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PLENARY SESSION

INVESTIGATING INSECT-ASSOCIATED FUNGI: A CASE STUDY OF THE INVASIVE BARK BEETLE POLYGRAPHUS PROXIMUS

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Four-eyed fir bark beetle *Polygraphus proximus*, is native to Far East (Pacific) Asia where it is harmless and economically unimportant, inhabiting dying trees weakened by other factors (fire, wind, pathogens, defoliating insects). In its invasive range in Siberia and European Russia (Moscow), the beetle has become a destructive pest of indigenous fir (*Abies* spp.). This resulted in massive infestation and killing of vigorous trees, and complete collapse of forest stands over 100 000's ha. In coming years, the beetle can potentially invade EU, where European white fir (*Abies alba*) is a crucial component of forest (mountainous) ecosystems expanding over large geographic areas from Poland to Spain. Bark beetles are known to be associated with numerous fungi representing wide range taxonomic, functional and ecological groups, and *P. proximus* is not an exception. The known examples are ophiostomatoid blue-stain fungi (*Grosmannia*, *Graphium*, *Ophiostoma* spp.) that cause bark necroses and dry/dead zones in sapwood, thus weakening tree defence reactions against beetle attack. While associations of *P. proximus* with ophiostomatoid fungi are well documented, other fungal associates of potential pathological importance remain poorly understood. In particular, resinous cankers frequently observed on beetle-attacked trees suggest involvement of additional pathogens. We investigated fungal communities associated with *P. proximus* using a combination of ITS2 rDNA metabarcoding from environmental samples (beetles), plus pure culture isolations, followed by identification based on mycelial morphology, and subsequent sequencing ITS4 rDNA from representative cultures from each morphotype. Beetles were collected from three infested sites in central Siberia, and fungal DNA was analysed using PacBio sequencing. In parallel, fungi were isolated from surface-sterilised beetles and from wood cores of attacked but externally symptomless trees. Metabarcoding revealed high fungal diversity, comprising 358 taxa, with yeasts and filamentous Ascomycota and Basidiomycota dominating communities, while ophiostomatoid fungi represented a minor fraction of total sequence abundance. Notably, a novel canker pathogen, *Corinectria* sp., was consistently detected across all sites, trees, and beetle samples. Viable cultures of this fungus were also isolated from surface-sterilised beetles, supporting its association with *P. proximus*. Culture-based isolations further revealed several beetle-associated ophiostomatoid fungi (incl. known pathogen *Grossmania aoshimae*, undetected by metabarcoding). Isolations from wood of the infested trees yielded root- and heart-rot pathogens *Armillaria borealis*, *Heterobasidion parviporum*, *Fomitopsis pinicola* and *Phaeolus schweinitzii*. Obtaining pure cultures (mycelia) provided possibility to check pathogenicity of isolated potential canker agent *Corinectria* sp. against several conifers; the fungus proved to be pathogenic exclusively to *Abies* (incl. European *A.alba*), while *Picea*, *Pinus*, *Larix* and *Pseudotsuga* had remained unaffected. Our findings demonstrate that *P. proximus* vectors a broader and more diverse fungal communities than previously recognised, including a novel canker pathogen *Corinectria* sp. This beetle – pathogen association may enhance invasion impacts and poses potential risks for European fir forests.

AGRONOMY, HORTICULTURE

SNOW MOULD RESPONSE OF ANTHOCYANIN-RICH WINTER WHEAT GENOTYPES UNDER THREE CROPPING SYSTEMS

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Snow mould can damage winter wheat during overwintering and impair spring recovery. Prolonged snow cover over unfrozen soil creates moist conditions favourable for disease development, while the extent of damage also depends on genotype susceptibility. Cultivar, sowing time and seed treatment can also influence infection by *Microdochium* species. Disease control is hampered by insufficient information regarding the resistance of varieties and complicated testing of resistance. Disease infrequent occurrence is not vewied by growers as a harmful situation.

This study examined whether greater snow mould severity was associated with poorer subsequent crop condition, lower grain yield or changes in grain quality in anthocyanin-rich winter wheat grown under three cropping systems. Twenty five winter wheat (*Triticum aestivum* L.) lines with purple, blue and black grains and three reference cultivars, Ada, Skagen and Artist, were evaluated in 2026 at central Lithuania in potassium and phosphorus rich soils.

Three cropping systems were evaluated: (i) continuous wheat, in which winter wheat followed spring wheat, (ii) a medium-intensity and (iii) an intensive systems which winter wheat followed bare fallow. Herbicides were applied in all systems but other pesticides were not used in monocrop system. One fungicide and one plant growth regulator were applied in medium-intensity system and twice more of mentioned pesticides were used in intensive system. Nitrogen 125, 150 and 200 kg N ha^{-1} were applied according intensity of systems.

Snow mould severity was visually assessed on a scale from 1 to 9, with higher scores indicating greater disease severity. Subsequent crop condition was assessed on a separate scale from 1 to 9, with lower scores indicating poorer crop condition. Protein, wet gluten, starch, sedimentation value and test weight were assessed by near-infrared spectroscopy. Spearman correlations were used to assess the relationships of snow mould severity with crop condition, grain yield and grain quality traits, based on replicate means for 28 genotypes. Snow mould severity averaged 7.23 in continuous wheat, 4.88 in the medium intensity and 2.61 in the intensive cropping system. In continuous wheat, grain yield ranged from 1.47 to 5.72 t ha^{-1} , average 3.98 t ha^{-1}. In the medium intensity cropping system, yield average was almost twice higher than in continuous wheat, reaching 7.85 t ha^{-1}, while in the intensive system it was a further 4.3 % higher at 8.19 t ha^{-1}. Insufficient differences between cropping systems was influenced by precipitation deficiency in spring and harmful heat wave in last decade of June. In continuous wheat, greater snow mould severity was associated with poorer subsequent crop condition ($P = 0.002$) and lower grain yield ($P = 0.008$). No significant relationship with yield was detected in the other two systems or with grain-quality traits in any system as medium diseases severity was low This study helps characterise the response of anthocyanin-rich winter wheat lines to snow mould. Further research is needed to confirm the observed relationships and identify lines with low snow mould severity and high grain yield.

Keywords: *Microdochium* spp.; *Triticum aestivum*; purple, blue and black grains; medium-intensity cultivation; intensive cultivation; grain yield; grain quality.

EFFECTS OF LITSEA CUBEBA ESSENTIAL OIL ON THE GROWTH AND PROTEIN MASS SPECTRAL PROFILES OF AGROBACTERIUM RADIOBACTER

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Bacterial diseases pose a challenge to vegetable production, motivating the evaluation of plant-derived antibacterial agents. This study investigated the *in vitro* effects of *Litsea cubeba* essential oil (LCEO) on the growth and protein mass spectral profiles of *Agrobacterium radiobacter* CCM 2926. Cultures with or without 0.1% (v/v) LCEO were incubated in Mueller-Hinton broth at 28 °C for 24 h. Growth was monitored by optical density at 850 nm (OD850). Samples collected after 1.5, 4.5, and 24 h were analysed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), followed by clustering of the main spectral profiles. The untreated culture showed increasing OD850, particularly during the second half of incubation, whereas the LCEO-treated culture maintained substantially lower values. At 24 h, OD850 was approximately 2.2 in the untreated culture and 0.28 in the treated culture, indicating growth inhibition under the tested conditions. Treated cultures exhibited distinct mass spectral peak patterns, while untreated cultures developed a more complex spectral profile at 24 h. Cluster analysis separated treated and untreated samples. LCEO treatment inhibited bacterial growth and altered the MALDI-TOF MS spectral profiles of *A. radiobacter*. LCEO inhibited the growth of *A. radiobacter* and altered its protein mass spectral profiles under the tested conditions. The findings provide an experimental basis for further investigation of LCEO as a plant-derived candidate for bacterial disease management in vegetable crops.

Key words: *Litsea cubeba*; essential oil; *Agrobacterium radiobacter*; growth inhibition; MALDI-TOF MS; plant protection

Acknowledgement: This work was supported by project SK-PL-25-0038 entitled "Integrated Use of Terpene Compounds for the Elimination of Bacterial Pathogens in Vegetables".

LIGHT SPECTRUM INFLUENCES GROWTH PERFORMANCE AND METABOLIC RESPONSES OF TWO THYMUS SPECIES UNDER CONTROLLED ENVIRONMENT AGRICULTURE (CEA)

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Light is one of the major environmental factors affecting plant growth. However, the metabolic and physiological response of congeneric species to different light spectra remains largely unexplored. In this study, we investigated the response of two thyme species (*Thymus serpyllum* L. and *Thymus daenensis* Celak.) to light spectrum compositions. The experiment comprised six light treatments, namely 0%B:100%R, 5%B:95%R, 10%B:90%R, 20%B:80%R, and 30%B:70% R in controlled environmental conditions. After germination, the seedlings were transferred to a deep water culture (DWC) hydroponic system under a 16-h photoperiod (23/19 ºC day/night; PPFD~250 µmol m-2 s-1). After 35 days, plant biomass, antioxidant activities, phenolic compound contents, chlorophyll content, organic acids, and sugars were evaluated. The results demonstrated that different compositions of blue and red light influence plant growth and metabolic features in both species. However, the plant species had different responses to the light treatments. Increasing the proportion of blue light to 20% enhanced plant performance and chlorophyll content in both thyme species, while having little effect on plant height. Blue light also altered the primary and secondary metabolites, with higher blue-light levels generally reducing soluble sugars, whereas antioxidant and phenolic compounds showed moderate increases at 10-15% blue light and distinct species- and organ-specific patterns. Organic acids were dominated by citric, fumaric, and malic acids, while rosmarinic acid, ferulic acid, and quercetin were the major phenolic compounds, with their responses to blue light differing between species. These findings show that light spectra modulate resource allocation between biomass production and bioactive compound accumulation. It was also found that the metabolic response was species-dependent.

Keywords: Blue light, Herbs, Red light, Secondary metabolites, Vertical farming.

GROWTH REGULATION WITHOUT VEGETATION ARREST: EFFECTS OF A FERMENTATION-DERIVED PHYTOHORMONE COMPLEX COMBINED WITH SOIL MICROBIOME ENHANCEMENT IN WINTER WHEAT AND WINTER OILSEED RAPE

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Synthetic plant growth regulators (PGRs) are widely used to control lodging in winter wheat and winter oilseed rape. They inhibit gibberellin biosynthesis and arrest plant growth for 2–3 days after each application, which may result in 6–9 days of reduced vegetative activity per season during critical developmental stages. The aim of this study was to evaluate a phytohormone complex obtained by controlled fermentation of Pseudomonas spp. (FFP), containing cytokinins and auxins in a defined ratio, as a growth regulator that does not interrupt vegetation. Field demonstration trials were conducted in the 2021/22 and 2022/23 growing seasons at the Latgale Agricultural Science Centre (Viļāni, Latvia) with winter wheat 'Skagen' and winter oilseed rape 'LG Ambassador' and 'Aganos'. Seven treatment variants were included, with FFP applied three times at 1.5–3.0 L ha^{-1} according to BBCH growth stages, including one variant combining FFP with soil microbiome enhancement (Trichoderma harzianum and Bacillus subtilis). Yield, grain and seed quality, and plant morphological parameters were assessed and compared with an untreated control and a synthetic PGR standard. In comparison with the untreated control, a tendency towards higher yields was observed in all FFP variants. The highest yield was recorded in the variant combining FFP with soil microbiome enhancement, which suggests a possible positive interaction between FFP and soil biological activity. Grain and seed quality in FFP variants was comparable to or higher than in the synthetic PGR standard. The preliminary results indicate that FFP may regulate crop growth without inhibiting vegetation and shows potential as a biological alternative to synthetic PGRs in integrated crop production. The combination with soil microbiome enhancement appears particularly promising and requires further investigation, including the role of FFP in strengthening plant resilience and reducing pesticide use.

Keywords: cytokinins; auxins; soil microbiome; winter wheat; winter oilseed rape

GREEN SYNTHESIS OF ANTIMICROBIAL SILVER NANOPARTICLES USING CUCURBITA MAXIMA PEEL WASTE FOR SUSTAINABLE CROP PROTECTION

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Food-processing industries generate large quantities of agro-industrial waste, posing significant environmental challenges despite its potential as a rich source of valuable bioactive compounds. Silver nanoparticles (AgNPs) have attracted considerable attention due to their potent antimicrobial properties; however, conventional chemical synthesis methods often rely on hazardous reagents. This study explores pumpkin (Cucurbita sp.) peel waste, an abundant agricultural by-product, as a natural reducing and capping agent for AgNPs synthesis, with the aim of developing a nano enabled strategy against Botrytis cinerea, a major fungal pathogen affecting crops. For 3D scaffold development, pumpkin peel waste was collected, washed, dried, and extracted using the magnetic stirring method. AgNPs were synthesized by reacting the extract with 1 mM silver nitrate ($AgNO_3$) solution at 60°C for 1 hour. Further characterization was performed using scanning electron microscopy (SEM), X-ray diffraction (XRD), and Fourier-transform infrared spectroscopy (FTIR) to determine morphology, crystallinity, and functional groups involved in reduction and capping of Ag ions. Additional analyses included pore size determination, biodegradation assessment, and color analysis. UV-vis spectroscopy confirmed AgNPs formation, showing a characteristic surface plasmon resonance peak at 380 nm, consistent with the optical signature of biosynthesized silver nanoparticles. SEM analysis revealed rough interlayered particles, while XRD confirmed the crystalline structure of the nanoparticles. FTIR spectra identified functional groups from the peel extract responsible for nanoparticle reduction and stabilization. Pore size analysis indicated mean pore size ranges between 74.05 to 280.61 micrometers supporting water absorption and controlled release of bioactive compounds. Biodegradation studies showed 95% degradation in 30 days, while color analysis confirmed AgNPs formation. In conclusion, Pumpkin peel waste serves as an effective, biodegradable, and eco-friendly precursor for AgNPs biosynthesis and exhibited strong anti-fungal activity against Botrytis cinerea, supporting their potential as a nano enabled tool for crop protection while offering a practical direction for agricultural waste valorization.

Keywords: Green synthesis, silver nanoparticles, 3D structures, biodegradable, antifungal activity, crop protection

DROUGHT-INDUCED FLAVONOID BIOSYNTHESIS AND CHALCONE SYNTHASE UPREGULATION REFLECT CULTIVAR-SPECIFIC RESPONSES IN LOTUS CORNICULATUS

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Drought limits the productivity of forage legumes, and flavonoids contribute to plant protection against water deficit. However, the role of chalcone synthase (CHS), the gateway enzyme of flavonoid biosynthesis, in cultivar-specific drought responses of *Lotus corniculatus* L. remains poorly understood. Three cultivars ('Gelsvis', 'Baco' and 'Izis') were grown at 100% (control), 50% (moderate) and 30% (severe) field capacity (FC) for 21 days. Morphological traits, chlorophyll content and biomass were recorded, flavonoids and phenylpropanoids were profiled by HPLC, and expression of LcCHS3, LcCHS4, LcCHS10, LcCHS11, LcCHS12, LcIFS2, LcFLS and LcF3'H was quantified by qRT-PCR. Data were analysed by two-way ANOVA with Tukey's HSD test and multivariate analyses. Drought significantly reduced plant height, bunch diameter, leaf dimensions, root length, leaf and branch number, chlorophyll content and biomass in all cultivars, with broadly similar declines; only 'Gelsvis' significantly maintained branch number. Water deficit shifted metabolism towards secondary metabolism, causing significant accumulation of quercetin and kaempferol derivatives, isoflavones, isoflavans and phenylpropanoid acids. CHS and downstream flavonoid genes were upregulated most strongly at 30% FC. 'Gelsvis' showed the most coordinated response, combining pronounced transcriptional induction with greater metabolite enrichment than 'Baco' and 'Izis'. Multivariate analyses revealed negative associations between growth traits and flavonoid pathway components, consistent with reallocation of resources from growth to protective secondary metabolism. *L. corniculatus* cultivars differ in their transcriptional and metabolic responses to water deficit, and CHS upregulation is closely associated with drought-induced flavonoid accumulation. 'Gelsvis' is a promising genetic resource for breeding drought-resilient forage legumes, although classical tolerance indicators were not measured and confirmed drought tolerance requires further validation.

CONSUMER ACCEPTANCE, SENSORY PREFERENCES AND CONSUMPTION POTENTIAL OF WALNUT-BASED FRUIT SNACKS AMONG GENERATION Z

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The walnut market is expected to undergo significant changes driven by evolving consumer preferences and increasing demand for innovative and nutritionally valuable food products. Walnuts represent a promising raw material for the food industry, with potential for use in the development of new food products. This study aimed to assess consumer acceptance and purchase and consumption intentions for walnut-based fruit snacks among Slovak Generation Z consumers. The study was based on a combination of a questionnaire survey and sensory evaluation involving a sample of 129 Generation Z respondents. Respondents were characterized based on selected sociodemographic factors, such as gender, education, place of residence, household size, and dietary habits. The respondents evaluated three variants of walnut-based fruit snacks: apple; apple, strawberry, and banana; and apple, plum, and cinnamon. The results indicated that the walnut, apple, plum, and cinnamon variant received the highest mean rating for purchase and consumption intention (5.07), followed by the walnut, apple, strawberry, and banana variant (4.24). On the other hand, the walnut and apple variant received the lowest rating (3.77). The most important sensory attributes shaping consumer preferences were overall taste (6.71), fruit flavour (6.03), aftertaste (5.63), and aroma (5.19). Factors potentially encouraging future purchase and consumption of walnut-based snacks included competitive pricing, recommendations, brand trustworthiness, and packaging appeal. Functional product benefits, the origin of ingredients, alignment with a healthy lifestyle, local production, and nutritional information can also play a positive role. The study results suggest that walnut-based fruit snacks have the potential to be accepted by young consumers and become a nutritionally valuable alternative to other snack products on the market. Furthermore, the findings provide insights applicable to consumer-oriented new food product development and the creation of market launch strategies reflecting key consumer preferences and motivations.

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OPTIMIZATION OF GROWING AND HEALING CONDITIONS IN TOMATO GRAFTING

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Pre-grafting light intensity and post-grafting healing relative humidity are important environmental factors influencing graft establishment, seedling growth, and physiological performance. This study aimed to identify favorable growing and healing conditions for producing high-quality grafted tomato seedlings by integrating graft success, growth, photosynthetic performance, and mineral nutrient responses. Tomato scion 'Jalila F1' was grafted onto four rootstocks 'Auroch', 'Ficus', 'Goldrake', and 'TOR23901'. Rootstock seedlings were grown under three pre-grafting light intensities: 150, 250, and 350 ±10 µmol m^{-2} s^{-1} for 18 days. After grafting, seedlings were healed under three relative humidity levels: 60, 75, and 90% ±5 RH for 5 days and 2 days for acclimatization under 60% RH. Pre-grafting light intensity and healing humidity significantly influenced seedling growth and photosynthetic performance, with responses varying among rootstocks. At 75% relative humidity, seedlings previously grown under 250 and 350 µmol m^{-2} s^{-1} achieved 100% graft success across all four rootstocks. A pre-grafting light intensity of 250 µmol m^{-2} s^{-1} resulted in significantly greater plant height compared with the other light treatments, while 350 µmol m^{-2} s^{-1} did not provide additional growth benefits. After grafting, healing at 75% relative humidity resulted in significantly higher net photosynthetic rate and maximum quantum efficiency of PSII (Fv/Fm) compared with 60% and 90% relative humidity. Mineral analysis revealed rootstock-dependent responses to pre-grafting light intensity, with significantly higher leaf calcium (25.48 mg g^{-1} DW) and sulfur (0.38 mg g^{-1} DW) concentrations under 250 µmol m^{-2} s^{-1} compared with the other light treatments. Overall, the results indicate that 250 µmol m^{-2} s^{-1} pre-grafting light intensity combined with 75% post-grafting healing humidity can improve grafting success and seedling physiological quality. These findings provide practical guidance for optimizing environmental conditions during grafted tomato seedling production.

