased the serum concentrations of 3-hydroxykynurenine (3-HK), anthranilic acid (AA), picolinic acid (PA), kynurenic acid (KYNA), and xanthurenic acid (XANA). Conversely, serum kynurenine (KYN) and quinolinic acid (QA) decreased, while 3-hydroxyanthranilic acid (3-HAA), remained unchanged. In urine, KYN, 3-HK, XANA and QA increased after fasting, whereas AA and PA did not change.

Conclusions: In conclusion, these findings indicate that fasting generally increases serum kynurenines (KYNs), which is associated with enhanced urinary excretion, suggesting that fasting may stimulate their synthesis. In the case of anthranilic acid (AA) and picolinic acid (PA), their increase in serum does not influence their urinary excretion. Conversely, a decrease in serum KYN and quinolinic acid (QA) may result from enhanced urinary excretion.

Keywords: kynurenine metabolites; picolinic acid; anthranilic acid; exercise; urine

ONE TICKET, TWO JOURNEYS: TWO APPROACHES TO EFFICIENT NEGISHI CROSS-COUPLING FOR ACCESSING DIARYLMETHANES - THE CASE OF A PHENOXIMINATO COBALT(II) CATALYST

Jakub Robaszkiewicz^{1,2}, Wojciech Chałada³, Maciej Zaranek^{1,2}, Piotr Pawluć^{1,2}

¹*Faculty of Chemistry, Adam Mickiewicz University, Poznan, Poland*

²*Center for Advanced Technologies, Poznan, Poland*

³*Institute of Organic Chemistry, Polish Academy of Sciences, Warsaw, Poland*

jrobaszkiewicz@amu.edu.pl

The transition from precious-metal catalysis toward sustainable alternatives remains a central challenge in modern cross-coupling chemistry. Although cobalt has emerged as a promising earth-abundant metal, practical homogeneous systems for Negishi reactions operating with low catalyst loadings and simple components remain rare. In particular, efficient access to sp²–sp³ carbon–carbon bonds leading to diarylmethane scaffolds—privileged motifs in medicinal chemistry—still relies largely on nickel or palladium catalysis.

Herein, we present a phenoximinato cobalt(II) catalyst enabling two complementary Negishi cross-coupling pathways that converge on diarylmethane synthesis. The first strategy employs aryl bromides and benzylzinc bromide, delivering high conversions and excellent selectivity under operationally simple conditions. Systematic optimisation identified THF as a key medium while maintaining catalyst efficiency at only 2 mol%.

Remarkably, reversing the polarity of the coupling partners establishes a second catalytic regime in which phenylzinc reagent react with benzylic electrophiles, allowing catalyst loadings as low as 0.5 mol% with near-quantitative conversions. Both approaches display broad functional-group tolerance, including heteroarenes and challenging electrophiles such as aryl chlorides. The synthetic relevance of the methodology was demonstrated through derivatisation of diarylmethanes and the direct preparation of pharmaceutically relevant structures, including tesmilifene derivatives. These findings reveal that structurally simple phenoximinato cobalt complexes can unlock distinct catalytic manifolds within a single platform.

This work positions cobalt as a practical alternative to noble metals and highlights ligand-design-enabled catalyst simplicity as a powerful strategy for sustainable sp²–sp³ cross-coupling chemistry.

Key words: catalysis, cross-coupling reaction, Negishi cross-coupling, cobalt

THE SECOND LIFE OF BREWER'S SPENT GRAIN: GREEN POLYPHENOL EXTRACTION

Łukasz Steczko¹, Renata Jastrząb²

^{1,2}*Adam Mickiewicz University, Faculty of Chemistry, Department of Coordination Chemistry, Uniwersytetu Poznańskiego 8, 61-614 Poznań, Poland*

**adres e-mail autora do korespondencji: lukasz.steczko@amu.edu.pl*

Brewer's spent grain (BSG) is the main by-product of the brewing industry, accounting for approximately 85% of the total waste generated during the beer production process. Over 38 million tons of BSG are produced worldwide. Despite its high fiber content and the removal of phenolic compounds, including ferulic acid, p-coumaric acid, and lignin derivatives, this raw material is primarily used as animal feed. At the same time, the bioactive polyphenols with antioxidant, anti-inflammatory, and antimicrobial properties that are available are underutilized as a potential source of energy, nutraceuticals, and other beneficial effects.

