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ABSTRACTS

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PLENARY SESSION

TOWARDS A HOLISTIC UNDERSTANDING OF FOOD AND MENTAL WELL-BEING: THE ONE HEALTH APPROACH

Acad. Prof. Dr Elena Bartkienė

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The One Health approach recognizes the intrinsic interconnection between human, animal, and environmental health. Within the field of food sciences, this concept highlights the need for an integrated strategy to ensure food safety, nutritional quality, and sustainability throughout the entire food chain. Food is fundamental for human survival, fulfilling essential nutritional and energy requirements. However, in recent years, public interest has shifted toward understanding the broader impact of nutrition on overall well-being, including its influence on mental health. Emerging research underscores that effective public health nutrition strategies can play a preventive role in mental health disorders. Our previous studies revealed that multiple factors shape food choice — ranging from individual characteristics (such as gender, age, education, and psychological traits) to habitual eating behaviors and food properties themselves. Although hunger remains a primary driver of consumption, what people choose to eat — when given options — is not determined solely by physiological or nutritional needs. According to the European Food Information Council (EUFIC), food choice can also be influenced by mood and emotional state. Our research further demonstrated that emotional responses triggered by different food tastes may be associated with Major Depressive Disorder (MDD) and could serve as potential early diagnostic indicators. Looking ahead, future food research should aim to develop novel food products that go beyond nutritional optimization. By refining sensory aspects — such as texture, aroma, and flavor profiles — it may be possible to evoke more positive emotional responses, particularly benefiting individuals suffering from mood-related disorders like MDD. Ultimately, integrating the One Health perspective into food science not only enhances physical and mental health outcomes but also supports the creation of a sustainable, ethical, and health-promoting global food system.

CLIMATE-SMART PRODUCTION PRACTICES TOWARDS A SUSTAINABLE PROTECTED CULTIVATION

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Global temperatures surpassed 1.5 °C above pre-industrial levels for the first time in 2024, marking a critical threshold in climate change and an increase in extreme weather events. Horticulture both contributes to and is affected by these changes. In protected cultivation systems, especially greenhouses, fossil fuel heating, intensive fertilizer and pesticide use, and non-renewable growing media such as peat contribute significantly to greenhouse gas emissions. Simultaneously, rising temperatures, drought, and irregular precipitation threaten crop productivity, quality, and stability.

Climate-smart agriculture (CSA) offers an integrated framework to reduce emissions while improving resource efficiency and resilience. In greenhouse vegetable production, CSA can be implemented through renewable energy use, precision irrigation and fertigation, and advanced environmental control systems. Closed and semi-closed greenhouse designs, soilless cultivation, and decision-support tools for managing climate, water, and nutrients can substantially reduce energy and input losses while maintaining yield and quality.

Transitioning to sustainable protected cultivation requires greater adoption of cleaner technologies, circular resource use, and adaptive management practices that respond to environmental variability. Collaboration among research, industry, and policymakers is essential to accelerate innovation and support practical, scalable solutions.

This presentation highlights climate-smart strategies for sustainable protected cultivation, focusing on technologies and management practices that lower emissions, optimize input use, and strengthen crop resilience. Advancing these systems is vital for sustainable intensification, ensuring food security, economic viability, and environmental protection in a changing climate.

MODERN AGRICULTURE NEEDS YOUNG SCIENTISTS

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The fourth industrial revolution, driven by digitalization and artificial intelligence, is reshaping agriculture and demanding a new generation of scientists and innovators. Smart farming technologies are becoming key to sustainable food production, resource efficiency, and environmental care — yet their full potential has not been reached.

In Latvia and across Europe, precision agriculture is proving that innovation pays off. From nitrogen sensors that optimize fertilizer use to autonomous robots that detect weeds, technology is helping farmers reduce costs, increase yields, and minimize environmental impact. Large farms are already using data-driven management systems and satellite-based soil analysis, while smaller farms are beginning to adopt tailored, cost-effective solutions.

Wireless sensor networks now allow real-time monitoring of soil, crops, and livestock. On Latvia University of Life Sciences and Technologies' research farm Vecauce, sensors and milking robots have increased milk yield by 30% and reduced diseases by 43%. Similar progress is seen in apiculture, where smart monitoring systems like the SAMS project improve bee health and honey production.

E-commerce and digital communication are also transforming rural economies. Farmers are connecting directly with consumers through social networks and mobile apps, making fresh products more accessible and boosting rural entrepreneurship.

However, to fully integrate agriculture into the digital economy, the sector needs more skilled people — data analysts, biotechnologists, and AI specialists who understand both technology and biology. Young scientists have a crucial role to play in building this resilient, sustainable future.

Modern agriculture is not only about machines and data — it is about people who can combine innovation with responsibility. To feed a growing population while protecting the planet, the world needs more bright young minds in the fields — literally and figuratively.

AGRONOMY, HORTICULTURE

INFLUENCE OF TILLAGE PRACTICES AND MUSTARD COVER CROPPING ON SOIL MICROBIAL DIVERSITY AND PATHOGENIC FUNGI ABUNDANCE

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Tillage intensity and cover cropping are agricultural practices that influence soil microbial diversity and community structure. Brassica cover crops, such as white mustard are known for their biofumigation properties, which can suppress soil-borne pathogens and modify microbial community composition. This study examined the effects of tillage practices and mustard cover crop use on the diversity and composition of soil fungi and bacteria, with a focus on pathogenic fungal abundance in a wheat field. Soil samples were collected in spring, summer and autumn of 2024 and 2025. DNA was extracted from lyophilized soil samples and microbial diversity was assessed using 16S rRNA and ITS metabarcoding via Illumina NovaSeq sequencing. The results showed that using white mustard reduced overall fungal diversity but increased evenness, indicating a more balanced distribution of taxa. Meanwhile, soil bacterial diversity was approximately 2.5 times higher than fungal, and bacterial alpha-diversity was significantly influenced by tillage intensity. However, beta-diversity analysis revealed that fungal community composition differed between tillage practices and cover crop treatments. Among the 20 most abundant fungal genera, three were identified as pathogenic: *Fusarium*, *Didymella* and *Plectosphaerella*. The DNA abundance of these pathogens in the soil across different seasons was assessed using qPCR. The abundance of *F. culmorum* in summer was significantly affected by tillage method across both years. In 2025, the abundance of this pathogen increased up to tenfold, with notably higher levels observed under conventional tillage. The abundance of *D. pinodes* remained consistent across both years and its suppression was influenced by white mustard. In conclusion, tillage method and cover cropping using white mustard affect microbial diversity and abundance of pathogenic fungi, but the effect is species-specific.

Keywords: tillage practices, cover crops, white mustard, soil microbiota, soil-borne pathogens

WHITE GRAPE MARC EXTRACT WITH DIVERSE AND HIGH POLYPHENOLIC CONTENT AS A POTENTIAL BENEFICIAL FEED ADDITIVE IN ANIMAL HUSBANDRY

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The overuse of antibiotics in animal husbandry has fuelled the spread of antimicrobial resistance (AMR), threatening both animal welfare and public health. Multidrug-resistant bacteria, such as Escherichia coli and Staphylococcus aureus, exacerbate this crisis, necessitating sustainable alternatives. Polyphenolic plant extracts, known for their antimicrobial properties, offer a promising solution. This study evaluates white grape marc extract—a polyphenolic-rich byproduct of winemaking—as a potential feed additive in animal husbandry, leveraging its economic and environmental benefits as a valorised waste product. A literature review covers antibiotic types, AMR mechanisms, polyphenol chemistry, and prior studies on grape-derived extracts, establishing a foundation for this work. Our research aimed to assess the extract's antimicrobial activity and its impact on resistance development. Experiments were conducted using *E. coli* and *S. aureus* strains, with antimicrobial efficacy measured via minimum inhibitory concentrations (MIC), IC95, IC90, and IC50 values. Mutation assays compared resistance induction by the extract versus ciprofloxacin, supported by PCR amplification of gyrA and parC genes in mutants. Results revealed robust antimicrobial activity against both pathogens, with MIC values indicating potency comparable to traditional agents. Tolerance assays showed limited resistance development with the extract, unlike ciprofloxacin, where gyrA and parC mutations were detected. These findings suggest that white grape marc extract could reduce reliance on antibiotics in animal feed, mitigating AMR while promoting sustainability. This study highlights its dual role in enhancing animal health and repurposing winemaking byproducts, offering a scalable, eco-friendly feed additive for future agricultural applications.