Keywords: tomato grafting; pre-grafting light intensity; healing relative humidity; graft success; photosynthesis; mineral nutrition

DEVELOPMENT OF AN *IN VIVO* CROSSLINKING AND FRACTIONATION WORKFLOW FOR STUDYING COLD-RESPONSIVE PROTEIN INTERACTIONS IN APPLE

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Cold acclimation is an important adaptive response that allows temperate perennial plants to survive freezing conditions. Dehydrins, members of the group II LEA protein family, are among the proteins that accumulate during low-temperature stress and help protect cellular structures. In apple (Malus × domestica), several dehydrins, including MdDHN2, MdDHN4 and MdDHN6, are known to respond strongly to cold treatment. However, much less is known about the protein interaction networks in which these stress-responsive proteins may participate. In this study, we aimed to develop and optimize a workflow for recovering cold-responsive protein complexes from apple microshoots. The approach combined *in vivo* formaldehyde crosslinking with differential protein fractionation, trichloroacetic acid precipitation and SDS-PAGE. Crosslinking was used to preserve weak and transient protein-protein interactions before extraction. Apple 'Gala' microshoots exposed to cold acclimation were analyzed under non-crosslinked and formaldehyde-crosslinked conditions, and protein recovery from soluble and nuclear fractions was assessed by SDS-PAGE followed by InstantBlue staining. The different fractions showed clearly distinct protein profiles. The second soluble fraction contained the highest amount of recovered protein, while the nuclear fraction showed a broader distribution of protein bands. Formaldehyde treatment also changed the electrophoretic pattern of the recovered proteins. One of the most consistent features was a prominent region around 40-45 kDa. This molecular-mass range is similar to that previously associated with MdDHN4 in cold-acclimated apple microshoots, although electrophoretic mobility alone is not sufficient for protein identification. These preliminary results show that the developed workflow can separate and recover distinct protein populations from cold-acclimated apple tissue. The method therefore provides a practical basis for further analysis of stress-associated protein complexes. Subsequent affinity purification and LC-MS/MS will be needed to determine whether the recovered fractions contain dehydrins and to identify their potential interaction partners.

HORTICULTURAL BY-PRODUCTS AS A SOURCE FOR ANTIOXIDANT AND PHENOLIC COMPOUNDS EXTRACTION

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Primary processing of fruits generates large quantities of by-products like pomace that are often discarded despite retaining high levels of polyphenols, dietary fiber, and antioxidant activity. The pomace of *V. opulus* and *H. rhamnoides* is rich in phenolic compounds, including chlorogenic acid and its derivatives, procyanidins, and flavonol glycosides of quercetin, and kaempferol. The aim of the study was to evaluate the total phenolic content and antioxidant capacity of *V. opulus* and *H. rhamnoides* pomace extracts. Dried pomace of *V. opulus* and *H. rhamnoides* were extracted with 50% ethanol (v/v) at a solid-to-liquid ratio of 1:10 (w/v) by maceration (24 h) and ultrasound-assisted extraction (5 min). Total phenolic content (TPC) was determined by the Folin–Ciocalteu method, and antioxidant activity was assessed using the ABTS and DPPH assays with a Genesys UV-Vis spectrophotometer. Results showed that *V. opulus* pomace UAE extract contained 525 mg GAE/ml, twice the value of the macerated extract. For *H. rhamnoides*, the UAE extract showed a TPC of 285 mg GAE/ml, which was 9.5 times higher than that of the macerated extract. The UAE extracts of both pomaces also exhibited higher ABTS and DPPH antioxidant activities compared to macerated extracts. In *V. opulus,* ABTS and DPPH activities were 1.5 and 9.7 times higher, respectively, while in *H. rhamnoides* the increase was 20 times (ABTS) and 3 times (DPPH). In conclusion, extraction method and solvent markedly influence phenolic recovery and antioxidant activity from horticultural by-products. UAE yielded extracts rich in natural phenolics and antioxidants with potential food and nutraceutical applications.

FORESTRY

GROWTH PERFORMANCE, STEM QUALITY, AND CLIMATIC RESPONSES OF LOCAL- AND SWEDISH-ORIGIN SWEET CHERRY (PRUNUS AVIUM L.) TREES IN LATVIAN PLANTATIONS

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Exploring non-traditional tree species and their genetic variation for timber production is a step closer toward ecosystem resilience in the face of global climate change. Sweet cherry (Prunus avium L.) has shown potential for rapid biomass accumulation and high quality timber production in Latvian conditions. To support future development of productive plantation forestry and timber diversification, we evaluated the productivity of already established small scale plantations. The aim of the study was to evaluate the influence of climatic factors on the growth dynamics and stem quality of local and Swedish-origin sweet cherry trees. Five sweet cherry plantations located in the Kurzeme and Zemgale regions were selected for the research. Dendrometric parameters were measured, stem defects were assessed, and wood samples were collected for tree-ring analysis. The relationship between radial growth and climate was evaluated using air temperature and precipitation data. Overall, the results showed that Swedish-origin clones were more productive with better stem quality than local-origin trees. There were significant differences in diameter and height among plantations. At 14 years of age, Swedish-origin clones already achieved growth results comparable to those of 28-year-old local-origin trees. The proportion of stem defects was substantially lower in Swedish-origin clones (3.5–3.8%) than in local-origin clones (16.2–18.1%). The analysis of climatic factors showed that radial growth was mainly associated with temperature, although the strength and timing of this relationship varied between plantations. Interestingly, higher temperatures were generally associated with narrower annual rings, while the influence of precipitation was weaker. Swedish-origin clones demonstrated greater productivity and better stem quality under Latvian conditions, thus, appearing promising for the production of high-quality timber. However, long-term monitoring is recommended to assess clone adaptation, growth stability, and responses to changing climatic conditions as the plantations mature.

INTEGRATED ASSESSMENT OF HYBRID POPLAR AND ASPEN CLONES FOR BIOENERGY PRODUCTION, BIOREFINERY APPLICATIONS AND CARBON SEQUESTRATION

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Identifying lignocellulosic feedstocks capable of simultaneously delivering high biomass productivity, favorable chemical characteristics, substantial energy output, and effective carbon sequestration is essential for the development of sustainable bioenergy systems and advanced biorefineries. This study evaluated nineteen hybrid Populus clones, comprising fourteen hybrid poplars and five hybrid aspens, grown under Lithuanian hemi-boreal conditions. A multidimensional assessment framework was applied to integrate dendrometric characteristics, aboveground biomass production and partitioning, chemical composition, theoretical energy yield, carbon storage potential, and suitability for biofuel production. Pronounced genotype-dependent differences were detected across the evaluated traits, demonstrating the substantial influence of genetic background on both biomass quantity and feedstock quality. Aboveground biomass production varied from 71.77 to 456.90 t ha^{-1}, corresponding to theoretical energy yields of 1332–8482 GJ ha^{-1} and estimated carbon sequestration potentials of 131.71–838.42 t CO_2 ha^{-1}. Clear compositional differences were also observed between biomass fractions. Stem tissues were characterized by significantly greater concentrations of cellulose, hemicellulose, neutral detergent fiber (NDF), and acid detergent fiber (ADF), whereas branch tissues contained higher levels of ash, lignin, water-soluble carbohydrates, and mineral elements, particularly Ca, K, Mg, Fe, Mn, Na, Cu, and Zn. Functional performance also differed considerably among hybrid combinations. P. trichocarpa × P. trichocarpa achieved the highest biomass productivity and theoretical energy output, while P. tremula × P. alba was characterized by comparatively lower lignin concentrations and a chemical composition more favorable for biochemical conversion. Correlation analysis further demonstrated strong positive relationships among cellulose, ADF, and NDF. In contrast, ash and water-soluble carbohydrates were negatively associated with structural carbohydrate fractions, suggesting coordinated patterns between cell-wall formation and mineral accumulation. To integrate these complementary characteristics, a biofuel suitability index was developed using biomass productivity, theoretical energy yield, carbon sequestration, cellulose, hemicellulose, lignin, and ash content. The integrated assessment identified SvSF Po 11 as the highest-performing clone, followed by SvSF Po 12, Nyd3261-Degrosso, D19, and Sv SF Po 7. Overall, combining dendrometric, compositional, energetic, and environmental attributes provides a more comprehensive basis for function-oriented selection of Populus genetic resources than evaluation based on biomass productivity alone. The proposed framework offers a practical decision-support tool for identifying high-performance hybrid poplar and aspen feedstocks for advanced biorefineries, sustainable bioenergy systems, and climate-smart forestry under Northern European conditions.

Keywords: Populus; hybrid poplar; hybrid aspen; lignocellulosic biomass; cellulose; hemicellulose; lignin; ash; bioenergy; bioethanol; carbon sequestration; clone selection.

RELATIONSHIPS OF FIRE, TREE GROWTH AND CLIMATE: A DENDROCHRONOLOGICAL STUDY OF SCOTS PINE IN HEMIBOREAL FORESTS OF LITHUANIA

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Lithuanian hemiboreal Scots pine (*Pinus sylvestris* L.) forests have historically been shaped by fire, forming open multi-cohort stands, yet fire suppression and high-yield wood production have simplified stand structure, species composition and forest resilience. This study explores the fire history of six multi-cohort Scots pine hemiboreal forest sites as a step towards developing Closer-to-Nature forest management practices. Applying a dendrochronological approach, we analysed, i) tree-rings with fire scars to establish the local fire history, ii) the effects of fire events on tree-ring growth, iii) seasonal climate effects on fire events, and iv) correlations between tree-ring growth and yearly climate indices. Results revealed median fire intervals of 5–11 years across sites, indicating frequent fire occurrence. Tree-ring analysis revealed contrasting post-fire growth trajectories, ranging from immediate release to prolonged suppression and delayed recovery, underscoring the complexity of tree-ring growth post forest fire events. Seasonal climate anomalies associated with fire event years were rare, site-specific, and dispersed across seasons both before and after the fire years, thus indicating inconsistent regional climatic signals. Correlation analysis showed weak and non-significant relationships between Scots pine growth and both short- and long-term drought indices, while precipitation and temperature exerted stronger but highly site-specific effects. Our findings highlight the incongruities between current forest management and the historical role of fire in shaping Scots pine forest ecosystems, underscoring the need for their reconciliation. Integrating disturbance-based practices such as prescribed burning for ecological purposes within Closer-to-Nature forest management could help restore structural complexity, sustain fire-dependent biodiversity, and enhance forest ecosystem resilience under changing climate conditions.

FROM INDIVIDUAL-TREE SEGMENTATION TO FOREST STRUCTURAL ESTIMATES: ERROR PROPAGATION IN MULTISPECTRAL AIRBORNE LIDAR

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Individual-tree segmentation from airborne LiDAR is increasingly used to support forest inventory, yet segmentation performance alone does not establish the reliability of derived tree- and stand-level structural estimates. This study investigates how individual-tree segmentation errors propagate into estimates of tree height, crown geometry, and forest structure. Experiments were conducted using the FGI-EMIT multispectral airborne laser scanning dataset. Six held-out forest plots containing 463 annotated trees were evaluated using a proposed individual-tree segmentation model across three random seeds. Predicted and reference tree instances were assessed using identical raw points, terrain estimates, and structural-measurement definitions. Tree height, crown projection area, crown diameter, and occupied crown volume were quantified after instance matching. Detection-related population bias and plot-level errors were also examined. A canopy-height-model watershed decoder sharing the predicted tree foreground was included as a comparative instance-separation approach, together with sensitivity analysis of geometric measurement choices. The proposed segmentation model detected approximately 35.2% of reference trees. Among successfully matched trees, mean absolute errors were 0.500 m for height, 9.578 m^2 for crown area, 1.341 m for crown diameter, and 33.320 m^3 for occupied crown volume. The watershed approach detected fewer trees but produced smaller errors for several matched-tree attributes. Plot-level analysis revealed substantial tree omission and changes in the recovered height distribution. Structural estimates were also sensitive to terrain estimation and crown-volume parameterization. Segmentation accuracy alone is insufficient for assessing the suitability of airborne LiDAR pipelines for forest structural estimation. Detection coverage, structural-attribute errors, and measurement sensitivity should therefore be evaluated jointly. The reported agreement is relative to annotated point-cloud instances rather than independent field measurements.

Keywords: individual-tree segmentation; multispectral airborne LiDAR; forest inventory; forest structure; crown geometry; error propagation

FROM AWARENESS TO ACTION: BARRIERS TO EFFECTIVE PREVENTION OF WOLF DEPREDATION IN LATVIA

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Wolf depredation of livestock is a major source of human-wolf conflict across Europe. Its occurrence and extent depend on several factors, many beyond farmers' control. Consequently, effective preventive measures (PM) are the main tool available to reduce depredation. However, State Forest Service (SFS) records indicate that PM are rarely implemented in Latvia, with farmers often relying on wolf hunting instead. In 2025, 78 interviews were conducted with farmers from randomly selected husbandries within the study area in eastern Latvia from the Estonian to the Lithuanian border. Information on farming practices, PM, and depredation during 2021–2024 was collected. SFS records of livestock depredation across Latvia during the same period were analysed. At least one depredation event was reported by 33 of the 78 husbandries. Wolves attacked sheep in 29 husbandries, killing 651 animals, and cattle in five, killing six animals. Approximately 15% of killed animals were not reported to the SFS. Overall, 1,042 killed livestock were reported to the SFS. Interviewed farmers used various PM, including electric fencing, night enclosures, and livestock guarding dogs, although detailed information on their implementation was unavailable. Among 247 SFS reports containing information on PM, only 2.0% involved measures considered effective. Even in these cases, shortcomings in implementation or maintenance often reduced their effectiveness. SFS data suggest limitations in farmers' knowledge, practical assistance, and financial resources, while interviews showed that most farmers are aware of effective PM and are willing to use them alongside limited wolf hunting and compensations. However, costs, insufficient practical information, and limited financial support remain important barriers. Improving access to knowledge, practical assistance, and financial support could promote use of effective PM, reducing livestock depredation in Latvia. Interviews were conducted as part of the project "Co-creating coexistence: Advancing policies, practices, and stakeholder engagement for integrating wildlife and livestock into sustainable multi-functional landscapes in Europe (CoCo)". Data analyses were supported by activity 1.1.1.9 "Post-doctoral research and Research" of the Specific Objective 1.1.1. of the European Union's Cohesion Policy Programme for 2021-2027 research application No. 1.1.1.9/LZP/1/24/041.

ASSESSMENT OF CLIMATIC FACTORS AND LONG-TERM GROWTH TRENDS OF EUROPEAN BEECH IN LITHUANIA

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Global climate change alters temperature and precipitation regimes, posing significant challenges to forest resilience, particularly for tree species located in transitional geographic zones. Understanding the climate-growth dynamics of European beech (Fagus sylvatica L.) at the northeastern edge of its natural range in Lithuania is a critical research problem for developing adaptive forestry strategies under intensifying thermal stress. This study evaluates the long-term radial growth dynamics and climate sensitivity of European beech in the Šilutė region, Lithuania. Utilizing a comprehensive dendroclimatological approach, we sampled 320 trees across 7 plots, categorizing them into small, medium, and large diameter classes. Tree-ring width (TRW) and ring-width index (RWI) chronologies were developed and analyzed against multi-decadal meteorological records (temperature, precipitation, and SPEI). Extreme environmental responses were identified via normalized pointer year analysis. Principal Component Analysis (PCA) was used to structure multidimensional climatic variance, while Linear Mixed-Effects Models (LMM) quantified the hierarchical influence of climate factors versus intrinsic tree characteristics. Meteorological analyses revealed a statistically significant multi-decadal warming trend for both the annual and vegetation periods, with no significant long-term changes in precipitation. The developed chronologies exhibited strong common signal strength (EPS > 0.95). Pointer year analysis highlighted severe, synchronized growth suppressions across the stands, most notably in 1992, reflecting acute vulnerability to extreme regional environmental anomalies. LMM results demonstrated that broad inter-annual meteorological fluctuations exert a dominant, synchronized forcing on tree-ring growth that heavily outweighs the intrinsic growth differences among individual trees and size classes. Ultimately, these findings indicate that inter-annual macroclimatic conditions govern European beech growth dynamics in Lithuanian transitional forests, overshadowing local, tree-level traits. This underscores the species' heightened sensitivity to shifting thermal regimes and extreme climatic events, providing vital empirical baselines for future vulnerability assessments and climate-adaptive forest management.

Keywords: Climate-growth relationships, European beech, increment

ASSESSING THE EFFECTS OF METEOROLOGICAL CONDITIONS ON THE NESTING SUCCESS OF THE BLACK STORK (CICONIA NIGRA) IN A PERIPHERAL POPULATION IN LATVIA

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The black stork (Ciconia nigra) is an internationally protected bird species that has shown a downward population trend at the northern periphery of its range, despite local conservation measures being implemented for the species and its habitats. Separate studies have reported low survival rates among young birds in the Baltic region, and it has been hypothesized that local climate variability may affect the nesting success of the black stork. However, no specific studies have been conducted on this topic, leaving a knowledge gap. To assess the effects of meteorological conditions on the nesting success of black storks in Latvia, a GLMM model was created. It incorporated the black stork nesting success obtained through annual bird monitoring and multiple meteorological variables. The nesting success was positively affected by increased soil moisture in early May and warmer days in the middle of May, whereas the rise in air temperature at the end of March reduced nesting success. The results indicate that meteorological conditions are a statistically significant but secondary driver of black stork nesting success in Latvia, as the three climatic variables retained in the final model collectively explained only 4.6% of the total variation in nesting success.

ENHANCING THE GREEN SYNTHESIS OF ANTIMICROBIAL SILVER NANOPARTICLES THROUGH BIOLOGICAL PREPROCESSING OF TILIA CORDATA

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This study investigates a sustainable approach for the green synthesis of silver nanoparticles (AgNPs) using biologically preprocessed extracts of *Tilia cordata* flowers and leaves. To assess the influence of biological preprocessing on nanoparticle synthesis and functional properties, crude plant extracts were compared with extracts subjected to fermentation using *Medusomyces gisevii* and enzymatic treatment. The synthesized AgNPs were systematically characterized using UV–Vis spectroscopy, scanning electron microscopy (SEM), transmission electron microscopy (TEM), X-ray diffraction (XRD), and Fourier-transform infrared spectroscopy (FTIR). Changes in the phytochemical composition of the extracts were further evaluated through total phenolic content analysis. The results demonstrated that biologically preprocessed extracts effectively promoted the reduction and stabilization of silver ions, resulting in successful AgNP formation with distinct morphological and surface chemical characteristics. Notably, AgNPs synthesized using fermented and enzymatically treated extracts exhibited enhanced antimicrobial activity against both Gram-positive and Gram-negative bacterial strains, as well as selected fungal species, compared with nanoparticles produced from untreated extracts. The antioxidant properties of the extracts and synthesized nanoparticles, evaluated using CUPRAC, ABTS, and DPPH assays, revealed distinct changes associated with biological preprocessing and nanoparticle formation. Overall, the findings highlight biological preprocessing of *Tilia cordata* as an effective strategy for modulating the synthesis, physicochemical characteristics, and biological performance of AgNPs. This approach provides a sustainable and versatile platform for producing antimicrobial and antioxidant nanomaterials from renewable botanical resources, with potential applications in environmentally friendly biomedical and functional material development.

DIVERSITY OF OPHIOSTOMATOID FUNGI ASSOCIATED WITH THE BARK BEETLE IPS ACUMINATUS AND ITS HOST TREE PINUS SYLVESTRIS IN LATVIA

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For many years Ips acuminatus was considered to be a minor forest pest. However, recently its significance has rapidly grown. Ips acuminatus hosts taxonomically rich fungal community, including blue-stain fungi. Economic losses associated with the blue-stain are significant and are expected to increase under climate change. This study aimed to assess the occurrence and taxonomic diversity of *Ophiostomatoid* fungi associated with the I. acuminatus beetles and its host tree *Pinus sylvestris*. In 2025, 14 pheromone-baited slit traps were installed in May and monitored for I. acuminatus until the end of September. Weekly, 1 to 20 beetles per trap were collected for fungal isolation. Additionally, 9 symptomatic trees were felled and sampled by cutting cross-section wood discs at 3 m intervals, which were subjected for fungal isolation. Furthermore*, I. acuminatus* beetles and larvae were collected from the felled trees and subjected for fungal isolation. A total of 620 *I. acuminatus* beetles were captured from slit traps and subjected for fungal analysis. Ten *Ophiostomatoid* fungal species were detected in association with I. acuminatus beetles. The most frequently isolated species were *Leptographium cuculatum* (20%) and *Ophiostoma minus* (16%). From 9 felled symptomatic trees, 288 wood discs were analysed, revealing the presence of 7 *Ophiostomatoid* species. The most common species was *Ophiostoma minus* (13%). Additionally, 163 beetles and 8 larvae were collected from the felled trees, from which 8 Ophiostomatoid fungal species were identified. *Leptographium cuculatum* was the dominant species, accounting for 47%. Further research is needed to better understand the ecological significance of fungal associations with I. acuminatus.