The aim of this work is to provide a review of polyphenol extraction methods from BSG, considering both process efficiency and compliance with green chemistry principles. Conventional extraction techniques employing organic solvents (ethanol, methanol) and alkaline solutions (NaOH) are discussed, alongside assisted methods such as ultrasound-assisted, microwave-assisted, and supercritical CO₂ extraction. Particular attention is given to deep eutectic solvents (DES/NADES) as a promising and more sustainable alternative to traditional extraction methods. Their physicochemical properties and influence on extraction yield and antioxidant activity of the obtained extracts are discussed.

A significant research gap has been identified in the lack of comprehensive comparative studies evaluating not only extraction efficiency, but also phenolic profiles, biological activity of the extracts, and the scalability potential of the processes under industrial conditions.

Keywords: brewer's spent grain, polyphenols, extraction methods, green chemistry, deep eutectic solvents

Critical Lithium Threshold for Chlorophyll Content in Maize Cultivated in Contrasting Brazilian Soils

Willian Cleisson Lopes de Souza^{1*}, Enilson de Barros Silva¹, Flávia de Jesus Costa¹, Ana Cláudia Nunes¹, Dawid Świstak², Małgorzata Wójcik², Jaco Vangronsveld²

¹ *Department of Agronomy, Faculty of Agricultural Sciences, Federal University of Jequitinhonha and Mucuri Valleys, Diamantina, MG 39100-000, Brazil*

² *Department of Plant Physiology and Biophysics, Institute of Biological Sciences, Maria Curie-Skłodowska University, Akademicka 19, 20-033 Lublin, Poland*

*corresponding author's e-mail address: willian.lopes@ufvjm.edu.br

Maize (*Zea mays* L.) is a strategic crop for lithium (Li) phytoremediation assays due to its high biomass and agronomic relevance. However, critical Li thresholds in Brazilian soils remain undefined. This study aimed to determine the critical Li concentration based on chlorophyll *a* and *b* contents in maize grown in three contrasting Brazilian soils classified as Typic Quartzipsamments and Typic Hapludox (clayey and medium-textured). A greenhouse experiment was conducted in a randomized block design with five replicates, using five Li concentrations (0, 12.5, 25, 50, and 100 mg kg⁻¹) applied to pots with 3 kg of soil at 60% field capacity. Four seeds were sown per pot and thinned to one plant 15 days after sowing. Chlorophyll *a* and *b* were measured 50 days after thinning using a portable chlorophyll meter. Data were analyzed by ANOVA followed by Tukey test (5%). Li significantly reduced chlorophyll *a* and *b* in maize, with effects intensifying as concentrations increased. Concentrations up to 25 mg kg⁻¹ remained similar to the control, whereas 50 mg kg⁻¹ promoted marked declines and 100 mg kg⁻¹ caused the greatest reductions, indicating photosynthetic impairment. Chlorophyll *a* showed greater sensitivity in Typic Quartzipsamments, with earlier decreases, while both Typic Hapludox soils remained comparatively stable until the highest Li dose. The observed pigment decline suggests Li-induced disruption of photosynthesis, possibly associated with altered nutrient uptake and structural destabilization of chloroplast membranes. Overall, chlorophyll reduction intensified above 50 mg kg⁻¹, indicating a critical Li threshold of 50-100 mg kg⁻¹ for maize.

Keywords: Lithium toxicity; Tropical soils; Soil contamination.

DROUGHT RESPONSE MECHANISMS IN THE FESTUCA AMETHYSTINA POLYPLOID COMPLEX: PHYSIOLOGICAL DIFFERENTIATION AND TRANSCRIPTOMIC PERSPECTIVES

Adnan Akbar^{1,2}, Aamir Hamid Khan¹, Marcin Kiedrzyński^{1*}

¹*Department of Biogeography, Paleoecology and Nature Conservation, Faculty of Biology and Environmental Protection, University of Lodz, Banacha 1/3, 90-237 Lodz, Poland*