Keywords: grape marc extract, polyphenols, antimicrobial resistance, feed additive, sustainability

VALORIZATION OF HEMP BIOMASS THROUGH GREEN TECHNOLOGIES FOR SUSTAINABLE FOOD PACKAGING APPLICATIONS

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Introduction: Growing concerns about plastic pollution and the need for renewable materials have stimulated interest in hemp (*Cannabis sativa* L.) as a sustainable biomass source. Hemp's high cellulose, hemicellulose, and lignin content make it suitable for producing biodegradable and functional materials. This abstract summarizes key findings from a published review focusing on green valorization strategies for hemp and their applications in food packaging.

Materials and Methods: The review involved a systematic literature search across databases including Scopus, Web of Science, and ScienceDirect. Studies emphasizing environmentally friendly green processing methods—such as enzymatic hydrolysis, microwave—and ultrasound-assisted extraction, and deep eutectic solvent (DES) systems—were critically analyzed for efficiency, sustainability, and biopolymer performance.

Results: The review revealed that enzymatic treatments effectively enhance cellulose accessibility and produce nanocellulose with excellent film-forming potential. Microwave and ultrasound-assisted processes significantly reduced energy consumption and processing time, while DES allowed selective lignin removal without generating toxic residues. Integrating these methods resulted in improved yield, mechanical strength, and barrier properties of hemp-derived biopolymers.

Conclusions and Future Perspectives: Green valorization of hemp biomass provides an eco-friendly and circular approach to next-generation food packaging. The reviewed findings support the transition toward sustainable materials within the bioeconomy. Building on this review, our ongoing research focuses on enzymatic valorization of hemp biomass for developing food-grade biopolymers, aiming to translate these laboratory insights into scalable industrial applications.

SPECTRAL AND MORPHOMETRIC RESPONSES OF WINTER WHEAT VARIETIES TO DROUGHT STRESS

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Understanding crop responses to water deficit is essential for improving drought tolerance in cereals. Recent advances in sensor-based phenotyping enable non-invasive quantification of morphological and spectral traits that reflect plant health under varying soil moisture conditions.

This study aimed to evaluate the responses of three winter wheat (*Triticum aestivum* L.) cultivars — 'Ada', 'Artist', 'Lakaja DS' — to drought stress using morphometric and spectral traits obtained from digital imaging. Plants were grown in loam soil under two irrigation regimes (70% and 30% of field capacity) in a greenhouse with semi-controlled conditions for four weeks. Wheat was scanned weekly using the TraitFinder system (Phenospex, Heerlen, The Netherlands), recording morphological (digital biomass, height) and spectral (Hue, NDVI, GLI, PSRI, NPCI) traits.

Parametric (two-way ANOVA, Tukey) and nonparametric (Kruskal—Wallis, Dunn) tests showed that digital biomass, height, Hue, NDVI, and GLI significantly decreased ($p < 0.05$) under drought, while PSRI and NPCI significantly increased ($p < 0.05$). These changes indicate stress effects on plants. Early physiological responses to water deficit were evident in PSRI, NDVI, and NPCI, which reflect pigment alterations associated with photosynthesis inhibition and leaf senescence. Most traits of 'Ada' and 'Lakaja DS' changed significantly by the second week of drought, while in 'Artist', major changes appeared in the third week, suggesting higher drought tolerance in this variety. Effect size analysis showed that interactions between watering regime and measurement week had the strongest effect (η^2 or $\varepsilon^2 > 0.5$). Principal Component Analysis revealed that the first two components explained over 94% of total variance, with PC1 mainly driven by pigment indices and PC2 by growth traits. Clear separation between treatments indicated distinct physiological responses. Significant trait correlations were strongest in 'Lakaja DS' ($r_S > 0.39$ or < -0.59, $p < 0.001$) and weakest but still significant in 'Artist' ($r_S > 0.27$ or < -0.41, $p < 0.05$).

GENOTYPE-DEPENDENT DIFFERENCES IN VIRUS INFECTION INTENSITY IN HONEY BEES (*APIS MELLIFERA*)

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Viral infections are a major factor contributing to honey bee (Apis mellifera) colony losses worldwide. Genetic variation among individual bees may influence susceptibility to infection, thereby affecting colony-level resilience. This study investigated the relationship between host genotype and total virus infection intensity in honey bees.

A total of 140 adult workers were collected from four regions in Lithuania and genotyped at SNP9–9224292 (AA, AG, GG). Viral presence was assessed using PCR targeting three common honey bee viruses—Black queen cell virus (BQCV), Chronic bee paralysis virus (CBPV), and Deformed wing virus (DWV)—and total virus infection intensity per bee was calculated as the number of detected viruses (ranging from 0 to 3). Non-parametric Kruskal–Wallis tests were used to compare infection intensities among genotypes, and Spearman's rank correlation examined the association between G allele count and infection intensity.

Bees with AA and AG genotypes exhibited higher median infection intensities (interquartile range [IQR] 1–2) than GG bees (IQR 0–1). AA bees showed the widest distribution (0–3), whereas AG and GG bees displayed narrower ranges (0–1 and 0–2, respectively). The Kruskal–Wallis test revealed significant genotype-dependent differences ($H = 57.296$, $df = 2$, $p < 0.001$). A moderate negative correlation was observed between G allele number and infection intensity ($\rho = -0.576$, $p < 0.001$), indicating that bees carrying more G alleles tend to harbor fewer viral infections.

These results suggest that variation at SNP9–9224292 is associated with differences in overall virus infection intensity, with the GG genotype showing lower susceptibility. The findings highlight the role of host genetics in shaping viral infection dynamics and support further exploration of genetic factors that may enhance colony health and resistance.

ADAPTIVE AGROTECHNICAL MEASURES FOR THE STABILITY OF PRODUCTIVITY UNDER CHANGING CLIMATE

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This research will raise the hypothesis of what would happen if less nitrogen and no fungicide seed treatment would be used in chosen crops and moreover if other alternative agrotechnical means could compensate for possible yield and quality loss.

The research object of this study was chosen to be a standard crop rotation used in Lithuania. These crops will be placed in two different fields, and they are peas, winter wheat, and winter oil seed rape followed by summer wheat. In total 13 treatments were performed. One treatment, with 50% higher nitrogen rate, will be compared with control and other treatments such as humic acids, nutritional seed treatment, hydrogel and foliar nutrition which were designed alone and in their various combinations.

The methods to evaluate different treatment outcomes were chosen such as yield, hectoliter weight, 1000 grain mass, leaf size, SPAD index, plant sap analysis, soil Haney analysis and root development done by ‘WinRhizo’ program.

After two seasons trials in pea crops the accumulated data showed that 50% higher nitrogen application rate resulted in lower yield compared to the control and the combination of all agrotechnical measures. However, at one year winter wheat trial, the treatment with higher nitrogen application produced the highest yield amongst all treatments, followed by the combination of all chosen means.

Regarding comparison among variants such as fungicide, nutritional seed and control treatments, in winter wheat trial both seed coating applications resulted in equal numbers and had better yield numbers than the control variant. While for the peas, for the 1st year trial the control treatment had slightly higher yield parameters than other two above-mentioned treatments, and in the 2nd year, the nutritional seed treatment substantially outperformed fungicide seed variant and had marginally better yield result than control treatment.

Acknowledgement: Supervisor Dr Virmantas Povilaitis

EVOLUTION IN MOTION: DECODING DAYLILY SELECTION'S PULSE AMID SHIFTING CLIMATES

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Over years daylily breeders had set goals to create tallest, biggest, smallest, brightest and in general the most unique daylilies. That resulted in over 100,000 cultivars registered in American Hemerocallis Society (AHS). Changing climate shifting climatic zones and raising challenges on breeding goals. This study aims to describe geographical distribution of daylily cultivars and identify possible prediction of climate zone changes and how it could shift breeding programs. The set of cultivar data covering all world was aligned with maps and assorted for trait analysis covering trait pressure and climate change modeling. We observed how human-driven daylily breeding and environmental constraints shaped geographic adaptation through anthropogenic and climatic selection pressures. Over the years certain traits were more suppressed while others evolved through mutation selection and breeding for both diploid and tetraploid lines. As projected—shifting climate zones would require adjusting breeding programs and selecting not only for aesthetics, but also resilience. In conclusion, this study elucidates climate dynamics and daylily trait tendencies over time and space, highlighting their critical impact on shaping future breeding strategies and selection criteria.