SENSORY PROFILING AND TEXTURE ANALYSIS OF WILD RED DEER AND ROE DEER MEAT

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As consumers pay increasing attention to food naturalness, interest in the meat of wild animals – red deer (*Cervus elaphus*) and roe deer (*Capreolus capreolus*) – is growing [1]. Since sensory properties directly determine product acceptability, their evaluation is necessary to define the culinary value of game meat [2]. The aim of this study is to investigate and compare the physical, textural, and sensory properties of red deer and roe deer meat. Samples of the Musculus medius muscle from 12–18-month-old red deer (n=6) and roe deer (n=6) were used for the study. Instrumental texture profile analysis (TPA) was performed to evaluate meat hardness, and color was measured using the objective CIE L*a*b* system. Sensory evaluation was conducted by a trained panel according to ISO standards. Roasted samples were evaluated using a 15-point numerical scale. Sensory evaluation revealed different meat profiles for the species. The cross-section color intensity of red deer meat was 18.6% higher than that of roe deer ($p<0.05$). This corresponded to instrumental measurements – the yellowness (b* value) of red deer meat was 67.2% higher. Red deer meat was characterized by a 17.7% stronger fat oxidation odor and an 86.4% higher perceived fattiness during chewing ($p<0.05$). Roe deer meat stood out with a 28.1% more intense sour taste and a 16.5% higher mass moisture during chewing ($p<0.05$). According to instrumental texture analysis data, roe deer meat was harder (a difference in hardness of 16.29 N). Although other instrumental texture parameters did not differ, during the sensory evaluation, the texture acceptability of red deer meat was rated 36.4% better ($p<0.05$) compared to roe deer. The overall acceptability of both products did not differ statistically significantly. The meat of both game species is highly acceptable to consumers, but red deer meat stands out with a more intense color and better texture acceptability, while roe deer meat is characterized by greater juiciness and a more sour taste.

Keywords: red deer, roe deer, sensory properties, meat texture, venison quality.

FOOD SAFETY AND VETERINARY MEDICINE

THE EFFECT OF WATER-SATURATED FAR-INFRARED (FIR) EMITTING BIOCERAMIC BANDAGES ON EQUINE DISTAL LIMB THERMOREGULATION

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Effective cryotherapy of the equine distal limb is essential for regenerative medicine and the mitigation of musculoskeletal pathologies. Emerging far-infrared (FIR) emitting bioceramic textiles are hypothesized to enhance cooling by counteracting cold-induced vasoconstriction, thereby promoting localized vasodilation and accelerating heat transport to the surface for more efficient evaporative cooling. This study evaluated the efficacy of water-saturated FIR-emitting bandages in cooling the equine distal limb compared to saturated polyester bandages and unbandaged controls. Secondary factors, including shoeing status and horse discipline, were also assessed. In a randomized controlled trial, twelve horses underwent a standardized 20-minute exercise protocol. Following exercise, a water-saturated FIR-emitting bandage was applied to one randomly selected forelimb for 15 minutes, while the contralateral forelimb received a standard saturated polyester bandage. Hind limbs served as untreated controls. Infrared thermography (IRT) was used to record thermal profiles at baseline, post-exercise, and at 15, 30, and 45 minutes after removal of the bandages. Both bandage types significantly reduced distal limb temperatures compared to controls ($p < 0.05$). For mean temperatures, a significant treatment-by-time interaction was observed ($p = 0.015$), with the cooling effect becoming most pronounced 30 and 45 minutes post-application ($d \approx 1.2$). For maximum temperatures, the cooling effect was significant and uniform from application through the final measurement ($p = 0.008$). However, no statistically significant difference in cooling efficacy was detected between FIR-emitting and standard polyester bandages ($p > 0.05$). Shoeing status and discipline did not significantly moderate these effects. Water-saturated bandages are effective cryotherapeutic tools; however, FIR properties provided no additional cooling advantage over conventional polyester under these specific conditions. Both garments rapidly reduced maximum temperature spikes, whereas reductions in mean temperatures required more time. Further research is needed to identify clinical applications where FIR textiles may offer distinct advantages.

ASSOCIATION OF RUMINATION TIME WITH BLOOD BIOCHEMICAL PROFILES IN EARLY-LACTATION HOLSTEIN COWS

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Rumination time (RT) is a sensitive behavioral indicator reflecting feed intake, rumen function, and physiological adaptation in dairy cows. Reduced RT during early lactation may accompany alterations in metabolic status before overt clinical signs become apparent. This study aimed to evaluate differences in blood biochemical parameters among early-lactation Holstein cows classified according to daily RT. 88 clinically healthy Holstein cows between 2 and 100 days in milk were included. Rumination activity was continuously recorded using an automated monitoring system. Cows were retrospectively classified into three groups: Group 1, >527 min/day (n = 31); Group 2, 412–527 min/day (n = 34); and Group 3, <412 min/day (n = 23). Serum biochemical parameters related to protein, energy, mineral, and enzyme metabolism were analyzed and compared among RT groups. Significant differences among RT groups were observed for C-reactive protein ($p < 0.01$), total protein ($p < 0.01$), urea ($p < 0.05$), alanine aminotransferase ($p < 0.05$), gamma-glutamyl transferase ($p < 0.001$), lactate dehydrogenase ($p < 0.001$), glucose ($p < 0.01$), magnesium ($p < 0.01$), and triglycerides ($p < 0.001$). Cows with the lowest RT generally showed higher urea, alanine aminotransferase, gamma-glutamyl transferase, lactate dehydrogenase, glucose, and magnesium concentrations, whereas triglycerides were lower. Albumin, calcium, iron, phosphorus, sodium, potassium, chloride, creatinine, aspartate aminotransferase, and non-esterified fatty acids did not differ significantly among groups. Reduced RT was associated with distinct changes in several blood biochemical indicators in clinically healthy early lactation cows. These findings support the potential value of automated rumination monitoring as a complementary tool for identifying subclinical physiological and metabolic variation during early lactation.

COMPARATIVE EVALUATION OF ANTIOXIDANT PROPERTIES AND BIOACTIVE PHENOLIC COMPOUNDS IN PLANTS WITH ADAPTOGENIC POTENTIAL

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Adaptogenic plants are a valuable source of biologically active compounds with potential applications in functional foods and nutraceuticals. This study aimed to evaluate the antioxidant activity and phenolic composition of four selected adaptogenic plants: *Tribulus terrestris* L. (flowering part), *Panax ginseng* C.A.Mey. (root), *Rhodiola rosea* L. (root), and *Rhaponticum carthamoides* (Willd.) Iljin (leaves). Antioxidant activity was assessed using four methods: DPPH, ABTS, phosphomolybdenum assay, and FRAP. In addition, total polyphenol, flavonoid, and phenolic acid contents were determined spectrophotometrically. The results demonstrated significant differences among the investigated species. *Rhodiola rosea* L. showed the strongest antioxidant potential in all assays. Its antioxidant activity reached 8.82 ± 0.19 mg TEAC/g in the DPPH assay, 111.99 ± 0.29 mg TEAC/g in the ABTS assay, 274.33 mg TEAC/g in the phosphomolybdenum assay, and 128.92 mg TEAC/g in the FRAP assay. *Rhaponticum carthamoides* (Willd.) Iljin also exhibited high antioxidant activity, with values of 6.66 ± 0.14 mg TEAC/g in DPPH and 68.37 ± 1.51 mg TEAC/g in ABTS assays. The highest total polyphenol content was observed in *Rhodiola rosea* L. (56.32 ± 2.48 mg GAE/g), followed by *Rhaponticum carthamoides* (25.24 ± 1.58 mg GAE/g). *Rhaponticum carthamoides* showed the highest flavonoid content (24.77 ± 0.79 mg QE/g), while *Rhodiola rosea* L. contained the highest amount of phenolic acids (31.25 ± 0.83 mg CAE/g). The evaluated adaptogenic plants differed considerably in antioxidant capacity and phenolic composition. *Rhodiola rosea* L. demonstrated the greatest potential as a source of natural antioxidants, while *Rhaponticum carthamoides* represented a rich source of flavonoids. These findings suggest that selected adaptogenic plants may be promising ingredients for functional foods, particularly antioxidant-rich beverages.

Keywords: adaptogens, antioxidant activity, polyphenols, flavonoid, phenolic acids

Acknowledgments: This study was supported by the project APVV-24-0190 Development of innovative, health-promoting beverages based on fruits, medicinal plants and snacks.

CLINICAL AND EPIDEMIOLOGICAL ASSESSMENT OF FELINE LOWER URINARY TRACT DISEASES

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Feline lower urinary tract diseases are among the most common conditions encountered in veterinary practice. Their occurrence may be associated with various animal-related and environmental factors, including sex, age, housing conditions, neutering status and nutrition. Accurate identification of clinical signs, diagnostic approaches and associated risk factors is important for appropriate management and prevention. The aim of this work was to evaluate etiology, risk factors, clinical signs, diagnostic methods and treatment approaches associated with feline lower urinary tract diseases. A retrospective analysis of 115 cats with lower urinary tract disease among 6100 cats presented to a veterinary clinic in Kaunas (2019–2022) was conducted. Statistical analysis was performed using IBM SPSS Statistics 25.0 ($p < 0.05$). The estimated prevalence of lower urinary tract diseases was 1.57–2.26% (95% CI; $p < 0.05$). Males accounted for 74% of affected cats ($p < 0.001$), mixed-breed cats for 63.8% ($p < 0.001$), and indoor cats for 79.1% ($p < 0.001$). Cats aged 4–7 years represented the largest age group (37.4%; $p < 0.001$). Significant associations were also identified between disease occurrence, sex and neutering status ($p < 0.01$), as well as food type and food class ($p < 0.001$). The most frequently diagnosed conditions were urinary tract infection (82.6%), urolithiasis (53%), urinary tract obstruction (21%) and idiopathic cystitis (6%). The most common clinical signs were stranguria (36.5%), frequent visits to the litter box (34%), pollakiuria and haematuria (33%). Urinalysis, urine microscopy, biochemical blood analysis and complete blood count were among the most frequently used diagnostic methods. Conservative treatment was predominant (92.17%), with antispasmodic, antimicrobial and anti-inflammatory medications commonly used. Feline lower urinary tract diseases were associated with several demographic, housing and nutritional characteristics. The findings highlight the multifactorial nature of these disorders and the importance of comprehensive diagnostic evaluation and individualized treatment.

EFFECTS OF SCOBY FERMENTATION AND QUERCETIN–LECITHIN ENRICHMENT ON THE PHYSICOCHEMICAL AND ANTIOXIDANT PROPERTIES OF A LINDEN-BASED BEVERAGE

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Fermented plant-based beverages offer opportunities for developing innovative products containing bioactive compounds. This study investigated the effects of symbiotic culture of bacteria and yeast (SCOBY) fermentation and quercetin–lecithin enrichment on the physicochemical and antioxidant properties of a linden flower-based beverage containing apricot purée and sea buckthorn juice. A base formulation (Mix A) and an enriched formulation (Mix B), containing *Sophora japonica* extract (450 mg/L; 95% declared quercetin, equivalent to 427.5 mg/L nominal quercetin) and lecithin (900 mg/L), were evaluated with and without SCOBY inoculation (K0–K3; three replicate vessels per variant). Inoculated variants received SCOBY pellicles and equal volumes of fermented starter liquid. Samples collected on days 0, 4, and 17 were analysed for pH, titratable acidity (TA), total polyphenol content (TPC), flavonoids, phenolic acids, and DPPH antioxidant capacity. Samples were filtered before spectrophotometric analysis. In SCOBY-inoculated variants, pH decreased from 3.0 to 2.6 over 17 days. TA increased from 0.508 ± 0.014% to 1.808 ± 0.018% in K2 and from 0.584 ± 0.030% to 2.172 ± 0.067% in K3 (acetic acid equivalents). The increase was greater in K3 (1.588 ± 0.096 percentage points) than in K2 (1.300 ± 0.030 percentage points; Welch's test, $p = 0.027$). On day 4, DPPH antioxidant capacity reached similar values across all variants (95.25–95.40 mg TEAC/L), including non-inoculated controls. DPPH showed a significant time effect ($p < 0.001$), but no significant variant-by-time interaction ($p = 0.650$). TPC decreased from 367.56 ± 7.02 to 259.11 ± 45.15 mg GAE/L in K2 and from 335.00 ± 15.40 to 272.00 ± 51.02 mg GAE/L in K3, with a significant overall time effect ($p = 0.006$). The enriched SCOBY-inoculated formulation showed a greater increase in TA, whereas antioxidant capacity followed a similar temporal pattern across formulations. These preliminary findings warrant further investigation of quercetin stability and the effects of sample preparation on measured bioactive compounds.

Keywords: SCOBY, linden flower, sea buckthorn, quercetin, lecithin, antioxidant capacity

Acknowledgments: This study was supported by the project APVV-24-0190 Development of innovative, health-promoting beverages based on fruits, medicinal plants and snacks.

DIAGNOSTIC VALUE OF BLOOD INFLAMMATORY INDICES IN DOGS WITH MENINGOENCEPHALITIS OF UNKNOWN ORIGIN

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Meningoencephalitis of unknown origin (MUO) is a common inflammatory disease of the canine central nervous system. The neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR), and monocyte-to-lymphocyte ratio (MLR) can be readily calculated from a routine complete blood count and may provide additional information about systemic inflammation. However, their diagnostic value in dogs with MUO remains unclear. This study aimed to compare NLR, PLR, and MLR among dogs with MUO, dogs with idiopathic epilepsy (IE), and clinically healthy dogs, and to evaluate their ability to differentiate MUO from IE. Pretreatment hematological data were retrospectively reviewed, and NLR, PLR, and MLR were calculated for each dog. Differences between groups were statistically evaluated, with Holm correction applied for multiple comparisons. Receiver operating characteristic (ROC) curve analysis was performed to assess the discriminatory ability of each index for differentiating MUO from IE. Dogs with MUO had significantly higher NLR, PLR, and MLR values than clinically healthy dogs (NLR, $p = 0.013$; PLR, $p < 0.001$; MLR, $p = 0.012$). In comparisons between dogs with MUO and those with IE, only PLR differed significantly ($p = 0.0048$), whereas NLR ($p = 0.255$) and MLR ($p = 0.317$) did not. PLR also demonstrated the best discriminatory performance in ROC analysis, with an area under the curve (AUC) of 0.743, compared with 0.619 for NLR and 0.581 for MLR. Among the evaluated inflammatory indices, PLR showed the greatest potential for differentiating dogs dogs with MUO from those with IE. Although PLR is unlikely to serve as as a standalone diagnostic marker, it may provide additional diagnostic value as a readily available hematological parameter. These findings contribute to a broader study investigation of systemic inflammation, oxidative stress, and gut microbiota in canine MUO.

EVALUATION OF ANTIOXIDANT POTENTIAL AND BIOACTIVE COMPOUNDS IN SEEDS OF DILL, NASTURTIUM, AND MALLOW AS PROMISING NON-TRADITIONAL RAW MATERIALS FOR FUNCTIONAL BEVERAGES

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Seeds of non-traditional plant species represent a promising source of biologically active compounds with potential applications in functional foods and nutraceuticals. This study evaluated the antioxidant activity and phenolic composition of seeds from three selected species: *Anethum graveolens* L., *Tropaeolum majus* L., and *Malva mauritiana* L., as potential raw materials for functional beverages. Antioxidant activity was determined using four spectrophotometric assays: DPPH, ABTS, ferric reducing antioxidant power (FRAP), and phosphomolybdenum assay. Total polyphenol, flavonoid, and phenolic acid contents were also determined spectrophotometrically. Significant differences in antioxidant potential and phenolic composition were observed among the investigated species. *Tropaeolum majus* L. seeds exhibited the highest antioxidant activity in all assays, reaching 6.51 ± 0.16 mg TEAC/g in DPPH, 47.69 ± 2.98 mg TEAC/g in ABTS, 34.81 ± 1.25 mg TEAC/g in FRAP, and 171.34 ± 3.17 mg TEAC/g in the phosphomolybdenum assay. *Anethum graveolens* L. and *Malva mauritiana* L. seeds showed lower antioxidant activities, although measurable values were obtained in all methods. The highest total polyphenol content was recorded in *Tropaeolum majus* L. seeds (12.24 ± 0.33 mg GAE/g), followed by Malva mauritiana L. (4.84 ± 0.17 mg GAE/g) and *Anethum graveolens* L. (4.47 ± 0.51 mg GAE/g). *Malva mauritiana* L. contained the highest total flavonoid content (6.32 ± 0.56 mg QE/g), whereas *Tropaeolum majus* L. showed the highest concentration of phenolic acids (10.75 ± 0.39 mg CAE/g). In conclusion, the investigated seeds differed considerably in antioxidant capacity and phenolic composition. *Tropaeolum majus* L. demonstrated the greatest potential as a natural source of antioxidants, while *Malva mauritiana* L. was characterized by the highest flavonoid content. These findings suggest that seeds of the evaluated species may serve as promising ingredients for the development of antioxidant-rich functional beverages.

Keywords: seeds, medical and culinary herbs, antioxidant activity, polyphenols, flavonoid, phenolic acids

Acknowledgments: This study was supported by the project VEGA 1/0192/26 Innovative non-alcoholic beverages based on medicinal plants, snacks and fruits.

CHANGES IN GENOMIC EVALUATION RESULTS OF DAIRY COW TRAITS RELATED TO MILK PRODUCTION SUSTAINABILITY ACROSS DIFFERENT EVALUATION PERIODS

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Genomic evaluation of dairy cattle enables selection for traits related to feed efficiency, health, and longevity, contributing to more sustainable milk production. Improving feed efficiency is important for achieving more sustainable milk production, as selecting animals with higher feed efficiency can contribute to reducing feed requirements and methane emissions . Genetic selection based on traits related to feed utilization, survival, and other environmentally important characteristics can serve as a long-term strategy for reducing the environmental impact of milk production. The study included 250 healthy dairy cows with genomic evaluations performed in the Netherlands using ear tissue samples. The analyzed traits included the Feed Efficiency Index, Feed Intake, Feed Saved for Maintenance, Saved Feed Costs for Maintenance, CRV (Cattle Improvement Cooperative) Health, and Longevity. The assessments were carried out in April, August and December 2024 - 2025 and April 2026. Over the study period, the genomic Feed Intake Index decreased by 65.00% ($p<0.01$), while the CRV Health Index decreased by 39.37% ($p<0.001$). The Longevity Index decreased by 8.37%, although the difference was not statistically significant ($p>0.05$). The Feed Efficiency Index remained relatively stable, decreasing by only 0.01% ($p>0.05$). In contrast, the Saved Feed Costs for Maintenance index increased from 1.50 to 11.52 ($p<0.05$), while the Feed Saved for Maintenance index increased from 0.02 to 0.12 ($p<0.05$). These findings highlight the importance of considering repeated genomic evaluations when selecting dairy cattle, planning herd replacement, and predicting changes in the breeding values of animals within a continuously changing population, it is important to consider genomic evaluation results obtained across multiple evaluation periods. This enables a more reliable selection of animals that will contribute, in the long term, to a milk production system that is more efficient, economically profitable, and environmentally friendly.