²*Doctoral School of Exact and Natural Sciences, University of Lodz, Poland*

**corresponding author's e-mail address: marcin.kiedrzyński@biol.uni.lodz.pl*

The grass species *Festuca amethystina* and *Festuca tatrae*, found across mountain–lowland gradients, are rare taxa exhibiting cytotypic variation at the diploid and tetraploid levels. Understanding their adaptive potential under increasing drought stress is critical in the context of climate change. We conducted a 14-day controlled drought experiment using 69 genotypes representing three cytotypes: *F. tatrae* (2x), *F. amethystina* (2x), and *F. amethystina* (4x). Physiological and biochemical parameters were assessed, including soil moisture, plant height, chlorophyll content, and reactive oxygen species (ROS) accumulation. The results revealed significant inter- and intra-specific variation in drought responses. Tetraploid *F. amethystina* (4x) demonstrated superior drought resilience compared to diploid cytotypes. This enhanced tolerance was associated with improved maintenance of chlorophyll content and more efficient regulation of oxidative stress. Principal Component Analysis (PCA) based on chlorophyll and ROS parameters clearly differentiated tolerant and sensitive genotypes. To uncover the molecular basis of these differences, three contrasting genotypes (plants 62, 60, and 44), originating from different geographic locations, have been RNA sequenced. Comparative transcriptomic analyses identified differentially expressed genes (DEGs) associated with drought tolerance and evaluated whether stress-response patterns correlate with cytotype and habitat origin. Genes and pathways have been identified for further studies. This integrative physiological and transcriptomic approach advances our understanding of polyploidy-driven adaptation in *Festuca* species and provides essential knowledge for conservation strategies in the context of ongoing climate change.

Keywords: drought, *Festuca*, polyploidy, RNA-seq, stress

PHARMACOMICROBIOMICS OF SELECTED ANTISEIZURE DRUGS: A REVIEW OF CURRENT SCIENTIFIC RESEARCH

Agata Matuła^{1,2*}, Piotr Właź², Katarzyna Socala²

*¹Doctoral School of Quantitative and Natural Sciences, Maria Curie-Skłodowska University,
Weteranów 18, 20–038 Lublin, Poland*

*²Biomedical Research Laboratory, Institute of Biological Sciences, Maria Curie-Skłodowska University,
Akademicka 19, 20–033 Lublin, Poland*

**agata.m.matula@gmail.com*

Epilepsy is a chronic neurological disorder characterized by recurrent seizures caused by excessive neuronal synchronization, which means excessive simultaneous excitation of many nerve cells. Antiseizure drugs such as valproic acid, lamotrigine, or levetiracetam have various mechanisms of action, including modulation of ion channels, GABAergic and glutamatergic systems, inhibition of enzymes responsible for neurotransmitter metabolism, or complex action. There is growing evidence that these drugs may also affect the gut microbiota, which in turn may modify the effectiveness of therapy and the patient's health and well-being. In preclinical studies investigating the role of the microbiota in epilepsy and its treatment using laboratory animals (mice and rats), various seizure models have been employed, including the MES test (maximal electroshock seizure) as well as models of seizures induced by PTZ (pentylene-tetrazol), kainic acid, or pilocarpine. The results obtained indicate that changes in the composition of the microbiota may be involved in antiseizure mechanisms, including modulation of short-chain fatty acids (SCFAs) metabolism and GABA/glutamate balance in the brain. These data highlight the significance of pharmacomicrobiomics in understanding differences in response to antiseizure therapy and open up prospects for personalized epilepsy treatment strategies, hence the need for further research in this area.

Keywords: epilepsy, antiseizure drugs, gut microbiota, seizure models, pharmacomicrobiomics

THE INFLUENCE OF ENCAPSULATION METHOD ON FLAVOR RELEASE FROM COATINGS

Agnieszka Kłosowska^{1,2}, Agata Wawrzyńczak¹, Agnieszka Feliczak-Guzik¹

¹ *Department of Applied Chemistry, Faculty of Chemistry, Adam Mickiewicz University in Poznań, Uniwersytetu Poznańskiego 8, 61-614 Poznań, Poland;*