PLANT GROWTH-PROMOTING PROPERTIES OF *RHODIOLA ROSEA* ROOT ENDOPHYTIC BACTERIA

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Plants growing in challenging environments often develop strong relationship with beneficial microbes that help them absorb nutrients and withstand environmental stress. *Rhodiola rosea* L., a succulent member of the Crassulaceae family, thrives in harsh habitats including sandy or rocky soils and dry tundra. The aim of the present study was to investigate plant growth-stimulating potential of R. rosea endophytic microbiota. Seventy-three endophytic bacterial isolates were recovered from rhizome of R. rosea plants and taxonomically classified into 14 distinct genera belonging to Firmicutes (26%) or Proteobacteria (74%). Functional screening revealed that these isolates possessed genes and traits associated with plant growth promotion, including nitrogen fixation (56% of isolates), siderophore production (40%), inorganic phosphorus solubilization (30%), and synthesis of indole-related compounds (51%). Based on these characteristics, the isolates grouped into 16 distinct functional clusters. To assess their growth-promoting potential, 45 selected isolates were co-cultivated with germinating Arabidopsis seedlings revealed 18 and 5 isolates that resulted in more than a 20% increase in root or shoot growth, respectively. These findings demonstrate the functional diversity within the R. rosea endophytic microbiome and highlight specific bacterial strains with promising agricultural applications. The identified isolates represent valuable candidates for developing phyto-stimulant formulations that could support sustainable, environment-friendly agriculture practices.

PROSPECTS OF REPURPOSING AIR CONDITIONING SYSTEM CONDENSATE FOR URBAN AGRICULTURE IN GHANA

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Urban agriculture is a promising way to reduce food insecurity and achieve “zero hunger.” Unfortunately, freshwater shortages threaten Ghana’s urban agriculture. This issue has forced some urban vegetable farmers to utilize water sources that exceed acceptable irrigation limits in terms of physicochemical and microbiological conditions. Inspired by this challenge, the study estimated the hourly condensate discharge of air conditioning (AC) systems and proposed its use for urban vegetable production by juxtaposing it with the estimated irrigation requirements of commonly grown vegetables in Nsawam in Ghana. The hourly condensate discharge was measured for a 30-day period, from January to February, for three separate AC systems in the Nsawam Government Hospital. The crop water requirement of tomatoes, cucumbers, cabbage, and chili peppers was estimated with FAO Climwat 2.0 and Cropwat 8.0 for the same location. The average discharges for the three AC systems were 1.98, 2.31 and 2.72 l/h. The irrigation requirements for the entire production period for tomato, cucumber, cabbage and chili pepper, from April, were 20.9, 1.9, 1.9 and 48.9 mm, respectively. For a vegetable bed size of 2.229 m^2 (4 x 6 ft) and an irrigation requirement of 48.9 mm (0.0489 m), the highest among the computed values, the volume of water to complement the water needs stands at 0.1090 m^3 (109 L). This study indicates that AC condensate could meet water needs in urban agriculture. We encourage further studies to assess the physicochemical and microbiological status of this water source to realize its full adoption.

EVALUATION OF CYANOGENIC GLYCOSIDE ACCUMULATION IN BLACK ELDERBERRY JUICE

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Black elderberries (BE) (Sambucus nigra) are rich in biologically active compounds such as polyphenols, phenolic acids and flavonoids, which contribute to their high antioxidant capacity and health benefits. The beneficial composition of elderberries makes them a valuable raw material for producing functional foods and beverages. However, the berries also contain cyanogenic glycosides (CG), such as amygdalin and prunasin, which can release toxic hydrocyanic acid upon enzymatic hydrolysis, raising potential safety concerns.

This study aimed to evaluate prunasin and amygdalin levels in BE, freshly pressed juice and juice subjected to sonication, to determine how processing affects the dynamics of these compounds.

BE harvested in 2024 (Ukraine origin) were purchased in April 2025. The berries were processed using a hydraulic juice extractor to obtain raw juice. 75 L of the obtained juice was subsequently sonicated for 50 minutes at an amplitude of 49 µm, with the temperature maintained below 24 °C. CG were quantified by LC-MS/MS, and statistical differences were evaluated using ANOVA ($p < 0.05$).

The raw and sonicated juices exhibited significantly higher ($p < 0.05$) prunasin concentrations than the whole berries. Prunasin concentration in the raw juice increased 6.9-fold, indicating its enhanced transfer from the berry tissues into the liquid phase during extraction. Although the prunasin content in the sonicated juice was 35% lower than in the raw juice, the difference was not statistically significant ($p > 0.05$). The amygdalin concentration remained comparable across all samples. This suggests that prunasin is more mobile and extraction-sensitive than amygdalin, and mild sonication does not substantially alter total CG content.

The accumulation of prunasin in elderberry juice highlights the need to balance the nutritional advantages of bioactive compounds with product safety considerations. Further optimisation of processing parameters is warranted to minimise potential risks while preserving the functional quality and stability of elderberry-based beverages.

HARNESSING GENETIC DIVERSITY FOR FUSARIUM STALK ROT RESISTANCE IN MAIZE: AN INTEGRATED PHENOTYPIC–GENOTYPIC APPROACH

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Maize (*Zea mays* L.) is one of the most important cereal crops worldwide; however, its productivity is greatly hindered by Fusarium stalk rot (*Fusarium verticillioides*), a major disease that diminishes both yield and grain quality. The present study was undertaken to assess the genetic diversity and resistance of segregating maize populations developed through wide hybridization. A total of 54 F2 lines (Kharif 2023) and 49 F2:3lines (Rabi 2023–24) were assessed using an Alpha Lattice Design for agro-morphological and molecular characterization. Genetic variability was analyzed through Mahalanobis' D^2 statistics, which classified genotypes into three distinct clusters based on key traits. To screen for resistance, a standardized toothpick inoculation method was employed in the pathological field, and disease severity was scored using a 1–9 scale. Molecular screening with 10 SSR markers identified resistant genotypes, with SSR93 and umc2059 proving effective in distinguishing resistance-associated alleles. Among 33 evaluated lines, six genotypes (2123859 X WS-5)^/4^-7, (2123426 X WS-5)^/6^-4, (2123401 X WS-5)^/10^-7, (2124008 X WS-1)^/5^-5, (2123792 X WS-1)^/10^-9, and (IC 0621166 X WS-5)^/5^-4 consistently exhibited resistance across both phenotypic and molecular evaluations. These findings highlight the genetic diversity within maize germplasm and provide valuable resources for breeding Fusarium stalk rot-resistant varieties. The identified resistant lines hold potential for use in maize improvement programs, ensuring sustainable production and enhanced disease resilience.

FORESTRY

POTENTIAL OF MODIFIED GREENWAYODENDRON SUAVEOLENS (ENGL. & DIELS) FIBERS AS RENEWABLE REINFORCEMENT IN BIOCOMPOSITES

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Forest-based fibers are continuously being explored and utilized as reinforcements in biocomposites because they are safe, non-abrasive, and eco-friendly. However, water-sensitive nature of bio-derived fibers always results to weak adhesion with polymer matrices such as Low Density Poly-Ethylene (LDPE), thus necessitating their modifications. Therefore, this study aims to evaluate the effect of chemical modification on the properties of Greewayodendron suaveolens (G.S) fibres as reinforcement for LDPE.

Fibres obtained from G.S. were chemically treated using potassium-permanganate ($KMnO_4$), nitric-acid (HNO_3), ethanol (C_2H_5OH), and acrylic-acid ($CH_2 = CH\text{-}COOH$), separately. Chemical composition, dimension and morphology indices of G.S fibres were examined. Characterisation of plant fibres was carried out using Fourier Transform Infra-Red (FTIR) spectroscopy. The LDPE was reinforced with modified and unmodified G. S fibres, respectively, at fibre contents of 2.5, 5.0 and 10.0% using twin-screw extruder. Morphology of the biocomposites was determined by SEM. Physicomechanical properties, and biodegradability of the biocomposites were determined using standard methods.

Chemical composition indicated G. S fibres as good reinforcing material. Dimension and morphology results showed that G.S fibres were discontinuous and could be easily delignified. The absorption peaks at 3411(O-H) and 1731(C = O) cm-1, in the unmodified fibres, disappeared after chemical modification, indicating improved hydrophobicity. Biocomposites with untreated G.S. fibres were more water sensitive than biocomposites containing modified G.S fibres. Water sensitivity also increased with increase in fibre content. Modified fibres formed stronger interfacial adhesion with LDPE than untreated fibres. Hence, stronger mechanical properties were obtained in biocomposites containing modified G.S fibres compared to biocomposites with untreated fibres. Also, biodegradability of the biocomposites (both treated and untreated) increased with increase in fibre content.