RELATIONSHIPS BETWEEN CORPUS LUTEUM BLOOD FLOW, PROGESTERONE AND VEGF-A IN MARES

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Early pregnancy maintenance in mares depends on adequate corpus luteum (CL) function and progesterone secretion. CL vascularisation is closely related to luteal activity, while vascular endothelial growth factor A (VEGF-A) plays a key role in ovarian angiogenesis. This study evaluated the relationships among serum VEGF-A, CL vascularisation, progesterone concentration and pregnancy status in mares, considering age and parity. Forty-six (n=44) Warmblood mares (3 – 20 years old) underwent a standardized artificial insemination protocol during 2024-2026 breeding seasons. At 14 days post ovulation, pregnancy status was assesed, blood sample for serum progesterone (P4) and VEGF-A were collected, centrifuged, and frozen at -70 for further analysis. CL vascularisation was assessed using frozen pictures of Doppler ultrasonography (Mindary DP-50 Vet). CL total area, vascularisation pixels and vascularisation percentage was obtained via Image J and Adobe Photoshop systems. Pregnant and non-pregnant groups were compared using non-parametric tests, and associations between continuous variables were evaluated using Pearson and Spearman correlations. Progesterone concentrations were significantly higher in pregnant than non-pregnant mares (median 13.87 vs 8.51; P=0.031). CL vascularisation also tended to be higher in pregnant mares (median 4329 vs 2584 pixels), although the difference did not reach statistical significance (P=0.062). Overall, progesterone showed weak positive associations with absolute CL vascularisation (Spearman ρ=0.17, P=0.464) and relative vascularisation (ρ=0.26, P=0.290). In non-pregnant mares, progesterone was strongly positively associated with relative CL vascularisation (ρ=0.83, P=0.042; n=6). VEGF-A did not differ between pregnancy groups (P=0.861), but tended to decrease with increasing age (Pearson r=−0.33, P=0.059). Pregnant mares had higher progesterone concentrations and a tendency toward greater CL vascularisation. The association between luteal vascularisation and progesterone may depend on reproductive status. Serum VEGF-A was not directly associated with pregnancy outcome, but its possible age-related variation highlights the need for larger studies integrating systemic angiogenic markers with local ovarian vascularisation.

EFFECT OF DRY PERIOD DURATION ON COLOSTRUM BRIX VALUES AND ESTIMATED COLOSTRAL IMMUNOGLOBULIN G CONCENTRATIONS IN DAIRY COWS

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The dry period is an important component of dairy cow management, allowing mammary gland involution before subsequent lactation. Colostrum quality is essential for transferring passive immunity to newborn calves through immunoglobulin G. Previous studies suggest that inadequate dry period management may affect mammary gland regeneration and influence colostrum composition and immunoglobulin transfer. The aim of this study was to evaluate the association between dry period duration and colostrum quality measured by Brix values and estimated IgG concentration. The study was conducted on a commercial dairy farm and included 112 clinically healthy cows, 1-5 lactation, sampled within 6 hours after calving. Cows were divided into groups according to dry period duration: 1–2 months and 2–3 months. Colostrum quality was assessed using a Brix refractometer, with values above 25% classified as very good quality. IgG concentration was estimated from Brix values using a published prediction equation. Descriptive statistics were calculated, and group differences were assessed using the Mann–Whitney U test. Cows with a 2–3 month dry period had higher mean Brix values than those with a 1–2 month dry period (26.02 ± 3.21% vs 24.43 ± 2.97%), corresponding to higher estimated IgG concentrations (93.38 ± 37.11 g/L vs 75.03 ± 34.33 g/L). However, differences in Brix and IgG values were not statistically significant ($p = 0.085$). The proportion of cows producing very good quality colostrum was numerically higher in the 2-3 month dry period group (70.0% vs 38.2%, $p = 0.088$). Cows with a dry period of 2-3 months produced colostrum with higher Brix values and correspondingly higher estimated IgG concentrations than cows with a dry period of 1-2 months. Although these differences were not statistically significant, the observed trends may indicate a potential effect of dry period duration on colostrum quality and warrant further investigation in larger populations.

HORTICULTURE, AGRONOMY, FOOD SAFETY, AND VETERINARY MEDICINE

BIOCONTROL POTENTIAL OF BACILLUS VELEZENSIS 12-45 AGAINST FUSARIUM SPP. FROM NON-GRAMINEOUS PLANTS AND WEEDS

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Non-gramineous plants and weeds may act as alternative hosts and asymptomatic reservoirs of Fusarium spp., allowing these pathogens to persist within agroecosystems and potentially contribute to Fusarium head blight (FHB) epidemiology. Therefore, evaluating the susceptibility of *Fusarium* isolates originating from non-gramineous (N) plants and weeds (P) to bacterial antagonists is relevant for sustainable disease management. This study evaluated the antagonistic activity of soil bacterial strain 12-45 against *Fusarium culmorum* and *Fusarium graminearum* isolates obtained from N and P plants. Whole-genome sequencing identified strain 12-45 as *Bacillus velezensis*, with 97.73% OrthoANI similarity to the reference strain *B. velezensis* NRRL B-41580T (GCA_001461825.1). Antagonistic activity was assessed by determining the effects of strain 12-45 on fungal mycelial growth, spore germination (SG), and hyphal morphology using scanning electron microscopy (SEM). Strain 12-45 inhibited mycelial growth of *F. culmorum* by 62% in isolates from N plants and by 65% in isolates from P plants, while inhibition of *F. graminearum* was 65% in isolates from N plants and 67% in isolates from P plants. In the untreated control, 98–100% of spores germinated after 8 and 24 h. After 8 h, SG reached 35% (19P) and 40% (30P) in the fungicide treatment, and 67% (19P) and 64% (30P) in the bacterial treatment. After 24 h, SG increased to 72–93% in both treatments. SEM revealed hyphal wrinkling and flattening following bacterial treatment, whereas fungicide treatment caused clear hyphal ruptures; hyphae in the untreated control remained morphologically unchanged. Functional genome annotation revealed genes associated with secondary metabolite biosynthesis and transport, defense mechanisms, signal transduction, chemotaxis, and motility. These genomic features may support mechanisms related to antifungal activity, nutrient competition, environmental adaptation, and colonization, providing genomic evidence for traits potentially underlying the observed antagonistic activity. Overall, the phenotypic and genomic results indicate that *B. velezensis* 12-45 could be a potential biocontrol agent against FHB-associated Fusarium spp. isolates originating from non-gramineous plants and weeds, although further evaluation is needed.

PRELIMINARY IDENTIFICATION OF FUNGI ASSOCIATED WITH EARLY BLIGHT SYMPTOMS ON POTATOES IN LATVIA

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Early blight is a foliar disease of potato commonly associated with *Alternaria* spp. However, the fungal diversity associated with early blight symptoms and similar foliar lesions in potato fields in Latvia remains insufficiently characterized. This study aimed to identify fungi isolated from symptomatic potato leaves collected during the 2025 and 2026 growing seasons in Latvia and assess the diversity of fungal groups associated with the observed symptoms. Potato leaves showing early blight symptoms were collected from organic and conventional potato fields in Latvia. Based on visual assessment, symptomatic leaves were classified into three types: numerous small, fine dark spots; predominantly solitary concentric lesions surrounded by yellow halos; and leaves showing both types simultaneously. Fungi were isolated on Rose Bengal agar medium, then subcultured and purified using the hyphal-tip method. Representative isolates were selected for molecular identification by sequencing the internal transcribed spacer (ITS) region. Preliminary results show that *Alternaria* was the most frequently isolated fungal genus, accounting for 46% of all isolates obtained from symptomatic potato leaves. ITS sequence analysis indicated that the identified isolates belonged to two sections of *Alternaria*: *Alternaria* and *Infectoriae*. In addition, several *Stemphylium* isolates were also obtained. The recovery of multiple fungal genera from leaves exhibiting early blight-like symptoms may indicate that these symptoms can be associated with a complex of fungi rather than a single causal species. However, isolation from symptomatic tissue alone does not confirm pathogenicity, and the role of individual taxa remains unclear. The identification process is ongoing; therefore, the current findings should be interpreted as preliminary. The presence of large-spored *Alternaria* species, including *A. solani* from section *Porri*, has not yet been confirmed in the studied fields. Further molecular analyses and pathogenicity tests are needed to clarify the identity of the isolates and their roles in potato foliar diseases in Latvia.

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Keywords: *Solanum tuberosum*, ITS sequencing, fungal diversity, *Alternaria, Stemphylium*.

SHOTGUN METAGENOMICS REVEALS DROUGHT-ASSOCIATED MICROBIAL TAXA AND FUNCTIONAL POTENTIAL IN THE WINTER WHEAT RHIZOSPHERE

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Drought can affect rhizosphere microbial communities and select microorganisms with traits potentially associated with stress adaptation. This study aimed to investigate drought-associated taxonomic and functional changes in the rhizosphere microbiome of winter wheat.

Three winter wheat cultivars ('Ada', 'Artist', and 'Lakaja D') were grown in a semi-controlled environment in a greenhouse under control and drought conditions. Plant responses were measured by digital phenotyping, and rhizosphere samples were analyzed using Illumina shotgun metagenomic sequencing. Taxonomic profiles were generated using Kraken2 and Bracken, while functional potential was annotated using KEGG and PLaBAse. Multivariate and differential abundance analyses were performed. The phenotypic plant response to drought included reduced plant growth and vegetation indices, while senescence-associated indices increased. Taxonomic analysis at the genus level showed significant differences between treatments in 'Artist' and 'Lakaja DS' (PERMANOVA, FDR = 0.044), although significant dispersion differences complicated their interpretation. Genotype-adjusted differential abundance analysis revealed enrichment of *Paenibacillus* ($log_2FC = 1.03$; FDR < 0.001), *Plantibacter* ($log_2FC = 1.85$; FDR = 0.005), and *Priestia* ($log_2FC = 1.21$; FDR = 0.005). According to the KEGG analysis, several genes involved in compatible-solute biosynthesis (gpgS), phenazine biosynthesis (phzD), siderophore-associated metabolism (pchD), and auxin-related biosynthetic potential (iaaM) were enriched under drought conditions (FDR < 0.05). Furthermore, PLaBAse indicated enrichment of spore formation and germination functions, suggesting potential bacterial stress-survival mechanisms. In parallel with the metagenomic analysis, 151 bacterial isolates were obtained from the roots of the same wheat plants and collected for subsequent taxonomic identification and functional screening. Overall, drought was associated with changes in both the taxonomic composition and functional potential of the winter wheat rhizosphere microbiome. The identified microbial taxa and functional markers provide a data-driven basis for targeted bacterial isolation and experimental evaluation of drought-associated and plant growth-promoting traits.

SALICYLIC ACID DECOUPLES OXIDATIVE PROTECTION FROM YIELD GAIN IN WHEAT ACROSS AN IRRIGATION GRADIENT

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Deficit irrigation is increasingly common in water-scarce regions, yet it constrains wheat yield. Foliar salicylic acid (SA) is a low-cost candidate for offsetting these consequences, but how its effectiveness changes across an irrigation gradient remains poorly determined. A pot experiment at Amir Muhammad Khan Campus, Mardan, Pakistan, during winter 2025 used wheat (*Triticum aestivum* L.) cv. Zincol-16. Four irrigation regimes (40, 60, 80 and 100% of field capacity, FC) and four SA concentrations (0, 1, 2 and 3 mmol L^{-1}; control, S1, S2, S3) were combined factorially in a randomised complete block design with three replications. Full irrigation maximised growth, yield, photosynthetic pigments and relative water content (RWC), whereas proline, hydrogen peroxide (H_2O_2), malondialdehyde (MDA) and peroxidase, catalase and ascorbate peroxidase activities peaked at 40% FC. SA improved performance at every irrigation level, but benefits differed between trait classes. Protective responses were largest under severe deficit, where 3 mmol L^{-1} SA (S3) raised RWC by 18.5% and lowered proline, MDA and H_2O_2 by 28.4, 27.1 and 18.6%, respectively. Yield gains were largest under full irrigation, where S3 increased grain weight per pot by 25.9%, against 8.1% at 40% FC. Principal component analysis separated irrigation regimes along PC1 (71.2% of variance), and path analysis attributed most of the SA effect on yield to a direct route (total standardised effect +0.56). Foliar SA at 3 mmol L^{-1} therefore limits oxidative damage and preserves tissue hydration under water deficit, while its yield advantage is expressed most fully when water is not limiting.

Keywords: antioxidant enzymes; deficit irrigation; oxidative stress; path analysis; salicylic acid; Triticum aestivum

PHENOLIC CONTENT AND ANTIOXIDANT POTENTIAL OF SALAD BURNET (SANGUISORBA MINOR L.) AT DIFFERENT HARVEST TIMES

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The growing interest in plant-based foods has highlighted the importance of identifying new sources of bioactive compounds. Salad burnet (*Sanguisorba minor* L.) is a perennial herb with a fresh, cucumber-like aroma that is traditionally used in salads. Its relatively high phenolic content and antioxidant potential make it an interesting candidate for further investigation as a plant-based food ingredient. This study investigated how plant age and harvest season influence the physicochemical properties, phenolic content, and antioxidant capacity of salad burnet. Aboveground plant material was harvested during summer and autumn in the first and second years of growth, freeze-dried, and analyzed for color coordinates CIELab, chlorophyll content, total phenolic content (TPC), total flavonoid content (TFC), and antioxidant activity using ABTS·+, DPPH·+, and FRAP assays. The results showed that TPC reached up to 280 mg gallic acid equivalents (GAE)/g dry weight (DW), while ABTS·+ antioxidant capacity reached up to 970 µmol Trolox equivalents (TE)/g DW, expressed relative to the dry plant material. Overall, second-year plants showed significantly higher values for nearly all measured parameters than first-year plants, whereas differences between summer and autumn harvests were generally not significant. Further research is needed to clarify the relative contributions of plant age and post-harvest storage conditions to these differences. These findings highlight the potential of salad burnet as a source of bioactive compounds for food applications, including formulations aimed at improving oxidative stability.

NETTLE SLURRY AS A PLANT BIOSTIMULANT: INTERACTIONS WITH MINERAL NITROGEN AND EFFECTS ON GROWTH TRAITS AND SOIL DEHYDROGENASE ACTIVITY IN SPRING WHEAT

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The integration of biostimulants with mineral nitrogen (N) fertilizers represents a promising approach to improve soil biological activity and crop growth while reducing reliance on synthetic inputs. This study evaluated the individual and combined effects of nettle (*Utrica dioica* L.) slurry and synthetic mineral N fertilizer on soil enzymatic activity and growth performance of spring wheat under controlled conditions. A pot experiment was conducted in a growth chamber using an unfertilized control (water), synthetic N at 45 and 75 kg ha-1 N, nettle slurry 5%, 10% and 20% concentrations, and their combinations. Plant growth parameters (root length, shoot length, dry weight) and soil dehydrogenase activity were determined. Nettle slurry applied alone with 20% concentration improved plant growth and soil enzymatic activity. Combined applications further enhanced these responses, indicating synergistic interactions between organic and mineral N sources. The nettle slurry 20% + 75 kg ha-1 N treatment produced the greatest increases in root length, shoot length, root and shoot dry weight, and soil dehydrogenase activity by 26%, 47.4%, 1.85%, 3.39 % and 12% respectively. Overall, integrated fertilization with nettle slurry and mineral N markedly stimulated soil microbial activity and spring wheat growth compared with single-source fertilization. These findings highlight the potential of nettle-based organic amendments to enhance resource use efficiency and soil biological activity in cereal production systems towards a less intensive agricultural system.

Keywords: stinging nettle, slurry, biostimulant, nitrogen fertilization, dehydrogenase, sustainable agriculture.

PTEROSTILBENE AND ITS EFFECTS ON HUMAN OVARIAN GRANULOSA CELL FUNCTIONS *IN VITRO*

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Pterostilbene, a naturally occurring dimethoxy analogue of resveratrol, exhibits antioxidant, anti-inflammatory and antitumour properties. However, its effects on ovarian granulosa cell functions remain insufficiently understood. This study aimed to evaluate the effects of pterostilbene on the viability and secretory activity of non-tumour human ovarian granulosa cells (HGL5) and ovarian granulosa tumour cells (COV434). HGL5 and COV434 cells were exposed to pterostilbene (1, 5, 10, 20, 50, 100 and 250 µg/mL) for 24 h. Cell viability was assessed using the AlamarBlue™ assay. The secretion of progesterone, 17β-estradiol and transforming growth factor β2 (TGF-β2) was determined by ELISA at selected concentrations (10, 50, 100 and 250 µg/mL). Pterostilbene significantly reduced the viability of both cell lines at 50, 100 and 250 µg/mL ($P \leq 0.001$). Progesterone secretion remained unchanged ($P \geq 0.05$), whereas 17β-estradiol secretion increased in HGL5 cells at 10, 100 and 250 µg/mL ($P \leq 0.001$) and in COV434 cells at 50 ($P \leq 0.01$) and 250 µg/mL ($P \leq 0.001$). TGF-β2 secretion decreased in both cell lines at these concentrations ($P \leq 0.001$), with an additional decrease at 10 µg/mL in HGL5 cells ($P \leq 0.001$). Pterostilbene modulated ovarian granulosa cell viability, estradiol secretion and growth factor production *in vitro*. These findings indicate biologically relevant effects on both non-tumour and tumour granulosa cell models, warranting further mechanistic investigation.

Key words: pterostilbene, ovarian granulosa cells, steroidogenesis, growth factors, viability

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ANTIMICROBIAL ACTIVITY OF BASIL (*OCIMUM BASILICUM*) AND IMMORTELLE (*HELICHRYSUM* SP.) HYDROLATES AGAINST SELECTED BACTERIA AND YEASTS

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Hydrolates (hydrosols) are aqueous products obtained during the steam distillation of essential oils. They contain relatively low concentrations of volatile bioactive compounds and have attracted attention as mild natural antimicrobial agents for potential applications in the food, cosmetic, and pharmaceutical industries. This study aimed to evaluate the antimicrobial activity of basil (*Ocimum basilicum*) and immortelle (*Helichrysum* sp.) hydrolates against selected reference bacterial and yeast strains. Antimicrobial activity was evaluated using the disc diffusion method. The hydrolates were applied to sterile 6-mm filter paper discs placed on Mueller–Hinton agar inoculated with bacterial strains or Sabouraud dextrose agar inoculated with yeasts. The tested microorganisms comprised five Candida species (*C. albicans, C. glabrata, C. krusei, C. parapsilosis*, and *C. tropicalis*), three Gram-positive bacteria (*Staphylococcus aureus, Listeria monocytogenes,* and *Enterococcus faecalis*), and three Gram-negative bacteria (*Escherichia coli, Salmonella enterica,* and *Yersinia enterocolitica*). Following incubation at 37 °C for bacteria and 25 °C for yeasts, the widths of the inhibition zones extending from the edges of the discs were measured. Cefoxitin, gentamicin, and fluconazole were used as positive controls. Both hydrolates exhibited only weak antimicrobial activity under the tested conditions. The widths of the inhibition zones measured from the edges of the 6-mm discs ranged from 1 to 2 mm, corresponding to total inhibition zone diameters of 8–10 mm, including the discs. The greatest inhibition was observed against C. glabrata, with a 2-mm inhibition zone extending from the disc edge for both hydrolates. Basil hydrolate showed slightly higher activity against yeasts, with a mean inhibition width of 1.2 mm, compared with 1.0 mm for immortelle hydrolate. No inhibition of C. krusei was detected with immortelle hydrolate. Activity against bacteria was very low, with a mean inhibition width of 0.5 mm for both hydrolates, and was observed mainly against Gram-positive strains. Most Gram-negative bacterial strains showed no measurable inhibition. Under the conditions of the disc diffusion assay, basil and immortelle hydrolates exhibited only weak antimicrobial activity. Yeasts, particularly *C. glabrata*, appeared slightly more susceptible than bacterial strains. The tested hydrolates therefore showed limited potential as standalone antimicrobial agents; however, their possible use as mild adjuncts or as components of combined antimicrobial systems warrants further investigation.

Acknowledgements. This research was co-funded by the project APVV-24-0190, Development of Innovative, Health-Promoting Beverages Based on Fruits, Medicinal Plants and Snacks.