² *Arcon Lab sp. z o.o., ul. Obornicka 309, 60-689 Poznań, Poland;*

**corresponding author's e-mail address: agnklo3@amu.edu.pl*

Flavors are complex mixtures of volatile organic compounds with diverse physicochemical properties that are highly susceptible to degradation under environmental factors such as temperature, UV radiation, oxygen, and humidity. Encapsulation is considered one of the most effective methods for protecting such sensitive ingredients and controlling their release. Numerous encapsulation techniques have been developed, each characterized by specific advantages and limitations, including capsule structure, stability, loading capacity, size, and release behavior. This study presents and compares two encapsulation methods: extrusion and an alginate-based dripping technique. In the extrusion process, flavor compounds were incorporated into a molten carbohydrate matrix under shear forces and subsequently solidified upon cooling, forming physically entrapped capsules. In contrast, the dripping method enables capsule formulation via ionic cross-linking of alginate during dripping into a solution. The loading capacity, encapsulation efficiency, and release of flavor compounds were evaluated using Gas Chromatography-Mass Spectrometry (GC-MS) and Solid Phase Microextraction- Gas Chromatography-Mass Spectrometry (SPME-GC-MS) analyses after application of the capsules to green tea. The results clearly show differences in encapsulation efficiency and release profiles between the two methods, highlighting the potential for optimizing flavor delivery in food applications.

Keywords: flavor encapsulation, alginate, ionic cross-linking, extrusion

STRUCTURAL FEATURES OF QUATERNARY AMMONIUM SALTS AS DETERMINANTS OF TOXICITY AND ENVIRONMENTAL BEHAVIOUR

Aleksandra Pomykała¹, Joanna Feder-Kubis¹, Marta Markiewicz², Stefan Stolte²

¹*Faculty of Chemistry, Department of Bioorganic Chemistry, Wrocław University of Science and Technology, Wybrzeże Wyspiańskiego 27, Wrocław 50-370, Poland*

²*Faculty of Environmental Sciences, Department of Hydrosociences, Institute of Water Chemistry, Technische Universität Dresden, Bergstrasse 66, 01069 Dresden, Germany*

**adres e-mail autora do korespondencji: aleksandra.pomykala@pwr.edu.pl*

Chemical research places strong emphasis on sustainable development and the principles of green chemistry, with particular focus on minimising environmental impact while maintaining functional performance. Quaternary ammonium salts (QAS), including surfactants, ionic liquids (ILs) and deep eutectic solvents (DES), are widely used in numerous industrial sectors. As a result of their extensive and growing use, both in academic research and industrial practice, global consumption of QAS is steadily increasing, leading to their growing presence in wastewater and aquatic environments. Their persistence and potential bioaccumulation raise significant environmental and toxicological concerns, and the environmental profile of QAS has become a key factor in determining their continued use and regulatory acceptance.

The current scientific literature discusses in detail the influence of the main structural components—the type of amine core, the length of the alkyl chain, and the anion type—on environmental behaviour and toxicity. Despite this well-established body of knowledge and the comparable maturity of symmetrical and asymmetrical QAS chemistry, the role of molecular symmetry within the QAS cation remains surprisingly underexplored in the context of environmental and toxicological evaluation.

By analysing structure–toxicity relationships with respect to cation symmetry, the present project addresses this critical knowledge gap and introduces a new perspective on the environmental classification of QAS. The resulting framework provides an additional, previously underexplored criterion for the informed design and selection of QAS with a defined and application-oriented environmental profile, supporting the future development of quaternary ammonium-based compounds whose functionality can be balanced with environmental considerations.

Keywords: Quaternary ammonium salts, toxicity, biodegradation

BEYOND APOPTOSIS: CALPAINS AS A GUARDIAN OF IMMUNE QUIESCENCE AND SELF-TOLERANCE – A SYSTEMATIC REVIEW

^{1*}Ashfaq Ahmad, ²Tamas Fulop, ^{1*}Jacek M. Witkowski

1 - corresponding authors; Department of Embryology, Medical University of Gdańsk, Gdańsk, Poland; jacek.witkowski@gumed.edu.pl, ashfaq.ahmad@gumed.edu.pl*

3 - Research Center on Aging, Graduate Program in Immunology, Faculty of Medicine and Health Sciences, University of Sherbrooke, Sherbrooke, QC, Canada