G.S. fibre is a promising bio-based reinforcement for LDPE. Also, chemical modification enhances adhesion of G.S fibre with the polymer matrix leading to improved physical and mechanical properties of the fibre reinforced LDPE biocomposites.

Keywords: greenwayodendron suaveolens, reinforcement, fibre adhesion, eco-friendliness, polymers

WOODEN ROOF FAILURE IN BENIN REPUBLIC: CAUSES, TYPES AND REMEDY

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Roof failure does not depict a total collapse, it entails all forms of deformation that can limit the prolonged shelf life of roof. There are incessant reports of roof failure occurrence which necessitates the need to assess the causes and types of roof failure to enable recommendation of effective remedies in eradicating its menace, especially in Benin Republic with prevalent use of young small girth roundwood for roof trusses fabrication.

The data were collected purposively with questionnaires administration to the building owners and personal field observation in Plateau Department of Benin Republic and analysed using descriptive statistics.

The major causes of roof failure opined by the respondents are the use of artisans with inadequate skills (93%), lack of roof inspection for immediate repair works (87%), ageing of the roof elements (86%), low-quality/strength materials (84%), design error (76%), lack of technical know-how of roundwood use resulting in poor jointing (75%), the ecological factors (61%), lack of motivation of the artisans (42%) and use of small girth roundwood (1%). The most observed roof failure types were leakage (69.7%), rusting (60.7%), nail withdrawal (53.7%) and roof ponding (53.7%). Other failure types were sheet removal (16.9%), wood decay (16.9%), roof blow-off (9%) and truss damage (5%).

The results of the study showed that the use of small girth roundwood for roof trusses fabrication does not contribute to roof failure and the causes of roof failure and types were not different from those reported for areas with prevalent use of lumber for trusses fabrication. To ensure structural integrity of roof constructed with small girth roundwood, there is need to design to specification, straighten up crooked part of the logs before use, not placing higher diameter logs over smaller ones and scheduling routine inspection for immediate repair works before aggravating to total collapse.

Keywords: roundwood, trusses, roof failure, roof ponding

CAPERCAILLIE AS THE INDICATOR OF FOREST HEALTH DIVERSITY AND GENETIC STRUCTURE OF IT POPULATIONS IN LITHUANIA AND LATVIA

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Introduction*:* *Capercaillie* (*Tetrao urogallus* L.) is considered an indicator species of naturally open coniferous forests with a high proportion of mature stands and diverse understorey vegetation, reflecting overall forest ecosystem health (Brugnoli, Brugnoli, 2006). However, its conservation status is currently threatened due to habitat loss, fragmentation, and intensive forestry practices across Central and Northern Europe (Brugnoli, Brugnoli, 2006; Mikoláš, Svitok, Tejkal et al, 2015). In the Baltic region, this species has transformed from a former hunting target into one of the most strictly protected forest indicator birds (Lõhmus, Leivits, Pēterhofs et al, 2017). Because T. urogallus populations are sensitive to forest structure and habitat quality, their genetic diversity can provide insights into ecosystem integrity and resilience. Therefore, this study aimed to assess genetic structure of T. urogallus populations in Lithuania and Latvia to evaluate connectivity, local adaptation, and to reveale conservation needs for this indicatory species.

Materials and Methods*:* To evaluate genetic diversity, feathers were collected non-invasively from wild and captive-bred birds in Latvia and Lithuania between 2023 and 2025. In total, 91 feathers were collected from Latvia, and additional samples were obtained from Capercaillie population raised in Viešvilė reserve in specialised breeding farm (Lithuania). Muscle tissue from two deceased birds obtained from Lithuania served as control material. DNA was extracted following the universal and rapid salt-extraction method (Aljanabi and Martinez 1997) using an optimized two-step NaCl–ethanol purification protocol with a 70% ethanol wash to enhance purity. The hypervariable fragment of the mitochondrial D-loop region was sequenced using the same primers as for amplification, and the resulting 324 bp fragments were aligned and analyzed in MEGA 11. Phylogenetic analysis between studied individuals was carried out using the Neighbor-Joining method with 1000 bootstrap replicates. Haplotype diversity and nucleotide diversity parameters were calculated to reveale distribution pattern of genetic diversity in studied Capercaillie populations.

Results*:* Initial DNA extractions yielded high concentrations but contained impurities inhibiting PCR. The optimized two-step purification significantly improved DNA quality and amplification efficiency. Agarose gel electrophoresis and PCR analysis confirmed successful primer binding after purification. High-quality mitochondrial D-loop sequences were obtained, revealing variable sites suitable for genetic differentiation and phylogenetic analysis of T. urogallus populations from Latvia and Lithuania.

Analyses revealed moderate haplotype diversity and limited genetic differentiation between Lithuanian and Latvian populations, indicating historical gene flow and shared ancestry. Nonetheless, several distinct haplotypes were detected, particularly in isolated forest areas, suggesting emerging sub-structuring linked to habitat fragmentation and differences in forest condition.

Analysis of mitochondrial D-loop sequences identified seven haplotypes (IBE-C6280, TuB39, Tu32, Tu37, Tu11, Tu10, TU16) among T. urogallus specimens from Latvia and Lithuania. Latvian specimens represented IBE-C6280, TuB39, and Tu37, whereas Lithuanian samples contained Tu32, Tu11, Tu10, TU16, and also Tu37.

The shared occurrence of haplotype Tu37 in both populations suggests a common maternal lineage and indicates partial genetic connectivity between Latvia and Lithuania. Although TU16 differs from Tu10 by only a single nucleotide substitution, it was considered a separate haplotype according to the strict definition.

Conclusions*:* The optimized non-invasive DNA extraction protocol provides a reliable method for obtaining high-quality DNA from feathers, enabling genetic monitoring of declining T. urogallus populations. The observed genetic diversity patterns reflect the ecological status and connectivity of forest habitats, confirming T. urogallus as a suitable bioindicator for forest health assessment. Integrating genetic monitoring with habitat restoration and sustainable forest management will strengthen conservation strategies and support biodiversity maintenance in the Baltic region.

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ASSESSMENT OF EMERGING LEAF PATHOGENS IN FAGUS SYLVATICA AND QUERCUS RUBRA STANDS IN LATVIA

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European beech (*Fagus sylvatica* L.) and Northern red oak (*Quercus rubra* L.) cover a small area in Latvian forests. Although European beech is relatively resistant to many pathogens (Jung *et al.,* 2005), leaf and shoot diseases can reduce tree vitality and growth, making them more vulnerable to other infections. Since no phytopathological risks have been assessed for beech and red oak in Latvia, this study, done in 2024 and 2025, evaluated together 19 young beech and red oak stands with focus on leaf pathogens.

Tree health was assessed along a 100-meter transect in each stand. Every 10 meters, two nearby beech trees were examined. For each tree, symptoms on leaves and shoots, including leaf chlorosis, wilting, drying, branch dieback, bark cracking, and wounds were recorded, and a sample was taken for fungal analysis. In the laboratory, two to three symptomatic leaves were selected from each sample and two small tissue pieces per leaf were placed on separate growth media. Fungal isolation and detection were carried out based on culture morphology and ITS region sequencing.

Over the two-year period a total of 159 beech and red oak leaf samples were analyzed. *Apiognomonia errabunda*, a known pathogen of deciduous trees, was detected in 33 of 125 beech samples. *Diplodia sapinea*, a fungus primarily associated with conifers, was surprisingly isolated from both tree species. Additionally, *Colletotrichum fioriniae* and *Colletotrichum godetiae* were isolated from beech and red oak, respectively.

Given that the changing climate facilitates pathogen emergence and host range expansion, continued research and monitoring of these species are critical to foresee and manage the likely increase in the quantity and diversity of tree pathogens.

INVASIVE FUNGAL SPECIES CAUSING NEEDLE BLIGHT IN SCOTS PINE (*PINUS SYLVESTRIS* L.) STANDS IN LATVIA

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Currently in Baltics and Latvia invasive fungal species causing needle blight diseases are threatening the vitality of Scots pines. Among these pathogens are *Diplodia sapinea*, *Dothistroma septosporum*, *D. pini* and *Lecanosticta acicola*, with *L. acicola* firstly detected in Latvia in 2021. This study aimed to assess the phytopathological risks of *L. acicola* and other mentioned pathogens in Scots pine stands in relation to tree vitality.