MATRIX-DEPENDENT RECOVERY OF BIOACTIVE COMPOUNDS FROM BEETROOT AND RASPBERRY BY-PRODUCTS USING ULTRASOUND-ASSISTED EXTRACTION

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Valorization of fruit and vegetable by-products offer a sustainable approach to recover high-value bioactive compounds and reduce agro-industrial waste. This study aims to compare beetroot and raspberry by-product powders as sources of natural antioxidants and pigments using ultrasound-assisted extraction (UAE). Three extraction treatments, varying in temperature, extraction time, and ultrasound power, were applied under identical conditions to both matrices for direct performance comparison. Extracts were analyzed for antioxidant activity (DPPH and ABTS assays), total phenolic content (TPC), total flavonoid content (TFC), pigment yield, color parameters (CIELAB), and UV–Vis spectra. Molecular weight distribution was determined by HPLC–SEC. The physicochemical and structural properties of the raw powders were assessed using FTIR, SEM, and ICP-OES to evaluate their impact on extraction behavior. The results showed that UAE parameters were non significantly on the recovery of bioactive compounds, with outcomes strongly dependent on the plant matrix, whereas total phenolic content showed relatively limited variation under the tested conditions. Raspberry extracts had higher flavonoid content (390–530 mg CE/100 g) and greater antioxidant activity, while beetroot samples yielded more pigments, especially with longer extraction times. Overall, the findings indicate that while extraction conditions affect process efficiency, the intrinsic composition and structure of the raw material are the main factors determining extract quality. This study offers new insights into the sustainable use of horticultural by-products as natural sources of antioxidants and colorants for value-added products.

Key words: Ultrasound-Assisted Extraction; Beetroot and Raspberry by-products; agro-industrial waste valorization; bioactive compounds; antioxidant activity

UPCYCLING OF FLORICULTURAL RESIDUAL BIOMASS: CHRYSANTHEMUM × MORIFOLIUM AS POTENTIAL SOURCE OF BIOACTIVE COMPOUNDS FOR CIRCULAR BIOECONOMIES

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Chrysanthemums rank among the most widely cultivated and commercially sold flowering plants worldwide. Intensive floricultural production generates significant amounts of plant biomass waste at various stages of the flower supply chain. This residual biomass may represent a valuable source of bioactive compounds as a part of circular bio-based value chain. Valorization of *Chrysanthemum* × *morifolium* by-products for different applications has been already. However, further comparative studies are needed to gain a more comprehensive understanding of the distribution and variability of bioactive compounds among different cultivars, plant organs and plant material from different sources. Such knowledge could help introduce the potential of Chrysanthemum × morifolium residual biomass for use in the circular bioeconomy applications. This study aims to combine literature analysis with experimental data to review current findings and future prospects of *Chrysanthemum × morifolium* waste valorization with a particular focus on opportunities for the recovery of valuable bioactive compounds. Comparative experimental analysis of five *Chrysanthemum × morifolium* cultivars, obtained from floriculture farm as unsold production, was conducted to characterize total phenolic content (TPC) across different cultivars and plant organs, including flowers, leaves, and stems

AGRICULTURE, AGROBIOLOGY, AGROECOLOGY

MICROPLASTICS AS EMERGING VECTORS OF HEAVY METAL TRANSPORT IN SOILS

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Microplastics (MPs) accumulating in agroecosystems, primarily via sewage sludge and compost, pose critical ecological risks due to their ability to adsorb environmental pollutants, particularly heavy metals. Subjected to abiotic and biotic aging processes, degraded MP particles can facilitate the entry of heavy metals into the food chain, threatening ecosystem stability. This study evaluated the sorption capacity of pristine and artificially aged low-density (LDPE, 5 mm) and high-density polyethylene (HDPE, 2–4 mm) particles for Zn, Cu, and Cd. MPs underwent combined mechanical, photochemical and chemical aging, while surface modifications were characterized using ATR-FTIR spectroscopy. Sorption experiments were conducted in 10 mL metal salt solutions (250 and 500 mg/L) using 5 and 15 MP particles over 4 and 10 days. To determine sorption capacity (Q_t, mg/g), pre- and post-interaction metal concentrations were measured via ICP-OES. The results revealed that complex abiotic aging induced severe polymer degradation, notable weight loss (up to 48.5% for HDPE and 26.6% for LDPE) and surface erosion. ATR-FTIR analysis showed localized surface oxidation in aged LDPE (C=O carbonyl peak at 1733 cm^{-1}). Furthermore, adsorption was highly selective: the strongest affinity occurred between Zn and damaged HDPE, reaching a sorption capacity of Q_t = 3.428mg/g after 10 days. Conversely, Cu and Cd adsorption remained minimal or unstable (Q_t = 0). In conclusion, aging processes do not yield abundant oxygen-containing functional groups. Instead, it occurs primarily via physical surface erosion and mechanical pore filling. Nevertheless, polymer-heavy metal interactions remain highly time and metal specific, with weathered HDPE particles acting as significant zinc vectors after extended contact. To confirm these findings and further evaluate metal ion interactions with the polymer surface, detailed future research, such as SEM-EDS analysis, is required.

Keywords: microplastic, heavy metals, ATR-FTIR

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INVESTIGATING THE SEED YIELD POTENTIAL OF DIPLOID AND TETRAPLOID RED CLOVER (TRIFOLIUM PRATENSE L.) CULTIVARS UNDER LITHUANIAN CONDITIONS

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Red clover (*Trifolium pratense* L.) is an important perennial forage legume in temperate regions, contributing to sustainable agriculture and the production of protein-rich animal feed. Although numerous cultivars are available, their genetic potential is not always fully realized because many exhibit limited adaptability to different soil and climatic conditions. The proposed research will focus on diploid and tetraploid cultivars, breeding material, and wild populations of red clover. Cytological and physiological methods will be used to determine ploidy levels and evaluate pollen viability, self-pollination capacity, reproductive traits, and responses to environmental stress. Particular attention will be given to differences between diploid and tetraploid red clover. Tetraploid cultivars often produce high vegetative biomass but generally have lower and less stable seed yields than diploid cultivars. Investigating the effects of ploidy on reproductive traits is therefore essential for identifying the factors that limit seed formation. Red clover is predominantly cross-pollinated and largely dependent on insect pollinators, although some genotypes may exhibit partial self-pollination. The relationships among ploidy, pollen viability, sterility, self-pollination capacity, and seed formation will be investigated to identify characteristics associated with stable seed production under unfavourable environmental conditions and limited pollinator activity. The inclusion of wild populations will enable the assessment of genetic diversity and adaptive potential. Comparing wild and cultivated materials may reveal valuable traits, including stable flowering, high pollen viability, efficient fertilization, and greater tolerance to environmental stress. The expected results may contribute to the development of red clover population combining high forage productivity, environmental adaptability, and stable seed yields under Lithuanian conditions.

Keywords: red clover, ploidy, pollen viability, self-pollination, seed yield.

ENDOPHYTIC BACTERIA IN AGRICULTURE: BIOLOGICAL NITROGEN FIXATION AND BENEFITS FOR PLANTS

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In order to ensure the increasing food supply of the population of developing countries, it is important to increase the productivity of agricultural plants, for which chemical fertilizers are most often used. Long-term use of these fertilizers reduces the diversity of soil bacteria and negatively affects the environment. Large amounts of nitrogen and phosphorus fertilizers are washed into groundwater, polluting soil and water bodies (Sun et al., 2015; Zhou et al., 2016). One way to increase sustainability in agriculture is to use microorganisms that are able to mobilize and make nutrients available to plants, thereby reducing the need for and dependence on chemical fertilizers (De La, 2016). Biological nitrogen fixation can be one of the ways to solve the problem of nitrogen supply to plants. 60 percent. of nitrogen fixed in the soil is biologically fixed nitrogen. Therefore, increasing its use and efficiency in agriculture is becoming increasingly relevant in order to meet the growing needs of global food production. The aim of this report is to review the importance of endophytic nitrogen-fixing bacteria in the nitrogen supply of plants and their potential in increasing nutrient use efficiency and contributing to sustainable crop production. Research methodology - an analysis and synthesis of scientific literature, project reports and other relevant sources of information on the topic under study was carried out. Results - the main research results, technological solutions and application possibilities are reviewed. The most important factors determining the effectiveness of the phenomenon under study are identified, and the main directions of scientific research are highlighted. Conclusions - summarize current knowledge on the topic, identify the most promising areas of application and the need for further research.

TRAIT ASSOCIATION STUDY OF WEEVIL DAMAGE, SEED PROTEIN, AND PHENOTYPIC TRAITS IN EIGHT FABA BEAN CULTIVARS INFESTED BY BROAD BEAN WEEVIL

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Faba beans is an important legume crop widely grown for their soil nitrogen-fixing ability, human food usage, and animal feeds. The broad bean weevil (BBW) *Bruchus rufimanus* is an economic pest of faba beans in which larvae development during pod setting and filling threaten production through seed damage and yield loss. A holistic study that determines reliable traits associated with weevil resistance under Lithuanian growing condition is needed to understand BBW-faba bean interaction and protect seed quality. The goal of this study is to provide insight into how measured traits of cultivars are associated with BBW damage traits and to determine traits that may contribute to BBW resistance. A field experiment evaluated eight selected faba bean cultivars under natural BBW infestation to assess the cultivar resistance effect on BBW activities. The analysis of variance, mean separation, correlation analysis, and multivariate analysis of measure traits were performed. Significant differences among cultivars were detected for several measured plant and BBW-related traits. Descriptive differences between the insecticide-treated and untreated sections were observed for egg deposition, adult emergence holes, and number of pods per plant.. Lower-node pods had higher egg deposition than middle-node pods. The pod and seed traits, and weevil damage trait were the major source of variation among the 8 cultivars as explained by the principal component analysis. An inverse relationship exists between most of the measure pod traits and seed hardness and protein. These preliminary results suggest that BBW susceptibility in faba bean may be associated with multiple plant and insect-related traits.

Keywords: Cultivar evaluation, Host plant resistance, Oviposition, Phenotypic traits, Seed damage

INTEGRATIVE CROSS-DATASET ANALYSIS OF THE TRITICUM AESTIVUM NON-CODING TRANSCRIPTOME UNDER CLIMATE STRESS

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Hexaploid wheat (*Triticum aestivum* L.) relies on complex, subgenome-asymmetric transcriptomic networks to regulate development and respond to climatic stress. However, integrated analyses of non-coding transcriptomes across developmental stages, environmental conditions, and spikelet micro-environments remain limited. In this study, we integrated three independent public RNA-seq datasets covering grain developmental stages (10, 20, and 30 days post-anthesis (DPA)), acute heat stress (42 °C), and spikelet positions within a unified computational framework. Filtering based on transcript structure and coding potential we identified a high-confidence set of novel wheat long non-coding RNAs (lncRNAs), classified as long intergenic, nested, or antisense transcripts. We identified a prominent D-subgenome-associated lncRNA locus, MSTRG.9649, with a distinct late grain developmental expression profile. Its abundance increased approximately 120-fold at 30 DPA , reaching 790.33 transcripts per million (TPM), but was undetectable under early heat stress and across different spikelet positions. In silico target mimicry analysis identified MSTRG.9649 as a putative competing endogenous RNA (ceRNA) decoy sponge with predicted base-pairing sites for tae-miR9667-5p and tae-miR5049-3p, suggesting a potential role in modulating miRNA-mediated regulation of basic helix–loop–helix (bHLH) transcription factors and DEAD-box RNA helicases during grain maturation. Genome-wide analysis using the Subgenome Expression Asymmetry Index revealed a substantial, dominant contribution of the D subgenome to non-coding RNA expression under acute heat stress (329,758.51 TPM). Graph-theoretic network topology analysis further indicated severe heat stress-associated changes in regulatory organization, with node-degree variance collapsing from 26.54 down to 4.20, tracking an environmental hub de-escalation. Finally, a machine learning Random Forest classifier identified GC content (48.69% feature importance) and transcript length (48.03%) as the strongest predictors of lncRNA stability. These findings highlight potential regulatory roles of wheat lncRNAs in grain development and stress responses, identifying high-priority candidates for functional validation and climate-resilient crop breeding.

FROM STRUCTURAL POTENTIAL TO BIOREGIONAL DEVELOPMENT: THE ROLE OF INSTITUTIONAL CAPACITY IN RURAL LATVIA

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Bioregional development offers opportunities to integrate agricultural resources, environmental objectives and local economic activities within a place-based approach. However, favourable structural conditions alone may not be sufficient to support bioregional initiatives. This study examines how institutional capacity may influence the ability of rural territories to transform their structural potential into development outcomes. The study focuses on 36 Latvian municipalities and applies a comparative analytical framework combining structural conditions, development trajectories and institutional capacity. Structural potential is assessed through socioeconomic, agricultural and environmental indicators, while development trajectories are examined using longitudinal data. Institutional capacity is conceptualised through three dimensions: coordination, absorptive capacity and adaptive capacity. Municipalities with similar structural characteristics are compared using peer benchmarking, followed by an assessment of the relationship between institutional capacity and differences in observed development trajectories. The analysis is designed to identify differences in development trajectories among municipalities with comparable structural potential. Particular attention is given to whether variation in institutional capacity is associated with differences between observed development outcomes and those expected from structural conditions. The findings will provide an empirical basis for assessing the relevance of institutional capacity to bioregional development opportunities. The study contributes to understanding the relationship between territorial resources, institutional capacity and bioregional development. By integrating structural and institutional perspectives, the proposed approach may support more differentiated municipal strategic planning and help identify governance conditions relevant to future bioregional initiatives in Latvia.

Keywords: bioregional development, institutional capacity, rural development, structural potential, local governance, Latvia.

DOSE-DEPENDENT EFFECTS OF MAITAKE (*GRIFOLA FRONDOSA*) EXTRACT ON HUMAN OVARIAN CELLS: FROM TGF-B1 SUPPRESSION TO CYTOTOXICITY

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Maitake (*Grifola frondosa*) is an edible medicinal mushroom used as a dietary supplement, among others to support ovulation in women with polycystic ovary syndrome. However, its direct effects on ovarian cells remain unclear. This study examined its effects on viability, progesterone release, TGF-β1 secretion and apoptosis-inducing factor (AIF) in human ovarian cell lines. Ovarian granulosa cells (HGL5) and ovarian granulosa tumour cells (COV434) were treated with Maitake extract (10–10,000 µg/mL) for 24 hours. Untreated and vehicle-treated cells (1% DMSO) served as control groups. Viability was assessed by AlamarBlue™ assay. Progesterone (both HGL5, COV434), TGF-β1 and AIF (HGL5) were quantified by ELISA. Data were analysed by one-way ANOVA (Dunnett's test). Viability of HGL5 cells was unaffected up to 500 µg/mL and significantly reduced at 1,000 µg/mL ($P \leq 0.001$), whereas 5,000–10,000 µg/mL reduced viability of both cell lines ($P \leq 0.001$). In HGL5 cells, the extract decreased TGF-β1 secretion at 100–5,000 µg/mL ($P \leq 0.05$ to $P \leq 0.01$) and progesterone release from 500 µg/mL onwards ($P \leq 0.01$ to $P \leq 0.001$). In COV434 cells, progesterone secretion was significantly reduced only at 10,000 µg/mL ($P \leq 0.001$). AIF in HGL5 cells increased only at 2,500–10,000 µg/mL ($P \leq 0.01$ to $P \leq 0.001$). Maitake extract affects human granulosa cells in a dual, dose-dependent manner: at non-cytotoxic concentrations it modulates secretory activity, whereas high concentrations induce cell death accompanied by increased AIF, without selectivity towards tumorous cells. The suppression of TGF-β1, a key local regulator of follicular development and ovarian fibrosis, may contribute to the reported effects of Maitake on ovarian function. As TGF-β1 itself inhibits progesterone synthesis, the parallel decrease in progesterone suggests an additional, independent action of the extract. This should be considered when evaluating the safety of Maitake supplements in women of reproductive age. These results suggest biologically significant impacts on both non-tumor and tumour granulosa cell lines, prompting additional research.

Key words: Maitake, ovarian granulosa cells, steroidogenesis, viability, medicinal mushrooms

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INFLUENCE OF WASTE-DERIVED ACIDIC ORGANIC-MINERAL FERTILIZERS ON PEAT CHEMICAL PROPERTIES AND BERRY POLYPHENOL CONTENT IN HIGHBUSH BLUEBERRY

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The increasing demand for more resource-efficient agricultural production highlights the need to improve nutrient recycling and develop alternative fertilizer sources from organic waste materials. In acidophilic crops such as highbush blueberry, fertilizer efficiency is closely linked not only to nutrient supply but also to the maintenance of an appropriately acidic substrate environment. Therefore, waste-derived fertilizers capable of simultaneously modifying substrate acidity and supplying plant nutrients may represent a relevant approach for more sustainable nutrient management. The aim of this study was to evaluate the influence of acidic organic-mineral fertilizers produced from alkaline manure compost on peat pH, macronutrient dynamics, and berry polyphenol content. Liquid fertilizers were produced using nitric acid (HNO_3), sulfuric acid (H_2SO_4), or a combination of HNO_3 and H_2SO_4. The treatments were compared with an unfertilized control and a commercial liquid fertilizer for blueberries. Peat pH and nitrogen (N), phosphorus (P), and potassium (K) concentrations were monitored throughout the growing season, and their relationships with berry polyphenol content were assessed. Fertilized treatments generally reduced peat pH and increased macronutrient availability compared with the control. Nitrogen concentrations increased during the fertilization period, particularly in the commercial fertilizer and HNO_3 treatments. Higher phosphorus concentrations were mainly observed in the commercial and HNO_3+H_2SO_4 treatments, whereas the H_2SO_4 treatment resulted in the highest potassium concentrations. Macronutrient concentrations were predominantly negatively correlated with peat pH, with the strongest relationship observed between phosphorus and pH. Negative correlations were also identified between peat macronutrient concentrations and berry polyphenol content. The results demonstrate that the chemical composition of waste-derived acidic fertilizers affects peat acidity, nutrient dynamics, and berry biochemical characteristics, supporting further evaluation of these fertilizers as a nutrient-recycling strategy for highbush blueberry cultivation.

EFFICACY OF *IN VITRO* CHEMOTHERAPY FOR RASPBERRY BUSHY DWARF VIRUS (IDAEOVIRUS RUBI) ELIMINATION IN RASPBERRY CV. 'PERSEYA'

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Chemotherapy is one of the methods used for the elimination of viruses in plants, based on the application of compounds with antiviral effects. Ribavirin is commonly used for this purpose, but it may cause severe phytotoxic stress in microshoots. To preserve the raspberry cultivar 'Perseya', for which virus-free clones were unavailable, we investigated the efficiency of raspberry bushy dwarf virus (RBDV) elimination via *in vitro* chemotherapy using ribavirin, acyclovir, oseltamivir, and rimantadine. Microshoots were cultivated on MS medium supplemented with ribavirin, acyclovir, and rimantadine at concentrations of 20, 40, and 60 mg/L, and with oseltamivir at concentrations of 40, 60, and 80 mg/L for 30 days. The effects of the treatment on microshoot height and multiplication coefficient were assessed. Ribavirin showed that the most pronounced phytotoxic effects, causing pale-yellow shoot tips, plant mortality ranging from 6.3% to 40.0%, and reduction in microshoot height to 70.0% of the control. In contrast, oseltamivir slightly stimulated growth, increasing shoot height to 106.4% of the control. The presence of RBDV was assessed by ELISA. The results presented here indicate the proportion of plants in which RBDV was not detected. No ELISA-negative plants were obtained following ribavirin treatment under the tested conditions. Acyclovir was the most effective treatment, resulting in 42.8% ELISA-negative plants at 60 mg/L and 14.3% at 40 mg/L. At the highest tested concentration of oseltamivir (80 mg/L), 14.3% of plants tested negative for RBDV. These results identify acyclovir at 60 mg/L as the most promising of the tested treatments for obtaining raspberry plants in which RBDV was not detected by ELISA. Cultivation and monitoring of the treated plants are ongoing to assess the persistence of their ELISA-negative status over time.