The immune system maintains a delicate balance between rapid pathogen defence and self-tolerance. Calpains (CAPN1 and CAPN2), traditionally viewed as executors of apoptosis, are now recognised as master regulators of lymphocyte quiescence and immune homeostasis. This systematic review (PRISMA 2020, PubMed/Web of Science/Scopus, 2000–2025) challenges the classical pro-apoptotic paradigm and demonstrates that calpains function as molecular checkpoints. Through limited proteolysis of key substrates (CD3 ζ , ZAP-70, LAT, NF- κ B p65, Cyclin D1, c-Myc, and mTORC1 regulators), calpains suppress spontaneous T-cell activation, enforce metabolic restraint, and set activation thresholds that prevent auto-reactivity. Dysregulation of the calpain–calpastatin system contributes to autoimmune diseases (RA, MS, SLE), chronic inflammation, and altered immune responses in cancer. We further discuss therapeutic potential: isoform-selective inhibitors (SNJ-1945, CYLA), CRISPR-based modulation, and calpain activity as a novel biomarker of immune dysregulation and immunotherapy response. Open questions include whether targeted calpain modulation can restore tolerance without broad immunosuppression and its role in T-cell exhaustion in cancer. By repositioning calpains as guardians of immune quiescence, this review opens new frontiers in precision immunotherapy and autoimmune disease management.

Keywords: Calpains, Lymphocyte quiescence, Immune homeostasis, Autoimmune diseases, APOPTOSIS

PRODUCTION OF FUNCTIONAL PECTIN-BASED MATERIALS BY EXTRUSION USING SELECTED PLASTICIZERS

Diana Magdalena Lesiak*¹, Marta Fiedot¹ oraz Konrad Szustakiewicz¹

¹*Department of Polymer Engineering and Technology, Faculty of Chemistry, Wrocław University of Science and Technology, 27 Wybrzeże Stanisława Wyspiańskiego; 50-370 Wrocław*

** the author's email address for correspondence: diana.lesiak@pwr.edu.pl*

Pectin is a natural polysaccharide that forms gels and polymer networks, its structure and ionic conductivity change under pressure. It is flexible and easily modifiable (amidated). It represents a promising raw material for the production of functional biodegradable materials with pressure-dependent sensory properties. The aim of this study was to produce pectin- and water-based materials using the extrusion method and to investigate the effect of the type of plasticiser on their thermal, mechanical and piezoresistive properties. Three different plasticisers were used in the process: polyethylene glycol (PEG 400), glycerol and xylitol.

The resulting materials were characterised in terms of extrusion process efficiency, in particular their ability to form a homogeneous strand of constant diameter, their elasticity, and changes in electrical properties in response to applied pressure.

It was demonstrated that each of the plasticisers used interacts differently with the pectin matrix, leading to variations in the final properties of the materials. Glycerol promoted the production of high-strength materials, PEG improved the cohesion of the mixture, facilitating its processing in the extruder, whilst xylitol increased stiffness and imparted gloss.

The results obtained show that by selecting the suitable plasticizer, it is possible to control the physicochemical properties of pectin-based functional materials produced by extrusion.

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Keywords: extrusion, pectin, plasticisers, functional materials

NANOPOROUS SULFUR-DOPED CARBON COMPOSITES FOR ADSORPTION OF PLATINUM-BASED ANTICANCER DRUGS

Marlena Bytniewska¹, Dominika Fila¹, Anna Michalicha², Mariusz Barczak¹,
Dorota Kołodyńska¹, Anna Belcarz-Romaniuk²

¹*Institute of Chemical Sciences, Faculty of Chemistry, Maria Curie-Skłodowska University,
Maria Curie-Skłodowska Sq. 5, 20-031 Lublin, POLAND*

²*Chair and Department of Biochemistry and Biotechnology, Faculty of Pharmacy, Medical University of
Lublin, ul. Chodźki 1 (Collegium Universum), 20-093 Lublin, POLAND*

marlena.bytniewska@mail.umcs.pl

Platinum-based anticancer drugs are used in up to 70% of chemotherapy treatments. A significant part of these compounds is excreted from the patient's body, mainly in urine, and enters wastewater, where they become persistent and potentially harmful environmental pollutants. Platinum compounds can interact with proteins, peptides, and DNA, causing damage to living cells and leading to allergic reactions or inflammation, for example during occupational exposure to platinum salts. At the same time, platinum is a metal of high economic value, and its recovery may provide both environmental and economic benefits by enabling its reuse in electrochemistry, pharmacy, dentistry, and industry.

To address this issue, hospital wastewater treatment systems are being developed, often based on adsorption due to its high efficiency and relatively low cost. However, the effectiveness of sorption processes depends on the use of efficient and affordable sorbents. Various materials have been studied for this purpose, including resins, MOFs, magnetic nanoparticles, polymers, biomass, and activated carbons.