In 2024, eight young pine stands, where *L. acicola* was detected previously, were surveyed. Using the transect method, trees were evaluated every five meters. In total, 450 trees were examined, observing morphological indicators and estimating needle cast intensity. From 161 trees needle samples were collected (20–21 symptomatic trees per stand) for morphological and molecular analyses.

The average needle cast intensity indicated partially damaged second-year and current-year needles, without significant needle loss in the crown. *Dothistroma septosporum* and *D. pini* were present in all surveyed stands and caused the highest needle cast intensity. *Lecanosticta acicola* was repeatedly detected in three stands were it was previously found in 2022 and 2023, for a total of 10 samples. Thus, the needle cast intensity of infected trees with this pathogen was low. An inverse correlation was observed between tree height and occurrence of *L. acicola* with higher occurrence in trees with lower height. In 2025, *L. acicola* was detected in two new stands, neighboring some infected ones from 2024 survey. Since all tested pathogens are recently established in forest stands of Latvia, monitoring their spread and impact to local forests is crucial.

ADAPTING TO CHANGE: INNOVATION DEVELOPMENT IN LITHUANIAN FORESTRY SECTOR

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The EU Green Deal policy has a significant impact on forest sector enterprises, promoting a sustainable economic growth strategy through the implementation of innovations in Lithuania. With the rapid advancement of new technologies, evolving consumer demands, and changing requirements for forest management, there is an increasing need for enterprises operating in forestry to adopt novel technologies. The evolving innovation landscape provides more favourable conditions for enterprises to leverage financing opportunities aimed at green transformation and digitalisation. In 2024, an expert survey was conducted to identify key trends in innovation development within forestry sector enterprises. The data collected were compared with findings from a previous survey conducted in 2005. The results indicated a significant increase in the implementation of innovations within enterprises operating in the forestry sector from 2005 to 2024. Innovation adoption has been stimulated not only by political decisions but also by enhanced access to financing and growing public awareness of the importance of forest conservation. However, enterprises within the forest sector continue to face substantial challenges, particularly due to a lack of specialised knowledge and skills required to implement sustainable practices, modernise operations, and comply with complex environmental regulations.

RELATIONSHIP BETWEEN SSR-BASED MOLECULAR MARKER AND COTTON F1 INTER SPECIFIC HYBRIDS PERFORMANCE FOR SEED COTTON YIELD AND FIBER PROPERTIES

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Knowledge of genetic diversity and relationships among breeding materials has a significant impact on crop improvement. Association between parental divergence and progeny performance has not been well documented in cotton (*Gossypium hirsutum* L.). The objectives of this study were to estimate genetic diversity among selected cotton genotypes on the basis of simple sequence repeat (SSR) markers, and to investigate the relationship between genetic diversity and F1 population performance and heterosis. The present study was conducted to investigate the relationship between parents molecular marker diversity and interspecific hybrids of cotton to evaluate the hybrid performance and heterosis using molecular markers. Twenty eight F4 lines of (*Gossypium barbadense* L.) were crossed with the four common diverse testers (*Gossypium hirsutum* L.) viz., DH 98-27 (T 1), ZCH8 (T 2), 178-24 (T 3) and DH 18-31 (T 4) to produce 112 F1 inter specific hybrids during 2010. These 112 F1 hybrids, their F5 barbadense lines with 4 hirsutum testers and ruling commercial check (MRC6918 and DCH32) were evaluated for yield and fiber quality traits and sown during kharif 2011 at University of Agricultural Sciences, Dharwad, India. Genetic distances (GD) among the parents were calculated from 40 microsatellite marker data, and their correlation with hybrid performance and heterosis were analysed. The dendrogram constructed from the pooled data revealed three distinct clusters. One cluster involved testers and other clusters showed all lines were placed which are already having proven record in giving good hybrids. The similarity coefficient values between the line DB 533 × DB 534.

F4 IPS 49 and the tester DH 98-27 showed 67%. It revealed that DB 533 × DB 534 F4 IPS 49 was closely related to DH 98-27 with 67% similarity between parents. The hybrid between DB 533 x DB 534 F 4 IPS 49 and DH 98-27 exhibited the highest yield of 2884.26 kg/ha. Similarity coefficient (88%) value between lines and testers showed between the line DB 533 × DB 534 F4 IPS 52 and the tester ZCH8, the hybrid between these recorded an yield of 2 040.757 kg/ha. Lowest similarity coefficient value was noticed between the line DB 533 × DB 534 F4 IPS 16 and tester DH 98-27 which revealed that they are far distinct from each other. This combination exhibited 2384.62 kg/ha yield. Genetic distance (GD) ranged from 0.041 to 0.429, with an average of 0.183. The result implied that each cluster dendrogram substantially reflected its own genetic relationship among parents. Overall, a low significant correlation of GD with hybrid performance and heterosis was detected in Table 2. Highly significant positive correlation were found between genetic distance (GD) and ginning outturn for F1 performance (0.277) and heterosis over MRC 6918 (0.279) and DCH 32 (0.279), while significant positive correlation were found between genetic distance (GD) and ginning outturn for mid parent heterosis (0.237). Highly significant positive correlation were found between genetic distance (GD) and seed cotton yield for F1 performance (0.359) and heterosis over Bt check MRC 6918 (0.336) and over non Bt check DCH 32 (0.362), while significant positive correlation were found between genetic distance (GD) and seed cotton yield for mid parent heterosis (0.226). Significant positive correlation were found between genetic distance (GD) and lint index for mid parent heterosis (0.227), F1 performance (0.251) and heterosis over MRC 6918 (0.250) and DCH 32 (0.250), while significant positive correlation were found only between genetic distance (GD) and fiber micronaire value for F 1 performance (0.241).

PATTERNS OF PRODUCTIVITY VARIATION IN LITHUANIAN LOTUS CORNICULATUS ACROSS ECOLOGICAL AND MANAGEMENT CONTEXTS

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Birdsfoot trefoil (*Lotus corniculatus* L.) is a perennial forage legume valued for its nutritional value, environmental flexibility and the fixation of nitrogen. This species occurs across a wide range of habitats in Lithuania, including meadows, where it exhibits considerable ecological and yield variability. The potential of the local populations is underutilized in the breeding programs, even though the species itself is widespread. This study examines the yield and diversity patterns of 43 wild populations of Lithuanian-origin *L. corniculatus* and 18 cultivated varieties to identify and develop superior genotypes for future breeding and conservation programs. For this study, *L. corniculatus* populations were collected *in situ* from habitats corresponding to EU Habitat Codes 6210, 6230, 6270, 6510, and 9070, as well as from two anthropogenic sites. Plants were grown *ex situ* from the collected seeds and established in a breeding nursery to evaluate yield and morphological traits. Yield performance was assessed based on total fresh biomass and total dry matter yield (g plant^{-1}) from the first and second cuts, while morphological traits included leaflet length and width and plant height. Cultivated varieties consistently exhibited superior dry matter yield relative to most wild populations throughout the dataset. On average, cultivated varieties produced significantly higher total dry matter yields (15–30% greater; $p < 0.05$) than wild populations, with mean yields of 320 g plant^{-1} and 220 g plant^{-1}, respectively. Nevertheless, considerable variability was observed among wild accessions, with several wild populations (130, 141, 144, 149, 150, 160, 165, 166, 168) achieving yield levels comparable to, or occasionally exceeding, those of the average of the population groups which is considered as control.

Dry matter yield of *Lotus corniculatus* populations varied significantly among meadow habitat types. The highest productivity was observed in populations from the 6270 semi-dry grasslands (average 243 g plant^{-1}), whereas populations from the 6510 lowland hay meadows showed slightly lower productivity (average 215 g plant^{-1}). Populations originating from 6210 dry calcareous meadows exhibited moderate productivity (average 206 g plant^{-1}), while those from 9070 wet fen-transition meadows produced lower biomass 65–75% (average 194.4 g plant^{-1}), attributable to nutrient-limited conditions. Populations from 6230 mesic meadows displayed the lowest yield of about 97.4 g plant^{-1}, likely due to impaired root aeration and growth under waterlogged conditions. These inter-habitat differences were statistically significant ($p < 0.05$), demonstrating that soil fertility and moisture regime constitute the principal ecological determinants of yield variation among meadow types. Populations from anthropogenic sites produced intermediate yields, similar to the lower range of natural meadow populations. Principal Component Analysis (PCA) revealed distinct separation between wild populations and cultivated varieties, reflecting substantive morphological differentiation between these groups. The first two principal components accounted for approximately 55% of total variation (PC1 = 35.9%; PC2 = 19.1%), capturing the predominant differences in plant architecture and biomass-related traits. Fresh biomass, dry matter yield, plant height, and leaflet length exhibited strong loadings on PC1, indicating that these productivity-associated characteristics were most influential in differentiating cultivated varieties from wild populations. Conversely, leaflet width and bunch diameter contributed primarily to PC2, representing secondary morphological variation related to plant structural form. Cultivated varieties formed a compact cluster, indicative of greater phenotypic uniformity resulting from selection for stable, high-yield characteristics. In contrast, wild populations displayed broader dispersion, reflecting enhanced natural variability and local adaptation across diverse meadow ecosystems.