Keywords: *Rubus idaeus,* RBDV, elimination, phytotoxicity, ribavirin

SYSTEMATIZATION OF BREEDING MATERIAL BASED ON KEY MORPHOLOGICAL AND AGRONOMIC TRAITS

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Systematizing breeding material makes it possible to track changes in its phenotypic structure over time, as well as to identify traits for which the distribution of lines has shifted toward desired categories. Comparing materials from different periods characterizes the development trends of the breeding stock as it undergoes renewal. The material consisted of 154 inbred lines of diverse genetic origin and from different periods of development, obtained from the collection of the Laboratory of Maize Breeding and Seed Production, as well as the National Center for Plant Genetic Resources of Ukraine. A comparison of breeding material across four periods (from 1950 to 2020) revealed that its structural transformation was driven primarily by the enhanced expression of traits associated with grain yield per ear. While breeding material from the earlier periods was characterized predominantly by intermediate trait values, the material from 1991–2020 showed an increased proportion of forms with a high number of grains per ear and greater grain weight. These trends indicate a gradual accumulation of traits that contribute to higher grain yield and create opportunities for the further selection of valuable genotypes. Analysis of breeding material from four periods revealed a gradual shifts toward the enhanced expression of traits associated with grain productivity specifically, a high number of grains per ear and greater grain weight. Breeding efforts should focus on combining high-yield traits with desirable morphological characteristics, while maintaining sufficient genetic variability for the development of improved genotypes.

PERFORMANCE AND ADAPTIVE STRATEGIES DEVELOPED BY SOME WOODY SPECIES UNDER ARID CLIMATE CONDITIONS

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Mediterranean woody species are increasingly exposed to prolonged drought and rising temperatures due to climate change, threatening the sustainability of arid ecosystems. Understanding the ecophysiological, biochemical, morphological, and anatomical mechanisms underlying drought adaptation is essential for predicting species resilience and supporting conservation and restoration strategies. This study aimed to compare the performance and adaptive strategies of four Mediterranean woody species (*Argania spinosa, Pistacia lentiscus, Olea europaea* subsp. *maroccana*, and *Tetraclinis articulata*) growing under natural arid conditions in southwestern Morocco and to identify the key functional traits associated with drought tolerance. Five mature individuals per species were monitored during winter, spring, and summer in the Mesguina forest (Amskroud, southwestern Morocco). Ecophysiological measurements included relative water content (RWC), gas exchange parameters (net photosynthetic rate, stomatal conductance, transpiration rate, and intrinsic water-use efficiency), chlorophyll and carotenoid contents, free proline concentration, leaf mass per area (LMA), leaf thickness, and stomatal traits. Principal component analysis (PCA) was performed to identify relationships between functional traits and drought adaptation. The study site was characterized by an annual rainfall of 73.83 mm, an Emberger aridity index of 20.47, and approximately six months of drought. PCA explained 70.76%, 77.38%, and 78.22% of the total variance during winter, spring, and summer, respectively. *Pistacia lentiscus* maintained the highest RWC and photosynthetic performance, whereas *Argania spinosa* combined efficient stomatal regulation with high carotenoid and proline contents and tolerated leaf water potentials below −5 MPa. *Olea europaea* subsp. *maroccana* developed early stomatal closure, thick cuticles, and protective trichomes, while Tetraclinis articulata exhibited reduced photosynthetic performance and poor stomatal regulation, indicating greater drought sensitivity. Mediterranean woody species exhibit distinct but complementary drought-adaptive strategies through coordinated physiological, biochemical, morphological, and anatomical adjustments. These findings improve our understanding of plant resilience under arid conditions and provide valuable functional traits for conservation programs and the selection of drought-tolerant species under future climate change.

AGRONOMY, AGROBIOLOGY, AGROECOLOGY, AND AGRICULTURAL ENGINEERING

SIMULATION ANALYSIS OF PARTICLE BEHAVIOUR DURING BIOCHAR AND MANURE FERTILIZER GRANULATION

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The use of biochar and manure as raw materials for granular fertilizer production is a sustainable way to recycle organic waste and recover essential nutrients for agricultural purposes. Particle movement and granule formation are influenced by complex interactions between particles and processing machinery throughout the granulation process. Investigating these processes and assessing particle behaviour during granulation is made possible by numerical modelling. The aim of this work is to analyse the granulation behaviour of biochar and manure-based fertilizer materials using EDEM software, with specific attention to particle movement and granule formation under selected processing circumstances. The design of the granulator is created using SOLIDWORKS Design 2025 Software and develop a model of the granulation process to simulate the particle interactions during granulation formation. The influence of selected operating and material parameters was investigated, and the simulation results such as angular velocity, compressive force were evaluated with simulation time. The obtained results provide a preliminary assessment of the granulation behaviour of biochar and manure-based materials, as well as demonstrating the potential of DEM modelling for investigating the organic granular fertilizer production. The use of biochar and manure as fertilizer feedstocks can contribute to sustainable agriculture by valorising organic residues, reducing waste and supporting the recycling of nutrients back into agricultural soils.

Key words: Biochar, Manure, Granular Fertilizer, Granulation, EDEM, Particle Behaviour, Numerical Modelling.

EFFECTS OF TILLAGE, CROP MANAGEMENT AND REDUCED NITROGEN FERTILIZATION ON SOIL CO_2 EMISSIONS AND WINTER WHEAT PERFORMANCE

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Sustainable crop production requires strategies that reduce mineral nitrogen inputs while maintaining soil functioning and crop productivity. This study evaluated the effects of tillage, crop management and reduced N fertilization on soil CO_2 emissions, soil temperature and moisture, winter wheat yield and grain quality. A long-term field experiment established in 2021 at the Lithuanian Research Centre for Agriculture and Forestry was arranged in a split–split–plot design with four replications. Conventional tillage (CT), reduced tillage (RT) and no-tillage (NT) were combined with integrated (I) or conventional (C) crop management and either no N fertilization or a 30% reduced N rate. Results from 2025–2026 showed clear temporal variation in soil CO_2 emissions, with the highest values generally observed in May. Fertilization tended to increase CO_2 emissions, although responses depended on tillage, crop management and sampling date. Soil temperature followed a seasonal pattern, while soil moisture varied among sampling dates and treatments. In 2025, CO_2 emissions were negatively correlated with soil moisture under conventional management and positively correlated with electrical conductivity. Winter wheat yield responses differed between years. In 2025, N fertilization significantly increased yield, whereas tillage and crop management had no significant main effects. In 2026, yield differences among tillage systems were more evident under integrated management, particularly without N fertilization, with CT producing the highest and NT the lowest yield. In 2025, fertilization generally increased grain protein and gluten contents, while starch tended to decrease. CT frequently resulted in higher protein, gluten and sedimentation values than RT and NT. Overall, these preliminary results indicate that soil CO_2 emissions and winter wheat performance depend on interactions among management practices and growing-season conditions, emphasizing the need for multi-year evaluation.

MICROBIAL DIVERSITY AND ANTIMICROBIAL RESISTANCE GENES IN HONEY BEE DRONES AND DANDELIONS: POTENTIAL ROUTES OF TRANSMISSION

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The microbiota of a honey bee colony (*Apis mellifera* L.) comprises a complex community of microorganisms associated with bees and the hive environment. These microorganisms support colony health by contributing to immune function, metabolic processes, and the maturation of bee-derived products. Honey bee microbiota is acquired and transmitted through interactions with nestmates, hive environment, and flowering plants during foraging. Consequently, honey bees and their associated microbial communities may harbor antimicrobial resistance genes (ARGs) and contribute to their dissemination within the hive and surrounding environment. This study aimed to characterize bacterial communities and investigate ARG prevalence in the entire body of honey bee drones at different developmental stages and in dandelions (*Taraxacum* spp.). Metagenomic DNA was extracted from drone and dandelion samples, and bacterial community composition was characterized using Next-Generation Sequencing of the PCR-amplified V3–V4 region of the 16S rRNA gene. Members of the family *Enterobacteriaceae*, particularly *Frischella* and *Gilliamella,* prevailed in unsealed larvae, pupae, and adult drones, whereas *Lactobacillaceae*, represented mainly by *Lactobacillus, Bombilactobacillus*, and *Apilactobacillus*, dominated in sealed larvae. In dandelions, *Lactococcus* and *Pseudomonas* were the most abundant genera. PCR-based screening revealed a high prevalence of ARGs conferring resistance to tetracyclines and sulfonamides, with the greatest ARG diversity and detection frequency observed in dandelion and larval metagenomic samples. The detection of shared bacterial taxa and ARGs in drones and dandelions highlights the potential for microbial exchange at the bee–plant interface. These findings provide insights into the distribution of antimicrobial resistance within honey bee-associated microbial communities and its potential transmission between bees and their foraging environment. This study has received funding from the Research Council of Lithuania (LMTLT), agreement No. S-MIP-24-55.

EFFECTIVENESS OF ADAPTATION MEASURES FOR AGRICULTURAL CROP PRODUCTIVITY UNDER CHANGING CLIMATE CONDITIONS

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Agriculture contributes around half of nitrogen entering the Baltic Sea. The EU Farm to Fork strategy demands a 20% reduction in synthetic fertilizer use by 2030. Meanwhile, fungicide seed treatments are being phased out of the market, and late-summer drought increasingly threatens grain fill in the Baltic region. This study tested whether biological and biophysical tools could address all three problems: maintaining yield and grain quality while reducing synthetic nitrogen by 30% across a pea–winter wheat–winter oilseed rape rotation on alkaline soils. A randomized complete block field trial with 13 treatments and 3 replicates was established on alkaline soil in central Lithuania. Treatments ranged from high nitrogen (180 kg N/ha wheat; 45 kg N/ha peas) to reduced baseline rates (120/30 kg N/ha) combined with biological seed treatment (fulvic acid + Mo, Zn, Mn, Cu), soil-applied humic acid granules (500 kg/ha per rotation), superabsorbent polymer hydrogel (200 kg/ha per rotation), and foliar nutrition (fulvic acid + Mo, Zn, Mn, Cu). A parallel vegetative pot experiment tested the same alternatives on leached clay and sandy soil. Excess nitrogen produced taller plants but not higher yield. High nitrogen produced the lightest wheat grain, but the highest protein percentage. Fungicide seed treatment suppressed root mass in both soil types in the vegetative pot experiment. Humic acid application produced the highest root and shoot biomass among soil-applied treatments. A combined biological and biophysical approach maintained or improved crop yield and grain quality while reducing synthetic nitrogen by approximately 30% across a pea–winter wheat rotation on alkaline Baltic soils. Biological seed treatment showed the best yield results across crops. This study provides evidence that the EU nitrogen reduction target is agronomically viable.

SEARCH FOR SOIL MICROORGANISM STRAINS EXHIBITING ANTIBACTERIAL ACTIVITY

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Due to the rapidly spreading bacterial resistance to antimicrobial agents, traditional treatment methods are becoming ineffective, therefore increasing attention is being directed towards the search for new antimicrobial compounds. Soil, characterized by high microbial diversity and resource competition, is a promising source for discovering bacterial strains with antibacterial activity. This study aimed to performe search for soil and cave microorganisms possessing antibacterial and antifungal activity by isolating bacterial isolates from forest soil, bog soil, and Kruberio-Voronja cave samples, evaluating their antibacterial activity against four plant pathogenic strains (*Agrobacterium radiobacter, Pectobacterium carotovorum, Pseudomonas syringae, Xanthomonas campestris*), determining antifungal activity against six fungal strains, and identifying the most active isolates using molecular methods. From forest and bog soil samples, using different culture media (R2A, *Acidobacterium medium, Granulicella medium*, 0.2×R2A), 56 bacterial isolates were obtained, while an additional 15 isolates originating from the Kruberio-Voronja cave were used from the laboratory collection. Antibacterial activity was assessed using the streak and well diffusion methods, while antifungal activity was evaluated using the dual culture method. Genomic DNA of the most active isolates was extracted, and their identification was performed using 16S rRNA gene PCR and electrophoresis. Two isolates (PA23 and E1) inhibited the growth of all four tested plant pathogens. In antifungal activity tests, isolate PR15, demonstrated the broadest effect by inhibiting the growth of *Rhizopus* sp., *Trichoderma harzianum* and *Mucor* sp. Isolates E9 and PR11 inhibited the growth of three tested plant pathogens. During molecular identification, genomic DNA was successfully extracted from isolates E9, E1, PA23, PR15 and PR11, and the 16S DNA gene fragment was amplified. Amplified isolates were identified as *Collimonas* sp. and *Pseudomonas* sp. Isolates E1, E9, PR11, PA23 and PR15 exhibited broad antogonisitc effects and are suitable for further studies.

INFLUENCE OF BOTANICAL ORIGIN AND DRYING TEMPERATURE ON THE ANTIOXIDANT POTENTIAL OF MONOFLORAL BEE POLLEN

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Bee pollen is a rich source of natural antioxidants. This study evaluated the antioxidant activity of monofloral bee pollen from different botanical origins and assessed the effect of drying temperature on its antioxidant potential. Antioxidant activity was determined using the DPPH radical scavenging assay in aqueous and methanolic extracts of monofloral bee pollen collected from five plant species: *Phacelia tanacetifolia* (lacy phacelia), *Tilia* spp. (lime), Papaver somniferum (opium poppy), *Brassica napus* Group Napus (rapeseed), and *Helianthus annuus* (sunflower). Each sample was analysed in five replicates and statistically evaluated by Tukey's test. Additionally, pollen samples from phacelia and lime were dried at 40 °C, 60 °C, and 80 °C to assess the influence of temperature on antioxidant activity. Marked differences in antioxidant activity were observed among the evaluated monofloral bee pollens, with values ranging from 26.5% (sunflower) to 61.3% (lacy phacelia) in aqueous extracts and from 38.5% (sunflower) to 93.7% (rapeseed) in methanolic extracts. The highest values of antioxidant activity were recorded when pollen was dried at temperatures up to 40 °C, reaching 52.5-59.5% in aqueous extracts and 62.9-93.7 in methanolic extracts. As the drying temperature increased, antioxidant activity gradually declined. At 80 °C, antioxidant activity was markedly reduced in both extracts, 37.0-47-2% in aqueous extracts and 55.4-86.6% in methanolic extracts. Overall, the results confirmed that antioxidant activity is strongly influenced by botanical origin, extraction solvent, and drying conditions, with methanolic extracts showing superior radical-scavenging activity and higher drying temperatures leading to a decline in antioxidant capacity. These findings highlight the importance of proper processing conditions and confirm the potential of monofloral bee pollen as a natural source of antioxidants for functional foods and nutraceutical applications.

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SCREENING AND GENOMIC ANALYSIS OF PYRETHROID-DEGRADING BACTERIAL CARBOXYLESTERASES

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Pyrethroids are widely used in agriculture for crop protection, with an average of 12.8 tonnes applied annually in Lithuania during 2020 – 2023 (FAOSTAT, 2026). Their persistence and lipophilicity may promote accumulation in soils and sediments, posing risks to non-target organisms and highlighting the need for sustainable remediation strategies. Microbial bioremediation involving lipolytic enzymes, including pyrethroid hydrolases, represents a promising approach for removing pyrethroid contaminants [1,2]. Pyrethroid-degrading bacteria were isolated from plant-growing substrates collected at five Lithuanian farmlands using enrichment cultures with permethrin as the sole carbon source. Among 79 isolates identified by 16S rDNA sequencing and screening for target hydrolytic activity, *Pseudomonas* sp. III8 and *Rhodanobacter* sp. II14 were selected for further characterization. Partially purified intracellular and extracellular protein fractions were analyzed using p-nitrophenyl butyrate (p-NPB) hydrolysis, agar diffusion, and zymography assays. Both isolates exhibited intracellular hydrolytic activity toward permethrin and tributyrin, with active bands at 35–70 kDa in *Pseudomonas* sp. III8 and approximately 70 kDa in *Rhodanobacter* sp. II14. Extracellular activity was additionally detected in Pseudomonas sp. III8, with active bands at 70–100 kDa. Whole-genome sequencing followed by ANI and dDDH analyses identified the isolates as *Pseudomonas knackmussii* III8 and *Rhodanobacter spathiphylli* II14. Genome annotation identified several candidate lipolytic enzymes potentially associated with the observed hydrolytic activity and permethrin transformation, including EstA (~68 kDa), CaeA (~58 kDa), and Aes (~34 kDa) in *R. spathiphylli* II14 and PytH (~30 kDa) and EstA (~68 kDa) in *P. knackmussii* III8. Conventional PCR product sequencing confirmed the selected candidates. Phylogenetic and bioinformatic analyses further supported the functional assignment of the candidate proteins by revealing conserved catalytic features and relationships to homologous esterases. Semi-quantitative RT-PCR detected *P. knackmussii* pytH and estA and *R. spathiphylli* estA transcripts under all tested conditions, with no clear differences among LB, M9P, and M9G media, suggesting constitutive rather than permethrin-induced expression. Together, these findings indicate that the selected strains and their lipolytic enzymes are promising candidates for pyrethroid bioremediation in agricultural environments and need further investigation.

MICROPLASTIC CONTAMINATION AND PHYSICOCHEMICAL CHARACTERISTICS OF SEWAGE SLUDGE AND ITS TREATMENT PRODUCTS: IMPLICATIONS FOR AGRICULTURAL SOILS

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The agricultural application of sewage sludge (SS) and its treatment products represent a potential strategy for nutrient recycling and improving soil fertility. However, these materials may also serve as carriers of microplastics into agricultural soils, raising concerns regarding potential environmental impacts. According to Eurostat data, in 2024 Lithuania utilized approximately 16,000 tons of SS in agriculture, compared with the European average of around 79,000 tons. In contrast, neighboring Latvia reported just over 1,000 tons. Although sewage sludge utilization varies considerably across European Union, these figures highlight the substantial quantities of SS applied to agricultural soils. Previous studies have demonstrated that sewage sludge contains microplastics, although their concentrations and polymer compositions vary significantly between countries and even cities. Despite increasing scientific evidence of microplastic contamination in sewage sludge and its effects for soil ecosystems, microplastics remain unregulated in terms of permissible concentrations in SS intended for agricultural application. This study aims to assess and compare microplastic contamination in sewage sludge and its treatment products: digestate, biochar and ash, while characterizing their physicochemical properties. Microplastic polymer composition and concentrations were determined using pyrolysis–gas chromatography–mass spectrometry. Additionally, physicochemical parameters: pH, electrical conductivity, organic matter content and cations concentrations, were evaluated to characterize differences among the materials investigated. The physicochemical characterization revealed expected trends associated with different SS treatment processes. Biochar exhibited the highest pH, while ash showed the highest electrical conductivity and the lowest organic matter content. Cation concentrations varied among the materials, with digestate generally exhibiting elevated Na^+, NH_4^+, and K^+ concentrations, whereas ash was characterized by higher Mg^{2+} content. These findings provide a physicochemical baseline for the comparative assessment of microplastic contamination in sewage sludge and its treatment products. Microplastic polymer composition and concentrations will be presented at the conference.

Keywords: microplastic, contamination, sewage sludge, digestate, biochar.

REVEALING MEIOTIC ABNORMALITIES AND CYTOLOGICAL APPROACH TO INDUCE 2N GAMETE FORMATION IN THE INTERSPECIFIC LILIUM HYBRID

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The role of 2n pollen, formed as a result of abnormal meiosis, has long intrigued researchers, particularly given its significance in chromosome doubling during mitosis in interspecific hybrids. Beyond this, its contribution to homologous recombination makes it a valuable tool for introgression breeding. In the present study, I set out to determine whether viable 2n pollen could be induced in the otherwise sterile oreinpet (OT) (2n=2x=24) interspecific Lilium hybrid 'OT Yelloween' a question that speaks directly to practical challenges in lily breeding. To this end, I conducted experiments using bulbs cultivated in 16 cm pots at the smart farm facility at Kyungpook National University in Daegu, South Korea. Flower buds of 'Yelloween' at early meiotic stages were exposed to N_2O at 600 kPa for either 36 or 48 hours. The results were striking: the 36-hour treatment reliably induced 2n pollen at a frequency of 17.75%. By contrast, extending the exposure to 48 hours proved lethal, with plants succumbing within days. During microsporogenesis, I observed a high frequency of meiotic abnormalities, including chromosome bridges, lagging chromosomes, and micronuclei, with Anaphase II being the stage most prone to these disruptions. These findings are consistent with earlier reports in Lilium and other genera, which connect meiotic irregularities to reduced fertility and the formation of unreduced gametes. My observations underscore that the early meiotic window, from prophase I to metaphase I, is critical for successful induction in lily hybrids. Taken together, these results point to the utility of carefully timed N_2O treatments in generating sexual polyploids and, ultimately, in advancing the field of lily breeding.