In this study, sulfur-doped carbon composites (STACs) were proposed as materials for the adsorption of chemotherapeutic drugs. Controlled sulfur content and tunable porosity make them promising for environmental applications. The materials were synthesized using the sustainable SASI method (Steam Assisted Sulfur Insertion).

Nanoporous STACs were applied for the removal of platinum-based cytostatic drugs (cisplatin, oxaliplatin, and carboplatin) from water and model hospital wastewater. The materials showed high adsorption efficiency, enabled partial recovery of platinum compounds, and demonstrated antibacterial activity.

Acknowledgements: This research was funded by the Polish National Science Centre, grant number 2023/51/B/ST5/01911, titled *Novel sulfur-tuned advanced carbons: synthesis, characterization and applications*.

Keywords: platinum, chemotherapy, adsorbents, wastewater, recovery

FROM SEIZURE CONTROL TO DISEASE MODIFICATION: EMERGING STRATEGIES IN EPILEPSY THERAPY

Nikola Gapińska^{1,2*}, Ewelina Mitura¹, Katarzyna Socala¹

¹ *Biomedical Research Laboratory, Faculty of Biology and Biotechnology, Institute of Biological Sciences, Maria Curie-Skłodowska University, Akademicka 19, 20-033 Lublin, Poland*

² *Doctoral School of Quantitative and Natural Sciences, Maria Curie-Skłodowska University, Weteranów 18, 20-038 Lublin, Poland*

*corresponding author's e-mail address: nikola.gapinska@poczta.umcs.pl

Over the past decade, epilepsy research has undergone a transformative shift, moving beyond symptomatic seizure control toward precision, disease-modifying, and preventive strategies. Advances in genetics, the development of novel preclinical models, and innovative drug discovery platforms have generated a rich pipeline of therapies spanning small molecules, gene- and oligonucleotide-based treatments, neuroactive steroids, and neuromodulation approaches.

The recent characterization of monogenic epilepsies has enabled the development of targeted therapies, including antisense oligonucleotides and gene supplementation strategies, exemplified by STK-001 for SCN1A-related Dravet syndrome. Novel pharmacological approaches targeting GABAergic transmission, glutamate receptors, voltage-gated ion channels, and cation–chloride cotransporters are under investigation, with some compounds demonstrating subtype selectivity to enhance efficacy while minimizing adverse effects. Additionally, repurposed drugs and multimodal compounds are being evaluated to optimize therapeutic outcomes.

Parallel efforts in epilepsy prevention aim to intervene during epileptogenesis following acute central nervous system insults, such as traumatic brain injury or stroke. Preclinical and early clinical studies suggest that early intervention with agents such as levetiracetam, vigabatrin, or statins may reduce the likelihood of developing epilepsy. Emerging biomarkers, including continuous EEG monitoring and advanced neuroimaging, may further guide individualized preventive strategies.

Collectively, these advances signal a paradigm shift in epilepsy therapy, integrating mechanistic understanding, precision medicine, and preventive interventions. The future of epilepsy treatment may not only suppress seizures but also modify disease progression, reduce comorbidities, and enable personalized therapeutic approaches.

Keywords: epilepsy, epileptogenesis, disease-modifying therapies, precision medicine, antiseizure therapies

STRUCTURE-FUNCTION OF RIBOSOME INACTIVATING PROTEINS

Prasad Kumar Mohite*¹, Przemysław Grela¹ and Marek Tchórzewski¹

¹*Department of Molecular Biology, Institute of Biological Sciences, Maria Curie-Skłodowska University in Lublin, Poland*