GENETIC IDENTIFICATION OF *TOXOPLASMA GONDII* IN BRAIN TISSUES OF WILD RODENTS FROM LITHUANIA

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Toxoplasma gondii is an obligate intracellular parasite infecting a wide range of warm-blooded animals, with felids as its definitive hosts. Oocysts shed by cats can contaminate soil, water, and food, posing infection risks to intermediate hosts, including rodents, birds, and humans. Despite its global importance as a food-borne zoonosis, *T. gondii* remains genetically unstudied in Lithuania. This study aimed to detect *T. gondii* DNA in brain tissues of wild rodents.

In 2024, brain samples from 401 wild rodents representing eight species: *Apodemus agrarius, Apodemus flavicollis, Clethrionomys glareolus, Microtus agrestis, Microtus arvalis, Micromys minutus, Mus musculus* and *Alexandromys oeconomus* were collected from various regions of Lithuania to investigate the presence of *Toxoplasma gondii*. The animals were trapped in diverse natural habitats, including forests, meadows, shrubby clearings, and orchards. Genomic DNA was extracted from the brain tissues and screened for *T. gondii* using nested PCR targeting the ITS1 region, followed by sequencing for parasite confirmation and genetic analysis.

Toxoplasma gondii DNA was detected in four rodent species (*Apodemus agrarius, Apodemus flavicollis, Clethrionomys glareolus* and *Microtus arvalis*), indicating neural infection across multiple locations. The overall prevalence of *T. gondii* was 14.7%, with no statistically significant differences observed between infected species. Sequence comparison with reference data confirmed the parasite's identity and revealed low genetic variability among detected isolates. In total, eight different ITS1 genotypes were determined, and the predominant genotype was found in 86.4% of samples. These findings provide the first molecular evidence of *T. gondii* in Lithuanian rodent populations, confirming its presence in the country's wildlife and highlighting the need for further research on its epidemiology.

METABARCODING OF THE MYCOBIOME OF *PHAENOPS CYANEA* AND *PISSODES* SPP.

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The study investigates the mycobiome of insect pests of Scots pine, specifically *Phaenops cyanea* and *Pissodes* spp. It has been proposed that these insect species can distribute plant pathogen fungi of *Ophiostomataceae*, *Heterobasidion* and other genera. This study will allow for the characterisation of fungal communities hosted by *P. cyanea* and *Pissodes* spp., potentially confirming these insects as a vector of Ophiostomataceae associated with "blue-stain wood", as well as other potentially aggressive fungal species. The results of this project could provide new data about the presence of entomopathogenic fungi in the populations of *P*. *cyanea* and *Pissodes* spp., serving as natural regulators of the pest population and potentially acting as agents of biological control. Considering the local events of massive dieback of pine stands in European countries promoting development of stem pests and the economic impact of the combination of such events, studies included in the proposal are needed to development containment strategies.

Massively parallel sequencing (MPS) will be used to generate metabarcoding data from the mycobiomes of various insect species. MPS will be performed on an Ion GeneStudio S5 Plus instrument or an integrated Oxford Nanopore P2 instrument, both of which are used in the Genetic Resource Centre, Latvian State Forest Research Institute "Silava".

Currently, in collaboration with specialists from the Forest entomology laboratory at LSFRI "Silava" a total of 376 samples were collected, including 132 adults of *P. cyanea* and *Pissodes* spp., 190 larvae, and 52 pieces of damaged wood. The obtained material will be used for isolating phytopathogenic and entomapathogenic fungi and for DNA extraction.

We would like to invite you to collaborate on this project and would be happy to receive laboratory samples for this project.

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PROFITABILITY ASSESSMENT OF SMART IRRIGATION SYSTEMS IN CHILLI (*CAPSICUM ANNUUM* L.) PRODUCTION

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A field experiment was investigated at Water Technology Farm fields, College Farm, College of Agriculture, Rajendranagar, Hyderabad, during rabi seasons of 2022–23 and 2023–24 entitled ‘Profitability Assessment of Smart Irrigation Systems in Chilli (*Capsicum annuum* L.). The investigation followed a split plot design, with drip irrigation methods (I) as main plots with 2 levels (I1—surface drip (laterals were laid at soil surface) and I2—subsurface drip (laterals were laid at 15 cm deep below the surface soil) and irrigation scheduling approaches as subplots with 4 levels (S1- soil moisture sensor based irrigation triggering (16.8 and 23.6% moisture contents were fixed as lower and higher threshold values), S2—Plant water stress sensor based irrigation triggering (0.3 and 0 crop water stress index were lower and higher threshold values for irrigation triggering), S3—ET sensor based irrigation triggering (irrigation was triggered based on crop evapotranspiration at set time) and S4- Irrigation scheduling at 1.0 Epan by manual. Linear regression technique was employed to model the behaviour of capacitance soil moisture sensor (SW-10) and evapotranspiration system coupled with solar radiation (EMC –01) and ambient temperature sensors. A logistic regression model with edge computing at the device level was used to analyse data from the canopy (NTC—10K) and ambient temperature sensors in the plant water stress system. After calibration, all sensors were installed in the field and monitored for performance and accuracy. The results indicated that subsurface drip irrigation (I2) registered lower man days (104) and cultivation cost (₹ 168056) and significantly higher net returns (₹ 669148) and B:C ratio of 4.98 compared to surface drip irrigation. Among the irrigation scheduling approaches, ET sensor based irrigation triggering recorded lower man days (102) and cultivation cost (₹ 166044) and significantly higher net returns (₹ 696735) and B:C ratio of 5.20 which was statistically comparable with manual irrigation scheduling at 1.0 Epan.

FOOD SAFETY AND VETERINARY MEDICINE

MILK FAT-TO-PROTEIN RATIO AS A MARKER OF BLOOD METABOLIC CHANGES RELATED TO SUBCLINICAL KETOSIS AND LOW-GRADE RUMINAL ACIDOSIS IN EARLY LACTATION DAIRY COWS

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Objectives: This study's primary objective was to investigate the connection between the milk fat-to-protein ratio (FPR) and the metabolic changes associated with subclinical ketosis and low-grade ruminal acidosis in Holstein dairy cows during early lactation. The researchers aimed to validate FPR as a non-invasive indicator for these metabolic disorders by correlating it with specific blood biochemical markers.

Methods: Twenty-seven cows, ranging from 9 to 59 days postpartum, were sorted into three distinct groups based on their FPR values:

- Low-grade ruminal acidosis (FPR < 1.2)
- Metabolically healthy (FPR 1.2–1.5)
- Subclinical ketosis (FPR > 1.5)

Milk composition was continuously monitored using a Brolis HerdLine in-line analyzer. To assess metabolic health, weekly blood samples were collected and tested for various parameters, including iron, glucose, and non-esterified fatty acids (NEFA).

Results: The analysis revealed significant differences among the groups:

• Cows with subclinical ketosis showed significantly higher NEFA levels compared to the ruminal acidosis group ($p < 0.01$), a finding consistent with the enhanced fat mobilization that occurs during a negative energy balance.

• Serum iron levels were significantly lower in the ketosis group than in the ruminal acidosis group ($p < 0.01$). Furthermore, the ruminal acidosis group also had significantly lower serum iron than the metabolically healthy cows ($p < 0.01$), highlighting that iron metabolism is disrupted in both conditions.

• Correlation analysis supported these findings: FPR positively correlated with NEFA ($r = 0.281$, $p < 0.01$) and negatively correlated with serum iron ($r = -0.308$, $p < 0.01$).

Conclusions: The study concluded that FPR is a reliable indicator of metabolic health in early-lactation dairy cows. It accurately reflects key metabolic alterations, such as elevated NEFA in ketosis and reduced serum iron in both ketosis and ruminal acidosis. These results confirm the utility of FPR as a simple and practical tool for the early detection and management of subclinical metabolic disorders in dairy cows.