Keywords: 2n pollen, Hybridization, Reduction Division, Ristitution, Lilium

OMICS ANALYSIS REVEALS THE INVOLVEMENT OF CARBON AND FLAVONOID BIOSYNTHESIS IN LOW PHOSPHORUS TOLERANCE IN COTTON

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Low phosphorus (P) is one of the limiting factors in sustainable cotton production. However, little is known about the performance of contrasting low P tolerant cotton genotypes that might be a possible option to grow in low P condition. In the current study, we characterized the response of two cotton genotypes, Jimian169 a strong low P tolerant, and DES926 a weak low P tolerant genotypes under low and normal P conditions. The results showed that low P greatly inhibited growth, dry matter production, photosynthesis, and enzymatic activities related to antioxidant system and carbohydrate metabolism and the inhibition was more in DES926 as compared to Jimian169. In contrast, low P improved root morphology, carbohydrate accumulation, and P metabolism, especially in Jimian169, whereas the opposite responses were observed for DES926. The strong low P tolerance in Jimian169 is linked with a better root system and enhanced P and carbohydrate metabolism, suggesting that Jimian169 is a model genotype for cotton breeding. Results thus indicate that the Jimian169, compared with DES926, tolerates low P by enhancing carbohydrate metabolism and by inducing the activity of several enzymes related to P metabolism. This apparently causes rapid P turnover and enables the Jimian169 to use P more efficiently. Moreover, the transcript level of the key genes could provide useful information to study the molecular mechanism of low P tolerance in cotton.

HORTICULTURE, AGRONOMY

EFFECTS OF SOIL AMENDMENTS ON THE GROWTH OF REPLANTED APPLE ROOTSTOCK G.41 AND SOIL FUNGAL COMMUNITY

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Apple replant disease (ARD) negatively affects the growth, development, and yield of apple trees. As new orchards are usually established on old orchard sites, understanding soil microbiota is key to sustainable production. The aim of this study was to evaluate the effects of soil amendments on G.41 rootstock growth parameters and to determine trends in microbiota composition. Rootstocks were grown in pots filled with soil from a former apple tree nursery in a high plastic tunnel. The soil was enriched with the following additives: Mycostop (*Streptomyces griseoviridis* K61); Bacteria (*Bacillus halotolerans, B. velezensis*); Activation (*Azospirillum brasilense, Agrobacterium pusense, Ochrobactrum pseudogrignonense,* and *Meyerozyma guilliermondii*); Asir Fruit (*Rhizoglomus irregularis, Funneliformis mosseae, Trichoderma koningii, Bacillus megaterium*, and NPK 8-6-4); and Rootex (NPK 7-47-6, free amino acids, and phytohormones). Soil without additives served as control. At the end of the growing season, we evaluated rootstock growth parameters and collected soil samples to analyse soil microbiota composition, targeting the ITS1 region via NGS (Biomarker Technologies, Germany). Biometric measurements revealed significant effects of Rootex and Asir Fruit on rootstock growth, whereas the other treatments had no effect. Compared with the control, Rootex treatment showed the greatest increase in shoot length (36.9 and 92.4 cm, respectively) and stem diameter (0.99 and 1.61 mm, respectively). In comparison, Asir Fruit increased stem diameter (1.85 mm) and shoot length (58.3 cm). Based on the relative abundance of fungal phyla in the root zone, Ascomycota remained the dominant phylum across all treatments, followed by Glomeromycota and *Mortierellomycota.* Principal component analysis highlighted the Bacteria and Rootex treatments as distinct outliers. Sequencing revealed shifts in the fungal community: Rootex increased the relative abundance of *Fusarium* spp. (from 8.19% to 19.24%) while reducing *Mortierella* spp. (from 15.59% to 4.48%) and *Tetracladium* spp. (from 4.42% to 0.89%). Conversely, the Bacteria treatment increased *Mortierella* spp. (from 15.59% to 31.52%) and *Penicillium* spp. (from 3.17% to 6.43%). Soil amendments affected both apple rootstock development and the composition of the rhizosphere fungal community. Further research is needed to clarify how these microbiota shifts contribute to ARD suppression and to develop effective, sustainable management strategies.

PROPOLIS EXTRACTS AS POTENTIAL BIOCONTROL AGENTS AGAINST BOTRYTIS CINEREA

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Apple postharvest diseases caused by fungi, including *Botrytis cinerea*, contribute to storage losses, while reliance on synthetic fungicides is increasingly constrained. Propolis contains antimicrobial compounds and may offer a plant-derived alternative. This study evaluated the *in vitro* antifungal activity of aqueous and ethanolic propolis extracts against *B. cinerea*. Three different host-origin *B. cinerea* isolates (38R – host strawberry Elkat, 129 – host apple Auksis and 176 – host apple Ligol) were evaluated on potato dextrose agar (PDA) mixed with aqueous propolis extract (VA), ethanolic extract (ET), or ethanolic extract re-extracting the aqueous extraction byproducts (ET-2), at concentrations of 1.5%, 3.0% and 4.5%. Mycelial diameter was measured at 2, 4 and 7 days post-inoculation (DPI), and growth inhibition calculated compared to control. A reinoculation performed to distinguish between fungistatic (fungi start to grow) and fungicidal (total absence of growth) effects. Antifungal activity varied by extract type, concentration, isolate and assessment time. At 4.5%, ET and ET-2 completely inhibited mycelial growth of all three isolates through 7 DPI (100% inhibition). Lower concentrations of ET and ET-2 showed variable but lower inhibition, while VA was least effective. Reinoculation indicated a predominantly fungistatic rather than fungicidal effect. Propolis extracts, particularly ET and ET2 at 4.5%, strongly suppressed B. cinerea growth *in vitro*. Further investigations are required to evaluate their effectiveness in controlling postharvest apple rot during storage.

Keywords: aqueous extract, ethanolic extract, inhibition, effectiveness.

USING HYDROPONIC SOLUTION SALINITY TO ENRICH PHYTOCHEMICALS IN FACULTATIVE HALOPHYTES

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Salinity has significant potential to improve the nutritional quality of hydroponically grown facultative halophytes but may also reduce plant biomass and survival. This study investigated whether controlled salinity alters nutritional and phytochemical profiles and assessed the associated impact on plant growth. Two *Amaranthaceae* halophytes, *Amaranthus passion* and *Amaranthus lividus*, were cultivated in deep-water culture within walk-in hydroponic growth chambers under constant environmental conditions (PPFD 250 µmol m^{-2} s^{-1}, Blue: Red: Far-Red LED spectrum at 22:65:13 ratio, and 18/22 ± 2 °C) in hydroponic solutions containing 0, 150, and 300 mM NaCl. Both species maintained survival rates of 96.7–100% at 150 mM NaCl, whereas 300 mM NaCl significantly reduced survival rate to 66.7% in *A. passion* and 56.7% in *A. lividus*, accompanied by decreased shoot dry weight. Despite these reductions, phytochemical quality improved, with species-specific responses to salinity. In *A. passion*, 300 mM NaCl resulted in the highest levels of fructose (10.2 mg g^{-1}), glucose (13.0 mg g^{-1}), citric acid (6.0 mg g^{-1}), DPPH radical-scavenging activity (23.6 µM TE g^{-1}), and nutrient-use efficiency for P, Ca, Mg, Fe, B, and Zn, while simultaneously reducing the antinutrient oxalic acid (3.0 mg g^{-1}). Conversely, 150 mM NaCl resulted in the highest total phenolic content (TPC) in *A. lividus* (30.6 mg g^{-1} DW) and the greatest FRAP activity (3.0 µM TE g^{-1}) in *A. passion*. Principal component analysis further differentiated the effect of salinity based on their phytochemical and mineral profiles. *A. lividus* at 150 mM NaCl represents the most practical option, maximizing phenolics while maintaining high survival and viable biomass, whereas *A. passion* achieves peak sugar content, antioxidant capacity, and micronutrient efficiency only at 300 mM NaCl. These results support using 150 mM salinity to improve nutritional and phytochemical attributes of tested species without unacceptable yield losses.

Keywords: facultative halophyte; salinity biofortification; phenolics; antioxidant capacity; nutrient-use efficiency.

FINDING THE BALANCE BETWEEN LIGHTING ENERGY USE EFFICIENCY AND PHYTOCHEMICAL YIELD IN LEONURUS CARDIACA CULTIVATED IN VERTICAL FARM

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Growing interest in high-value pharmaceutical crops of standardized quality encourages the development of precision cultivation methods. Growing crops in controlled environment agriculture (CEA) could help obtain plant material year-round, get predictable and planned yields of uniform and standardized phytochemical quality. Artificial lighting is one of the main factors, affecting plant growth and metabolism, but together electricity costs are one of the largest expenses in CEA. Therefore, our aim was to explore the highest light energy use efficiency by balancing lighting intensity, biomass and phytochemical yield of well-known *Leonurus cardiaca* medicinal plant. Plants were cultivated in CEA chambers (21/17°C, 16 h photoperiod) in hydroponic systems. Light emitting diode (LED) artificial lighting with spectra, consisting of 21.6% blue (455 nm), 65% red (660 nm) and 13.4% far-red (740 nm) light was applied at three different lighting intensities of 150, 300 and 450 µmol m-2 s-1. Plant material was collected at two growth stages: branching (BBCH 21-29) and early flower bud stage (BBCH~51). Biomass productivity and total phenolic contents in leaves were measured and energy use efficiency evaluated. The results show significant lighting intensity effects on total phenolic contents and biomass of *Leonurus* plants, but also meaningful change in electricity costs at different lighting intensities applied. We disclose, which lighting intensity level in terms of phytochemical yield justify the expenses for electricity, seeking for profitable phytochemical-rich medicinal plant material cultivation in CEA.

BIOCHEMICAL POTENTIAL OF FERMENTED BIRCH SAP SUPPLEMENTED WITH BERRY LEAVES

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Blackcurrant (*Ribes nigrum* L.) is an aromatic deciduous shrub rich in bioactive compounds, including phenolic acids, organic acids, polyunsaturated fatty acids, and polyphenols. Due to their polyphenolic content, the leaves exhibit anti-inflammatory, antioxidant, and antimicrobial properties, which may increase when fermented. Therefore, the aim of the study was to investigate biochemical composition changes in fermented birch sap supplemented with black currant leaves. Birch sap supplemented with dried black currant leaves powder (FBL) (powder-to-liquid ratio 1:20, w/v) and fermented for 6 days in sterile jars at 28 °C, with sampling points at days 0, 3, and 6. Birch sap without black currant leaves was fermented in parallel. Biochemical composition was determined by measuring antioxidant activity using ABTS and DPPH assays, as well as by spectrophotometrically determining the total phenolic content (TPC) using the Folin-Ciocalteu method, all measurements were performed in triplicates. The antioxidant activity of FBL, as measured by the ABTS assay, increased during fermentation from day 0 to day 6, with little to no change observed between days 3 and 6. The DPPH assay also showed a trend toward increased antioxidant activity in FBL throughout the fermentation process, with values rising from 10,35 mmol TE/mL to 14,39 mmol TE/mL. The TPC of FBL increased between days 0 and 3 (from 37,55 mg GAE/ml to 48,80 mg GAE/ml) and subsequently decreased to 26,38 mg GAE/ml by day 6. The experimental results show that fermentation enhances the antioxidant activity of birch sap when fermented with the addition of blackcurrant leaves. The phenolic content peaks on the third day and subsequently declines. These findings indicate that such a product possesses antioxidant potential; however, further research is required.

THE EFFECTS OF DILL ESSENTIAL OIL ON THE GROWTH OF FUSARIUM SPP. *IN VITRO*

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Following the goals of the European Green Deal and the declining use of chemical pesticides, alternatives for plant protection are needed. Therefore, researchers are widely investigating plant essential oils (EO). This study evaluated the inhibitory effect of dill (*Anethum graveolens*) EO against *Fusarium* spp. *in vitro*. The dill EO experiments were conducted *in vitro* at 1000 (0.10%), 1500 (0.15%), 2000 (0.20%) and 2500 µL/L (0.25%) concentrations (D1000–D2500) added to potato dextrose agar (PDA) medium. The *Fusarium* spp. used in this study were: FO – *F. oxysporum* (host: strawberry, fruits), FG – *F. graminearum* (host: pea), FA-1 – *F. avenaceum* (host: asparagus), FA-2 – *F. avenaceum* (host: strawberry, stems), FA-3 – *F. avenaceum* (host: strawberry, leaves). Petri incubated at 22 ± 2 °C. Mycelial growth (mm) was measured 2, 4 and 7 days after inoculation (DAI). At 7 DAI, reinoculation was done onto fresh PDA without EO and measured at 2 and 4 DAI. Fungistatic (fungi started to grow after reinoculation) or fungicidal (after reinoculation, total absence of growth) effect was evaluated. The results at 7 DAI revealed that treatment with dill EO D2500 completely (100%) suppressed FO, FG, FA-1 and FA-2 mycelial growth. In addition, dill EO D2000 completely suppressed FG and FA-2 growth. In the control treatments, the average colony growth was 65 mm for FO, 64 mm for FG, 85 mm for FA-1 and FA-2, and 42 mm for FA-3. Treatment D2500 inhibited FA-3 mycelial growth by 69.7% (average growth 13 mm) and D2000 by 65.4% (average growth 15 mm) compared with the control. After reinoculation, all pathogens resumed mycelial growth, showing a fungistatic effect. The results reveal that the efficacy of EO varies among pathogens from different plant hosts and at different EO concentrations.

Keywords: *Anethum graveolens*; growth inhibition; reinoculation, fungicidal, EO

BIOCHEMICAL PROPERTIES AND ANTIOXIDANT ACTIVITY OF APPLE CIDER VINEGAR

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Apple cider vinegar (ACV) is a naturally fermented product with potential health-promoting properties, which may vary depending on the apple cultivar used for its production due to differences in biochemical composition, particularly acetic acid and phenolic compounds, which may exert beneficial effects on human health through their combined activity. The aim of this study was to evaluate changes in the biochemical properties and antioxidant activity of ACV produced from three different apple cultivars. The physicochemical and biochemical properties of the samples were evaluated by measuring CIE L*a*b* colour parameters, organic acid content, soluble solids (°Brix), and total phenolic content using the Folin–Ciocalteu method. In addition, *in vitro* antioxidant activity was assessed using three different assays: ABTS, DPPH, and FRAP. The results indicated that the biochemical properties of ACV varied among the apple cultivars. The soluble solids content ranged from 3.10 to 6.70 °Brix, while the acetic acid content varied from 1.67% to 2.76%. The highest total phenolic content was observed in ACV produced from the cultivar, reaching 35 mg/g. The ABTS antioxidant activity ranged from 5.49 to 7.43 mg TE/mL, while the DPPH and FRAP values ranged from 6.39 to 7.38 mg TE/mL and from 1.97 to 3.09 mg TE/mL, respectively. These findings highlight the importance of apple cultivar selection for producing ACV with improved biochemical properties and antioxidant potential, supporting the valorisation of local apple varieties and their application in the development of value-added fermented products.

GENOTYPIC EVALUATION OF UPLAND COTTON FOR DROUGHT TOLERANCE USING PHYSIOLOGICAL TRAITS AND DROUGHT TOLERANCE INDICES

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Cotton production is negatively affected by abiotic stress mainly drought stress. It is challenging for breeders to develop tolerant genotypes which can withstand dry conditions without reducing yield. For this purpose 50 genotypes of upland cotton were evaluated under control and drought stress condition using drought tolerance indices and physiological traits. Significant variations were observed among tolerance indices and yield under normal and drought condition. Seed cotton yield under both conditions showed significantly positive association with mean productivity (MP), yield index (YI), geometric mean productivity (GMP), and stress tolerance index (STI), respectively. Relative water content (RWC) showed positively significant association with seed cotton yield under stress. In principal component analysis, PC1 and PC2 expressed 98.84% cumulative contribution in overall variability. Biplot analysis showed that Yp, MP, GMP were the highly significant indices for drought tolerance. Cluster analysis grouped genotypes into four major clusters based on yield, physiological traits and stress tolerance indices. From multivariate analysis, NIAB-111, MNH-1016, FH-142, MNH-886, NIAB-820, VH-295, CYTO-511 and CYTO-513 were recognized as the most stable genotypes under drought stress. Therefore, these genotypes can be used in future breeding programs for drought tolerance.

GENOMIC PREDICTION AND HERITABILITY ESTIMATES OF PHYSIOLOGICAL AND AGRONOMIC TRAITS IN PROCESSING TOMATO

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Genomic selection (GS) offers a powerful approach to accelerating genetic gain in plant breeding by predicting complex phenotypes from genome-wide marker profiles. However, optimizing prediction accuracy and understanding heritability estimates across diverse physiological and agronomic traits remain critical for processing tomato (*Solanum lycopersicum* L.) improvement. This study evaluates phenotypic variability, broad-sense heritability, and genomic prediction performance across 172 genotypes evaluated using an augmented randomized complete block design (RCBD). The genotypes were characterized using 5,000 single-nucleotide polymorphism (SNP) markers. Raw phenotypic data were processed to obtain best linear unbiased estimates (BLUEs), incorporating spatial adjustments. Genomic prediction was performed using ridge-regression best linear unbiased prediction (rrBLUP), and predictive ability (r) was assessed through leave-one-out cross-validation (LOOCV). Results indicate substantial phenotypic variation across traits, with coefficients of variation (CV) ranging from 2.23% for maximum quantum efficiency of photosystem II (Fv/Fm) to 45.97% for total marketable yield (g). Broad-sense heritability estimates (H^2), calculated from phenotypic data, varied across traits, with moderate heritability observed for Fv/Fm (H^2 = 0.32) and marketable yield (H^2 = 0.29), whereas total chlorophyll content (TotCH) and plant weight (g) exhibited lower heritability estimates. Genomic prediction demonstrated positive predictive ability for TotCH (r = 0.31) and marketable yield (r = 0.25). These findings provide baseline genetic parameters for integrating high-throughput phenotyping and genomic prediction into processing tomato breeding pipelines, guiding future model optimization for multi-trait selection.

Keywords: genomic selection; broad-sense heritability; predictive ability; SNP markers; photosynthetic efficiency

DIFFERENTIATION OF MAIZE HYBRIDS BASED ON KERNEL HARDNESS: CLASSIFICATION, METHODOLOGICAL ASPECTS, AND TECHNOLOGICAL SIGNIFICANCE

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Corn kernel hardness is an important breeding trait that determines the grain's physical, technological, and economic properties. It depends on the ratio of horny to floury endosperm, the structure of the starch, and the specific structural characteristics of the kernel. Differentiating corn hybrids based on kernel hardness holds significant value for both breeding and processing, as it enables the targeted selection of genotypes that meet the specific requirements of the processing industry. The experimental material consisted of 8 inbred maize lines of diverse genetic origin from the collection of the Maize Breeding and Seed Production Laboratory, as well as 110 hybrids. The research established the range of grain hardness variation within the current assortment of maize hybrids. A classification scale for maize samples based on grain hardness was developed, and reference lines were identified for each phenotypic class. The metrological characteristics (repeatability and reproducibility) of the method for assessing maize grain hardness were determined, and optimal sample sizes were established to ensure the required accuracy of the results. Classifying maize hybrids based on grain hardness can serve as a basis for selecting raw materials for various types of industrial processing. The introduction of maize hybrids with genetically determined grain hardness parameters will facilitate the development of technologies for the food, starch and syrup, animal feed, and bioenergy industries, and will enable an expansion of the range of industrial products derived from maize.

SYSTEMATIZATION OF BREEDING MATERIAL BASED ON KEY MORPHOLOGICAL AND AGRONOMIC TRAITS

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Systematization of breeding material based on key morphological and agronomic traits makes it possible to trace changes in its phenotypic structure over time and identify the traits for which the distribution of lines shifted toward desirable categories. Comparing materials from different periods in terms of the proportions of low, medium, and high trait values characterizes not only the level of phenotypic expression but also the directions of breeding pool development during its renewal. The research material consisted of 154 inbred lines of diverse genetic origin and from different periods of development, sourced from the collection of the Laboratory of Maize Breeding and Seed Production and the National Center for Plant Genetic Resources of Ukraine. A comparison of breeding material across four periods (1950–1970, 1971–1990, 1991–2000, and 2000–2020) revealed that its structural transformation was driven primarily by increased expression of traits associated with grain yield per ear. While early breeding material predominantly exhibited intermediate values for row number, kernels per row, and grain yield per plant, material from 1991–2020 showed a higher proportion of forms with high kernel density per ear and greater grain weight. Concurrently, reduced coefficients of variation for ear diameter, leaf number, and kernels per row indicated increasing phenotypic uniformity. These trends demonstrate the progressive accumulation of traits associated with higher grain yield, while persistent variation in grain yield per plant provides opportunities for further selection of high-value genotypes. The analysis of breeding material across four periods revealed a gradual shift toward increased expression of traits associated with grain productivity, particularly high kernel density per ear and greater grain weight. Future breeding efforts should focus on combining high-yielding traits with desirable morphological characteristics while maintaining sufficient genetic variability to develop superior genotypes.