*e-mail: kunalakaprasad@gmail.com

Ribosome-inactivating proteins (RIPs) constitute a diverse family of cytotoxic enzymes produced predominantly by plants, although related proteins are also found in bacteria and fungi. RIPs function as highly specific RNA N-glycosidases that irreversibly inhibit protein synthesis by depurinating a single, universally conserved adenine residue within the sarcin–ricin loop (SRL) of 28S rRNA. This modification disrupts binding of translational GTPases and thus abolishes elongation factor–dependent GTP hydrolysis, effectively inactivating the eukaryotic translational machinery. RIPs are structurally classified into: type I categories, consisting of a single catalytic A chain (e.g., Saporin, Trichosanthin); type II, composed of an enzymatic A chain linked to a lectin-like B chain (e.g., Ricin and Shiga toxins), where the B subunit mediates cell surface binding and endocytic uptake; type III, (e.g., MOD) where they exist as inactivated proenzymes which upon proteolytic processing becomes active. High-resolution crystallographic studies, cryo-electron microscopy, and biochemical analyses have revealed key determinants of ribosome recognition, showing that interactions with ribosomal P-stalk proteins facilitate recruitment of RIPs to the SRL. Also, structural insights into active-site organization, substrate mimicry, and conformational dynamics have clarified the molecular basis of catalytic specificity and extraordinary efficiency.

Here, we present recent advances integrating structural biology, cell biology, and molecular mechanistic studies, that have substantially refined our understanding of RIP–ribosome interactions, and ribosome inactivation. These findings show fundamental aspects of RIP architecture and function, but also may lay the foundation for translational medicine, where we can repurposed them from natural toxins into precision tools for targeted oncology, antiviral strategies, and other applications.

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Keywords: ribosome-inactivating proteins (RIPs), ribosome, sarcin–ricin loop (SRL), depurination, P-stalk proteins, translational inhibition

THE EFFECT OF CEFIDEROCOL AND POLYMYXIN B IN MONOTHERAPY AND COMBINATION THERAPY ON THE GROWTH AND BIOFILM FORMATION OF *PROTEUS MIRABILIS*

Wanesa Sasal¹, Dawid Gmitter²

¹*Department of Microbiology, Faculty of Exact and Natural Sciences, Institute of Biology, Jan Kochanowski University in Kielce, Uniwersytecka 7, 25-406 Kielce, Poland*

²*Faculty of Biology, Institute of Microbiology, University of Warsaw, Miecznikowska 1, 02-096 Warsaw, Poland*

*corresponding author's e-mail address: wanesa.sasal.ujk@gmail.com

Proteus mirabilis is an important opportunistic pathogen associated with urinary tract infections and a strong ability to form biofilm. The increasing antibiotic resistance necessitates the search for effective therapeutic strategies, including combination therapy. The aim of this study was to evaluate the effect of cefiderocol and polymyxin B, used both in monotherapy and in combination, on planktonic growth and biofilm formation of the reference strain HI4320 and selected clinical isolates.

Growth kinetics (OD₆₀₀, 24 h) were analyzed in the presence of various concentrations of polymyxin B (5–30 µg/mL), Cef (0.25–2.5 µg/mL), and their combinations. Biofilm formation was assessed using the crystal violet staining method (OD₅₉₅).

In growth kinetics experiments, combination therapy demonstrated stronger growth inhibition compared to selected monotherapy regimens; however, the effect was concentration-dependent. In biofilm analysis, strain-dependent differences were observed. In the case of *P. mirabilis* HI4320, higher concentrations of cefiderocol were associated with increased biofilm production compared to the control, while polymyxin B exhibited a dose-dependent effect. Combination therapy did not consistently reduce biofilm formation and, in some variants, resulted in increased biofilm production compared to the control.

The obtained data indicate a complex, concentration-dependent effect of cefiderocol and polymyxin B on the physiology of *P. mirabilis*. The results highlight the need for careful interpretation of combination therapy effects in the context of biofilm-forming capacity and the necessity for further research to optimize treatment regimens.

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Keywords: *Proteus mirabilis*, Cefiderocol, Polymyxin B, Antibiotic resistance

PROBIOTICS IN THE TREATMENT OF EPILEPSY

Weronika Woźniak^{1*}, Piotr Właz¹, Katarzyna Socąła¹

¹Laboratory of Biomedical Research, Faculty of Biology and Biotechnology, Institute of Biological Sciences, Maria Curie-Skłodowska University, ul. Akademicka 19, 20-033 Lublin

* corresponding author's e-mail address: weronika.wozniak@mail.umcs.pl

Epilepsy is one of the most common neurological disorder worldwide. It is characterized by recurrent epileptic seizures resulting from incorrect electrical activity of neurons in the brain. It is estimated that approximately 65 million people worldwide suffer from this condition. Despite significant advances in medical diagnostics and therapy, epilepsy remains a major clinical challenge. Only 60–70% of patients achieve seizure control with a single antiepileptic drug. The remaining 30% of cases are classified as drug-resistant epilepsy. Moreover, long-term use of antiepileptic drugs is often associated with adverse effects that can significantly reduce patients' quality of life. For this reason, there is a need to search for new, alternative, or adjunctive therapeutic strategies.