OXIDATIVE STRESS-INDUCED ALTERATIONS IN BONE MARROW CYTOMORPHOLOGY IN BALB/C MICE

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Background: Bone marrow (*medulla ossium*) is the principal hematopoietic organ in mammals, accounting for 1.5–2% of body weight in mice. Oxidative stress, defined as an imbalance between the production of reactive oxygen species (ROS) and antioxidant defense, is not only a physiological by-product of metabolism but also a key pathological factor when excessive. Elevated ROS can disrupt bone marrow homeostasis, impair hematopoietic balance, and promote inflammatory responses.

Aim: To investigate *in vivo* the cytomorphological alterations of bone marrow under oxidative stress in BALB/c mice.

Methods: Male BALB/c mice were randomly allocated into two groups: (1) control (physiological saline) and (2) oxidative stress ($AlCl_3$ solution). Oxidative stress symptoms appeared within 30 minutes of $AlCl_3$ administration. Bone marrow smears were prepared from femurs. For each specimen, 500 cells were counted and classified into myeloid and erythroid lineages. Megakaryocytes were quantified across 10 high-power fields (HPF). The myeloid-to-erythroid (M:E) ratio was calculated for comparative evaluation.

Results: Control animals showed a physiologically balanced hematopoietic profile, with segmented neutrophils predominating and active erythropoiesis represented by rubricytes and metarubricytes. The mean M:E ratio was 1.69, consistent with reported physiological values (1.6–1.9). In the oxidative stress group, a significant increase in segmented neutrophils and their precursors (promyelocytes, metamyelocytes, myeloblasts) indicated enhanced granulopoiesis. Megakaryocytes averaged 15/10 HPF, a 1.9-fold increase compared to controls. The M:E ratio rose to 2.96, demonstrating hematopoietic imbalance and an inflammatory marrow environment.

Conclusion: $AlCl_3$-induced oxidative stress significantly alters bone marrow cytomorphology in BALB/c mice, characterized by increased granulopoiesis, elevated megakaryocyte density, and a pathologically high M:E ratio. These findings confirm that oxidative stress profoundly disrupts hematopoietic homeostasis and highlight the suitability of this *in vivo* model for studying ROS-mediated hematological alterations.

Keywords: oxidative stress, bone marrow, hematopoiesis, cytomorphology, BALB/c mice

EFFECT OF PROBIOTIC EDIBLE COATINGS ON THE NUTRITIONAL AND BIOCHEMICAL PROPERTIES OF EDAM-TYPE CHEESE

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Improving the nutritional quality of semi-hard cheese through functional ingredients is a growing focus in dairy research. Edible coatings containing probiotic-type bacteria offer a promising strategy to enhance cheese composition and digestibility during ripening.

In this study, *in vitro* digestion simulations of ripened Edam-type cheese samples (control, coated with liquid acid whey protein concentrate (LAWPC) coating, and coated with LAWPC coating containing *Lacticaseibacillus paracasei* A11 at approximately 7 log10 CFU/g) were performed using the standardized static method (Minekus et al., 2014), combined with size exclusion chromatography for the evaluation of digested protein concentration. Volatile fatty acids (VFA) were quantified by gas chromatography and expressed as percentages of total volatile fatty acids (% of total VFA).

After 45 days of ripening, digestion results showed that the soluble protein fraction ranged from 189.2 mg in cheese coated with LAWPC + A11 to 191.1 mg in cheese coated with plain LAWPC and 195.4 mg in control, corresponding to 80.3%, 77.5%, and 76.7% of total soluble protein, respectively. The degree of simulated enzymatic cheese digestion increased significantly from 66.1% in the control cheese to 66.9% in the cheese coated with plain LAWPC coating, and further to 69.4% in the cheese coated with LAWPC + A11 ($p < 0.001$), demonstrating enhanced enzymatic breakdown due to probiotic incorporation. Moreover, VFA analysis revealed no significant differences among most VFA, except for a significant decrease in lauric acid in cheese coated with LAWPC + A11 (3.09% ± 0.12) compared to cheese with plain LAWPC-coated (3.21% ± 0.01) and control (3.21% ± 0.14) cheeses ($p < 0.05$), suggesting a beneficial shift toward a healthier fatty acid profile.

These results demonstrate that edible coatings, particularly the LAWPC + A11 formulation, enhanced nutritional quality, protein solubilization, and digestibility, highlighting their potential as an effective strategy to improve the properties of cheese.

COOLED STALLION SEMEN TRANSPORTED WITHOUT QUALITY CERTIFICATION: THE FIRST LITHUANIAN STUDY ON SEMEN QUALITY BIOMARKERS AND FERTILITY AFTER 24-HOUR SHIPMENT

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In Lithuania, the growing equine breeding industry has increased the use of artificial insemination with cooled stallion semen imported from abroad and delivered within 24 hours of collection. Upon arrival, motility is routinely assessed, but pH is rarely measured despite its potential as an early biomarker of semen quality deterioration before motility visibly declines. This study aimed to evaluate correlations between semen pH and key morphological and functional parameters.

Twenty semen samples were collected from Warmblood stallions aged 4–22 years at breeding centers in Europe, cooled and sent to Lithuania. Following 24 hours of transport, semen concentration, pH, total sperm motility, sperm viability (eosin/nigrosin staining) and morphology were determined in specialized Animal Reproduction Laboratory according to the methodologies used there. Then, the semen was used to artificially inseminate the mares. Conception rates were observed after 14 days.

Despite all sperm samples quality meets international limits, some tendencies were noted. Semen motility ($\rho = +0.40$, $p = 0.040$) and concentration in sperm dose ($\rho = +0.68$; $p = 0.000039$) statistically significantly correlated with conception rates. Tail and sperm midpiece pathologies also correlated statistically significant ($\rho = +0.67$, $p = 0.001$). Semen pH values in the analyzed samples ranged from 7.61 to 9.63. A statistically significant positive correlation was observed between pH and detached pathological sperm heads ($\rho = 0.54$, $p = 0.036$) also pH and sperm heads with a narrow base ($\rho = 0.68$, $p = 0.0057$). The analysis revealed positive statistically significant associations between semen pH and conception rates ($\rho = 0.65$, $p = 0.0158$).

Our study results suggest that although all semen samples met international standards, higher motility, sperm concentration, and pH were positively correlated with conception rates. In stallions, increased numbers of detached heads and narrow-base heads may be associated with handling stress, pH changes, or osmotic imbalance. Monitoring pH alongside morphological assessment, total sperm motility, and viability could improve the evaluation of stallion semen quality and serve as an early biomarker of alterations in the seminal environment. Further investigation with a larger sample size is warranted.

ASSOCIATIONS BETWEEN MICROPLASTICS AND SPERM MOTILITY PARAMETERS IN BOAR SEMEN

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Microplastics (MP) are environmental contaminants that pose a potential risk to male reproductive health. The presence of MP in semen may influence sperm functionality by inducing oxidative stress and altering motility or the seminal environment. This study aimed to evaluate the relationship between MP characteristics and boar semen quality.

Undiluted semen samples ($n = 12$) collected from healthy adult boars were analyzed to determine MP particle characteristics using Fourier-transform infrared (FTIR) spectroscopy. Particles were classified by polymer type (nine polymers identified) and size (<50, 50–100, 100–250, 250–500, 500–1000, and ≥1000 µm; particles equal to the lower bound of an interval were included in that interval). Sperm motility parameters were assessed by Computer-Assisted Sperm Analysis (CASA). Associations between MP and CASA parameters were evaluated using Spearman's rank correlation.

Statistically significant correlations were observed between MP concentrations and motility parameters. The percentage of motile spermatozoa in semen was negatively correlated with polyethylene and polyamide particle counts per mL ($\rho = –0.608$, $p = 0.036$; $\rho = -0.616$, $p = 0.033$, respectively). The total number of MP/mL showed a significant negative correlation with rapid velocity ($\rho = –0.608$, $p = 0.036$). Specifically, polyester and polyethylene were negatively correlated with sperm rapid velocity ($\rho = -0.803$, $p = 0.002$; $\rho = –0.755$, $p = 0.005$, respectively), while MP size fractions (250–500, 500–1000, and ≥1000 µm) also correlated negatively with this parameter ($\rho = –0.769$; $\rho = –0.727$ and $\rho = –0.736$, respectively, $p < 0.01$). Conversely, slow velocity parameters were positively correlated with total MP counts, as well as polyester and polyethylene particles.