FOOD SAFETY AND VETERINARY MEDICINE

NON-INVASIVE MONITORING OF WELFARE-RELATED BEHAVIORAL AND PRODUCTION DYNAMICS AROUND METRITIS AND SUBCLINICAL MASTITIS IN DAIRY COWS

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Automated monitoring enables non-invasive assessment of behavioral and production changes associated with health disorders in dairy cows. This study compared welfare-related behavioral and milk-production dynamics around metritis and subclinical mastitis. A retrospective repeated-measures study included 52 dairy cows: 17 clinically healthy controls, 16 cows with metritis, and 19 cows with subclinical mastitis. Data from three days before to three days after diagnosis were analyzed. Day 0 represented clinical diagnosis and treatment initiation in diseased cows; healthy controls were assigned a central pseudo-Day 0 within a disease-free 7-day period. Feeding time, rumination, daily milk yield, lactose, somatic cell count (SCC), fat-to-protein ratio, milk fat, and protein were evaluated. Generalized estimating equations included group, relative day, group-by-day interaction, days in milk, and parity. SCC was analyzed as log(SCC+1). Milk-yield trajectories differed significantly among groups (group-by-day $P<0.001$). In cows with subclinical mastitis, milk yield decreased from 32.8 kg/day before diagnosis to 29.4 kg/day on Day 0 and recovered to 32.1 kg/day during Days +1 to +3; the Day 0 decrease versus the pre-diagnosis mean was significant ($P=0.008$). Rumination and feeding-time trajectories did not differ significantly among groups ($P=0.205$ and $P=0.138$, respectively). SCC differed strongly between groups overall ($P<0.001$), with the highest values in cows with subclinical mastitis, while the group-by-day interaction was not significant ($P=0.583$). Automated monitoring detected clear disease-related differences in milk-yield dynamics and SCC, whereas rumination and feeding time remained comparatively stable. Combining behavioral and milk-related indicators may support non-invasive monitoring of short-term health-related changes and early post-treatment recovery.

EXPLORING THE POTENTIAL OF WALNUTS FOR BEVERAGE DEVELOPMENT FROM A CONSUMER PERSPECTIVE

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The beverage industry faces numerous challenges arising from shifting consumer preferences and an increasing emphasis on healthy lifestyles and sustainability. The non-alcoholic beverage segment is undergoing significant changes, with consumers increasingly seeking products with favourable nutritional profiles and attractive sensory characteristics. In this context, walnuts represent a promising ingredient with high nutritional value and considerable potential for use in the development of innovative food products, including beverages. This study aimed to examine walnut consumption patterns, assess consumer acceptance of walnuts as an ingredient in beverage development, and identify consumer preferences for different categories of walnut-based beverages. The research was conducted through a questionnaire survey involving 290 respondents. The inclusion criteria were being born before 1997, Slovak nationality, and the absence of walnut allergies. The results indicated relatively low walnut consumption, with an average annual intake of approximately 1.2 kg per respondent. Despite predominantly occasional consumption, perceived nutritional and health benefits were identified as the key reasons for including walnuts in the diet. Furthermore, nearly 70% of respondents expressed interest in the incorporation of walnuts into innovative food products. Among walnut-based beverages, walnut liqueurs received the highest mean preference rating (3.579), followed by non-alcoholic walnut beverages (2.924) and walnut teas (2.631). The key factors associated with the acceptance of innovative walnut-based products included favourable nutritional properties, their perceived value as healthier alternatives to existing products, attractive flavour combinations, natural composition, and the use of local ingredients. These findings highlight the potential of walnuts as an ingredient for the development of innovative beverages and emphasise the importance of incorporating consumer preferences into the new product development process. Moreover, the study contributes to the existing body of knowledge on consumer acceptance of food innovations and offers practical insights for food companies involved in the development and commercialisation of novel beverage products.

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AERATION-ENHANCED ACID WHEY PERMEATE VALORISATION: INCREASED PROTEIN-RICH YEAST BIOMASS PRODUCTION AND REDUCED BY-PRODUCT ACCUMULATION

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The high lactose content of acid whey permeate contributes substantially to its organic load while providing a valuable carbon source for yeast single-cell protein (SCP) production. Sustainable valorisation requires efficient conversion of the substrate components into protein-rich biomass while limiting fermentation by-product accumulation in the residual liquid. This study aimed to evaluate whether active aeration, applied following optimisation and validation of cultivation conditions, could enhance Kluyveromyces marxianus SCP production efficiency while limiting ethanol and volatile-acid accumulation in the fermentation liquid. Lactose in acid whey permeate sourced from a local dairy producer was hydrolysed using Bifidobacterium bifidum-derived β-galactosidase (NOLA™ Fit 5500, Novonesis, Denmark), followed by inorganic salt and vitamin supplementation. K. marxianus DSM 5422 (DSMZ, Germany) was cultivated under controlled batch conditions for 48 h. A 15-run, three-factor Box–Behnken experimental design was employed to plan cultivation trials with temperature, pH and agitation as independent variables. The resulting biomass production and protein content responses were subsequently modelled using response surface methodology (RSM) in RStudio (Posit Software, USA) to identify protein-oriented conditions. The selected regime was experimentally validated and compared with and without active aeration. Total sugars, ethanol and total volatile acids were monitored at defined sampling points using an OenoFoss analyser (FOSS Analytical A/S, Denmark). Apparent crude-protein yield was expressed per gram of consumed total sugars. Despite comparable sugar consumption (36.52 versus 35.39 g L^{-1}), active aeration increased wet biomass by 53.6% (21.39 to 32.85 g L^{-1}) and volumetric crude-protein output by 46.0% (2.19 to 3.20 g L^{-1}). Apparent crude-protein yield per gram of consumed total sugars increased by 50.7% (0.060 to 0.091 g g^{-1}), while biomass protein content changed from 48.85 to 46.45% dry matter. Without active aeration, ethanol accumulated to 1.51% at 48 h; with aeration, it declined from an early observed maximum of 0.95% to 0.64%. Final volatile-acid readings decreased from 0.42 to 0.14 g L^{-1}. Active aeration increased apparent crude-protein yield per unit of consumed total sugars while reducing ethanol and volatile-acid accumulation. These findings highlight the potential of controlled fermentation to improve SCP production efficiency while limiting undesirable metabolite accumulation in the residual liquid, supporting more sustainable dairy side-stream valorisation.

LITTER SIZE AND BIRTH WEIGHT INFLUENCE THE ASSOCIATION BETWEEN EWE COLOSTRUM BRIX CLASSIFICATION AND LAMB GROWTH

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Brix refractometry is widely used to assess ewe colostrum quality. Because litter size affects both colostrum characteristics and lamb performance, apparent associations between Brix values and lamb growth may be misleading. This study investigated whether litter size and birth weight influence the relationship between colostrum Brix classification and lamb growth. Fifty-eight clinically healthy Ile de France ewes and their 108 lambs from a commercial flock were monitored during the 2026 lambing season. Colostrum was measured within 2 hours after lambing using a handheld refractometer with a measurement range of 0–30% Brix. Samples exceeding the upper measurement limit were classified as above-scale, the rest as within-scale. Birth weight was recorded, and average daily gain was calculated from follow-up body weights obtained at 43–88 days. Litter size effects on Brix classification were assessed by logistic regression, and associations with lamb growth by linear mixed models with ewe as a random effect, adjusted separately for litter size and birth weight. Colostrum from 40 of 58 ewes (69%) exceeded the upper measurement limit. The proportion of above-scale samples increased with litter size: 40% in singletons, 78% in twins and 86% in triplets (trend $p = 0.010$; odds ratio 4.00 per additional lamb, 95% CI 1.35–11.88). Lambs from above-scale ewes gained less than those from within-scale ewes (−0.041 kg/day, $p = 0.040$), but this was no longer significant after adjustment for litter size ($p = 0.157$) or birth weight ($p = 0.136$). Birth weight remained a significant predictor of growth (0.046 kg/day per kg, $p < 0.001$). The association between Brix category and lamb growth was largely explained by litter size and birth weight. Because most samples exceeded the measurement range, a single Brix classification has limited value for lamb triage. Refractometers with a wider range may improve colostrum assessment in ewes.

Keywords: ewe, colostrum quality, Brix refractometry, litter size, lamb growth

MILK COMPOSITION AND PERIPHERAL BLOOD LEUKOCYTE PROFILES IN MARES UNDER DIFFERENT PRE-MILKING SUCKLING PRACTICES

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Foal suckling stimulates milk ejection and may influence mares' physiological parameters. This study compares milk composition and peripheral blood leukocyte profiles between farms with different pre-milking practices and examines milk-blood associations. Paired milk and blood samples were collected from 40 mares (20 per farm). Farm 1 used machine milking without prior suckling; Farm 2 permitted a short-term of suckling before milking. Milk constituents and blood smear leukocyte differentials were evaluated. Between-farm differences were tested using Welch's t-test; Within-farm associations were assessed by Spearman correlation with Benjamini-Hochberg correction. Farm 2 showed higher milk fat (1.168 ± 0.237% vs 0.101 ± 0.054%), protein (2.203 ± 0.142% vs 1.979 ± 0.192%), casein (1.834 ± 0.098% vs 1.625 ± 0.144%), and total solids (11.218 ± 0.280% vs 10.057 ± 0.226%), but lower lactose (6.832 ± 0.115% vs 7.042 ± 0.131%; all $p < 0.001$) than Farm 1. Farm 2 showed lower young neutrophil percentages (0.25 ± 0.58% vs 1.50 ± 1.67%; $p = 0.0046$; $n = 16$ and 20, respectively). At Farm 1, segmented neutrophils correlated positively with casein ($\rho = 0.723$; $q = 0.011$) and protein ($\rho = 0.663$; $q = 0.026$), whereas lymphocytes correlated negatively with casein ($\rho = -0.616$; $q = 0.046$). No Farm 2 correlations survived correction. Milk collected after brief suckling contained more fat, protein, casein, and total solids, showing enhanced availability of fat-rich alveolar milk following oxytocin-mediated ejection. Farm-specific leukocyte-milk protein associations were also identified. As milking protocols differed by farm, the observed compositional differences cannot be attributed solely to suckling.

ULTRASONOGRAPHIC CHARACTERIZATION OF OVARIAN FOLLICULAR PHENOTYPES IN WARMBLOOD MARES

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AFC and follicular size distribution have been studied in mares, their associations with pregnancy outcomes remain unclear. This study investigated size distribution in Warmblood mares at insemination and its associations with age and pregnancy outcome. Forty-six (n=46) Warmblood mares (3 – 20 years) underwent a standardized artificial insemination protocol. On insemination day, both ovaries were examined by the same experienced operator transrectally using a Mindray DP – 50 Vet system, videos of each ovary were saved. Follicles 2 – 35mm were counted and categorized into size classes based on Claes et al. (2015) methodology. Analyses used Spearman's correlation and Mann – Whitney U tests. Including exploratory analysis excluding zero 2 – 5mm counts. Follicles measuring 11 – 15mm and 6 – 10mm predominated in young (32.2% and 29.7%) and older mares (31.9% and 30.0%). Per – mare counts did not differ significantly between age groups ($p=0.740$ and $p=0.283$; ≤ 0.05). Mean AFC was 14.9 (SD 7.7; median 12, range 3 – 35). Age group medians were 11 and 14.5 ($p=0.389$, ≤ 0.05). Correlations between age and AFC ($p=0.176$, ≤ 0.05) were non statistically significant. In an exploratory analysis of mares with 2 – 5mm follicles (n=19), older mares exhibited higher median counts than younger mares (3 vs 1; $p=0.011$, $p<0.05$). AFC did not differ between pregnant (n=29) and non – pregnant mares (n=17; $p=0.444$, ≤ 0.05). Non – pregnant mares showed numerically higher mean 20 – 35mm follicle counts (1.59 vs 1.31, $p=0.085$, ≤ 0.05). Warmblood mares showed AFC variation, with 6-15 mm follicles dominating across age groups. AFC and 20-35mm follicle counts did not differ significantly by pregnancy outcome. Older mares had higher 2-5 mm counts, suggesting an age – related difference in small follicle population. Size category analysis adds descriptive detail to AFC.

UNINVITED GUESTS IN PIGS: *SARCOCYSTIS* SPECIES ACROSS DIFFERENT TISSUES IN LITHUANIA

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Sarcocystis is a genus of protozoan parasites comprising more than 220 described species. *Sarcocystis* species have an obligatory two-host life cycle involving an intermediate host, in which sarcocysts develop in tissues, and a definitive host, in which sexual reproduction takes place in intestine. Pigs (*Sus scrofa domesticus*) are intermediate hosts for several *Sarcocystis* species. Some of these parasites are of particular importance, as humans can serve as definitive hosts and become infected through the consumption of contaminated pork. Furthermore, there is scarce recent data considering *Sarcocystis* infection in pigs from Europe. The aim of this study was to evaluate prevalence and parasite load of *Sarcocystis* in different tissues of pigs raised in Lithuania by microscopical examination and to identify the species molecularly. A total of 47 pig muscle samples were collected from Lithuanian slaughterhouses. For microscopic analysis, skeletal and cardiac samples were examined using the methylene blue-stained tissue compression technique. For the molecular assessment of *Sarcocystis* species composition, samples were subjected to artificial pepsin digestion followed by genomic DNA extraction. *Sarcocystis* species were identified using conventional and nested PCR with species-specific primers targeting the mitochondrial *cox1* gene. The microscopical analysis revealed that three cardiac samples of pigs were infected by *Sarcocystis*. The molecular analysis confirmed that ten samples of skeletal muscle were positive for parasites investigated. Based on *cox1*, a single *Sarcocystis* species *S. miescheriana* was established. The identified species employ domestic and wild canids for their transmission. Zoonotic *S. suihominis* was not detected primarily suggesting that pork is not important source for human *Sarcocystis* infection. However, further studies involving larger sample sizes and various tissues are needed to better assess *Sarcocystis* prevalence and the potential occurrence of zoonotic species in Lithuanian pigs.

ORANGE PEEL POWDER AS A NATURAL GROWTH PROMOTER FOR SUSTAINABLE BROILER CHICKEN PRODUCTION

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The increasing restrictions on the use of antibiotic growth promoters in poultry production have intensified the search for sustainable and environmentally friendly alternatives. Orange peel, an abundant agro-industrial by-product, is rich in flavonoids, essential oils, vitamin C, and other bioactive compounds with antimicrobial and antioxidant properties. This study aims to evaluate the potential of orange peel powder (OPP) as a natural growth promoter capable of improving growth performance, gut health, and economic efficiency in broiler chickens. A feeding trial is proposed using day-old broiler chicks randomly assigned to dietary treatments containing graded levels of OPP (0, 2, 4, and 6 g/kg feed) over a 42-day production cycle. Growth performance indicators, including body weight gain, feed intake, and feed conversion ratio, will be recorded weekly. Immune response, selected blood biochemical parameters, intestinal morphology, carcass characteristics, and production economics will also be evaluated. Data will be analyzed using one-way analysis of variance, with statistical significance declared at $P < 0.05$. It is anticipated that dietary supplementation with OPP will improve feed efficiency, enhance body weight gain, promote beneficial intestinal development, strengthen antioxidant status, and improve immune competence without adverse effects on bird health. Improved economic returns through reduced feed cost and enhanced productivity are also expected. Orange peel powder has strong potential as a sustainable phytogenic feed additive for antibiotic-free broiler production. The proposed study is expected to provide scientific evidence supporting the valorization of citrus processing waste into a value-added poultry feed ingredient, contributing to sustainable agriculture, circular bioeconomy, and environmentally responsible livestock production.

Keywords: Orange peel powder; Phytobiotics; Broiler chickens; Growth promoter; Sustainable agriculture; Circular bioeconomy.

PHYSIOLOGICAL VARIATION AMONG LENTIL ACCESSIONS UNDER THE AGROECOLOGICAL CONDITIONS OF AZERBAIJAN

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The evaluation of physiological traits in lentil accessions is important for identifying genotypes with favorable adaptive characteristics under local agroecological conditions. This study aimed to assess variation in leaf chlorophyll content, canopy temperature, and specific leaf mass among lentil accessions grown on the Absheron Peninsula, Azerbaijan. A field experiment was conducted during the 2024-2025 growing season at the Research Institute of Crop Husbandry in Baku, Azerbaijan. Ten lentil accessions, including nine ICARDA-derived accessions and the local cultivar Arzu, were evaluated. Relative leaf chlorophyll content was measured using a SPAD-502Plus chlorophyll meter, canopy temperature was recorded using an infrared thermometer, and specific leaf mass was determined from leaf dry mass and leaf area. Measurements were taken at the branching, budding, and flowering-pod formation stages. SPAD values increased across the evaluated growth stages in most accessions, reaching a maximum of 53.5 in F.2014-009 at flowering-pod formation. This accession also exhibited the highest specific leaf mass (0.07 mg mm-2) and the lowest canopy temperature (23.4 °C) at the same stage. In contrast, F.2013-22 showed the highest canopy temperature (27.3 °C). SPAD values were strongly correlated between budding and flowering (r = 0.999), as were canopy temperatures between branching and budding (r = 0.848). Specific leaf mass was negatively correlated with canopy temperature (r = -0.695). The evaluated lentil accessions exhibited considerable variation in physiological traits. F.2014-009 demonstrated a combination of high chlorophyll content, high specific leaf mass, and relatively low canopy temperature, making it a promising candidate for further evaluation under Absheron conditions.

Keywords: lentil, physiological traits, chlorophyll content, canopy temperature, specific leaf mass.

EVALUATION OF BARLEY GENOTYPES FOR RESISTANCE TO YELLOW AND BROWN RUST UNDER DIFFERENT AGROECOLOGICAL CONDITIONS IN AZERBAIJAN

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Yellow rust (*Puccinia striiformis*) and brown rust (Puccinia hordei) are important fungal diseases affecting barley (*Hordeum vulgare* L.) production and potentially causing significant yield losses. Identifying resistant genetic resources is essential for developing high-yielding, disease-resistant, and climate-resilient barley cultivars. This study aimed to evaluate the resistance of barley genotypes introduced from the International Center for Agricultural Research in the Dry Areas (ICARDA) to yellow and brown rust under field conditions in Azerbaijan. Field experiments were conducted during 2018–2021 at the Jalilabad and Gobustan Regional Experimental Stations. The experimental material consisted of 40 introduced barley genotypes, including 20 early-maturing and 20 late-maturing accessions. The locally adapted cultivar 'Jalilabad 19' was used as the standard. Disease responses were assessed using a nine-point scale under the agroecological conditions of both locations, allowing comparative evaluation of the introduced genetic material. Three promising genotypes were identified as resistant to both yellow and brown rust: Alanda/Regina (ICB06-1821-0AP-8AP-0AP), BREA/DL70//TOCTE/3/BREA/DL70/CABUYA/4/CALI92/ROBUST (ICB09-1441-0AP-OTR-0AP-OTR-0AP-0TR), and Hispanic/Sararood (ICB06-2099-21AP-0AP-0AP). These genotypes represent valuable potential sources of resistance for barley breeding programmes. Their resistance scores for each pathogen should be reported according to the original field observations and the applied rating methodology. The identified accessions may serve as parental material in breeding programmes aimed at improving rust resistance and stabilising barley production under diverse agroecological conditions. Their use could contribute to the development of cultivars with improved disease resistance and better adaptation to variable environmental conditions. Further multi-environment evaluation is recommended to confirm the stability of resistance and assess their potential for practical breeding applications.

Keywords: yellow rust, brown rust, disease resistance, barley breeding, genetic resources