In recent years, an increasing number of studies have indicated a potential role of the gut microbiota in the pathogenesis of epilepsy. One promising direction of adjunctive therapy is modulation of the microbiota–gut–brain axis, among others through the use of probiotics.

Probiotics play an important role in maintaining proper gut microbiota function. A balanced gut microbiome contributes to preserving the integrity of the intestinal barrier, thereby limiting its permeability. A sealed intestinal barrier prevents the development of chronic inflammation. In addition, the gut microbiota participates in the synthesis of neuroactive compounds, including serotonin and γ -aminobutyric acid (GABA), the main inhibitory neurotransmitter in the central nervous system.

Evidence from preclinical studies and limited clinical data suggest that probiotics may contribute to a reduction in the frequency and severity of epileptic seizures. However, further well-designed preclinical and clinical studies are necessary to conclusively assess the efficacy and safety of probiotics as an adjunctive therapy in the treatment of epilepsy.

Keywords: epilepsy, drug-resistant epilepsy, probiotics, microbiota

VARIABLE SENSITIVITY OF GLIOBLASTOMA CELLS TO SORAFENIB – CYTOTOXICITY STUDIES AND TYPES OF INDUCED CELL DEATH

Karolina Surowiec¹, Joanna Jakubowicz-Gil²

^{1,2} *Katedra Anatomii Funkcjonalnej i Cytobiologii, Wydziału Biologii i Biotechnologii, Instytut Nauk Biologicznych, Uniwersytet Marii Curie-Skłodowskiej, ul. Akademicka 19, 20-033 Lublin*

karolina.surowiec898@gmail.com

Glioblastoma (GBM) belongs to a group of malignant tumors of the central nervous system. It is characterized by infiltrative growth, significant molecular heterogeneity, and high resistance to treatment. Standard therapy involving surgical resection, radiotherapy, and chemotherapy allows only limited prolongation of patient survival. One of the key mechanisms underlying therapeutic resistance are disturbances in signaling pathways regulating cell proliferation and survival (including PI3K/Akt/mTOR and Ras/Raf/MEK/ERK), as well as reprogramming of lipid metabolism.

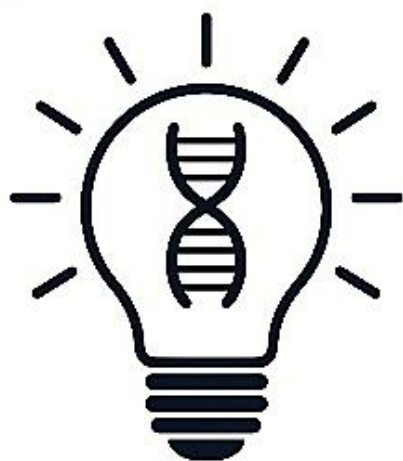
Sorafenib, an inhibitor of serine-threonine kinases including Raf kinase, induces programmed cell death in cancer cells by modulating the Ras/Raf/MEK/ERK pathway. Literature data indicate that monotherapy is less effective than combination therapy. Compounds that modulate fatty acid synthesis appear to play an important role in this context. Therefore, the aim of the study was to evaluate the effect of sorafenib in single and combination therapy with a very long-chain fatty acid (VLCFA) synthesis inhibitor on the induction of programmed cell death in primary cultures (GW01, GW06). Cell viability was analyzed using the MTT assay to determine the optimal concentration of sorafenib. The type of programmed cell death was assessed using fluorescence microscopy with specific fluorochromes—Hoechst 33342 and propidium iodide to identify apoptotic cells, and acridine orange to identify autophagic cells.

The results indicate varied sensitivity of the tested cell lines to sorafenib and the VLCFA inhibitor. Microscopic analyses showed that both compounds induce programmed cell death, with apoptosis as the dominant type.

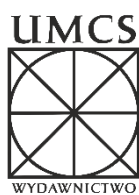
Keywords: Glioblastoma, Sorafenib, Programmed cell death, VLCFA synthesis inhibitor

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