These initial findings indicate that certain types of MP and particle sizes are associated with reduced sperm motility characteristics in boar semen, particularly decreasing rapid velocity while increasing slower motion patterns. This exploratory study highlights a potential link between microplastic contamination and impaired motility of boar sperm, warranting further investigation into the underlying mechanisms and effects of specific polymers.

QUANTITATIVE PROFILING OF TICK-BORNE ENCEPHALITIS VIRUS IN HOSTS AND VECTORS USING DIGITAL PCR IN CELL CULTURE MODELS

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Tick-borne encephalitis virus (TBEV) is a major neurotropic virus circulating in Lithuania, maintained through a natural cycle between ticks and vertebrate hosts. Although RT-qPCR is widely used for virus detection in field samples, quantitative data on viral replication, particularly from infected cell cultures, remain limited.

To investigate this aspect, we analyzed 139 TBEV-positive samples originating from ticks ($n = 16$), rodents ($n = 69$), dogs ($n = 32$), horses ($n = 7$), goats ($n = 4$), and raw goat milk ($n = 11$). Viral RNA copy number per microliter was determined using absolute quantification with digital PCR. Additionally, positive samples were cultured through ten consecutive passages in three different cell lines - MARC-145, Vero, and N2a, followed by digital PCR to evaluate their capacity for viral amplification.

Mean viral loads measured in native samples (viral copies/µL) were: horse blood 6.14 (95% CI 0 – 12.59), ticks 3.36 (95% CI 1.95 – 4.77), rodent tissues 6.72 (95% CI 3.82 – 9.63), goat blood 2.56 (95% CI 0 – 5.52), goat milk 4.54 (95% CI 2.28 – 6.8), and dog blood 4.25 (95% CI 2.76 – 5.74). Inferential analysis confirmed a statistically significant passage-dependent increase only in MARC-145 cells (slope = 0.20, 95% CI 0.12 – 0.27), ($p < 0.001$), although overall viral load remained very low. Furthermore, comparison of viral loads before and after cell culture revealed a strong increase only in the vector group ($p < 0.001$), while the domestic and synanthropic groups did not change significantly.

These findings highlight the utility of digital PCR for precise viral quantification in diverse biological matrices, aiding improvement of diagnostic approaches and risk assessment in veterinary and public health contexts. Moreover, despite being rarely used for TBEV culture in practice, MARC-145 cells could be a promising first-choice system for experimental applications. However, due to very low viral copy numbers, amplification in cell culture is not a suitable method for sample preparation when a high viral load is required.

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INTERACTION OF BOVINE HERPESVIRUS TYPE 1 WITH COPPER AND ZINC SURFACE MATERIALS

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Introduction: With viral infections becoming increasingly common, effective inactivation of viruses on different surfaces has gained significant attention. While human viruses have been widely studied, the behavior of animal viruses like bovine herpesvirus type 1 (BoHV-1) on metal surfaces remains poorly characterized. The objective of the present study was to evaluated the effect of copper (Cu) and zinc (Zn) surfaces on BoHV-1 and it's DNA.

Materials and methods: MDBK-adapted BoHV-1 was used to investigate the virucidal effect of copper (Cu) and zinc (Zn) surfaces, with stainless steel (Fe) serving as a control material. The virus was exposed for 1 and 24 hours under both humid and dry conditions. Inactivation was assesed based on changes in TCID50 log10 values, real-time PCR Ct results, and calculating half-lives of the virus and it's DNA.

Results: Copper-coated surfaces showed the most rapid inactivation of herpesviruses under all tested conditions. After 1 hour of exposure, a strong virucidal effect was detected in both humid and dry conditions (3.25 ± 0.29 log10 TCID50 and 4.5 ± 0.1 log10 TCID50; $p < 0.01$, $p < 0.05$), with similar reduction persisted after 24 hours (4.5 ± 0.25 log10 TCID50 and 4.5 ± 0.1 log10 TCID50; $p < 0.05$). Shorter inactivation half-live time for the virus and viral DNA were under dry conditions (4 minutes and 27 minutes) compared with humid conditions (6 minutes and 10 minutes). However, after 24 hours, this relationship reversed, with faster inactivation observed in humid conditions (1 hour 31 minutes and 6 hours 20 minutes) than in dry ones (1 hour 36 minutes and 4 hours 7 minutes). Viral activity studies in cell culture correlated with real-time PCR, confirming copper's strong effect on viral DNA under both conditions.

Conclusion: Copper surfaces demonstrated superior virucidal activity against BoHV-1, characterized by biphasic inactivation kinetics with an initial rapid reduction under humid and prolonged effect under dry conditions. These results indicate that copper can be effectively used as a surface material to inactivate BoHV-1.

EFFECTS OF ANTIFUNGAL DRUGS AND BACTERIAL AGENT M20G ON FISH PATHOGENIC OOMYCOTA

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Aquatic oomycetes (latin: *Oomycota*) are freshwater fungus-like stramenopiles. These water molds are mostly saprotrophs, however, some species, usually of Saprolegnia genus, can become pathogenic and cause mycosis — saprolegniosis — to fish, crustaceans and amphibians. Oomycetes can infect not only mature fish but also their eggs. Saprolegniosis appears on the gills, body or head of the fish as grey or white patches. In the later stages of infection the filamentous hyphae can causing trouble breathing, spread into deeper tissues, cause inflammation, dermal necrosis and fluid retention. Malachite green, before its worldwide ban for cancerogenic properties, was the main cure for saprolegniosis. Oomycetes' high morphological and genetic variability, ecological plasticity and survivability can complicate identification and treatment of saprolegniosis. Absence of efficient saprolegniosis treatment method is still a problem to this day. The aim of this study was to test different antifungal drugs and bacterial agent M20G against oomycetes in search of saprolegniosis cure or prevention methods. Oomycete colonies were isolated from water samples of lotic freshwater bodies and their identity was confirmed by morphological and sequence-based molecular diagnostic methods. Antifungal drugs tested were Amphotericin B, Nystatin, Itraconazole, Griseofulvin and Flucytosine. Discs or strips of these drugs were placed on an agar medium with a piece of oomycete mycelium and kept at room temperature to observe inhibition zones. Tests with bacterial agent M20G were done by growing oomycete colonies in water and M20G solution of different concentrations. The results show that Amphotericin B, Itraconazole, Nystatin, Griseofulvin and bacterial agent M20G have an antagonistic effect on *Saprolegnia* spp. pathogens and have potential to be used in the treatment of saprolegniosis infected fish. Flucytosine did not show any effect on oomycete growth and vitality.

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CYTOLOGICAL EVALUATION OF SOMATIC CELLS IN GOAT MILK: A STEP TOWARD MORE ACCURATE UDDER HEALTH ASSESSMENT

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Somatic cell count (SCC) is routinely used to evaluate udder health in dairy animals; however, its interpretation in goats remains challenging. Due to apocrine milk secretion, goat milk naturally contains higher numbers of cells and cytoplasmic particles than cow milk. Moreover, the cellular composition differs: macrophages typically dominate in healthy cow milk, while neutrophils prevail in goat milk even under physiological conditions. These differences make it difficult to apply bovine SCC thresholds to goats.

This study aims to characterize the cytological composition of somatic cells in goat milk and to explore its potential for improving the interpretation of SCC values used in mastitis diagnostics.

Bulk milk samples from dairy goats at various lactation stages were analysed in a standardized laboratory to determine total SCC. Cytological smears were prepared from the same samples and microscopically evaluated to quantify neutrophils, macrophages, lymphocytes, and epithelial cells.

Preliminary observations confirm the predominance of neutrophils, comprising approximately 60–80% of total somatic cells, consistent with previous findings reporting 64% in healthy and 79% in mastitic goats (Shah *et al*., 2017). Samples with SCC values between one and three million cells per millilitre frequently displayed mixed cytological profiles indicative of physiological rather than inflammatory variation. In contrast, samples exceeding three million cells per millilitre exhibited degenerative neutrophils and decreased macrophage counts, suggesting inflammatory changes.

Cytological assessment provides more precise information on mammary gland condition than total SCC alone. Establishing cytology-based SCC reference ranges could enhance the accuracy of mastitis diagnostics in dairy goats and reduce the risk of misinterpreting physiological cell variations as pathological.

Keywords: goat milk, somatic cell count, cytology, neutrophils, udder health, mastitis diagnosis

IMPACT OF CAPACITIVE-RESISTIVE MONOPOLAR RADIOFREQUENCY ON MECHANICAL NOCICEPTIVE THRESHOLD IN JUMPING HORSES: A PILOT STUDY

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Intensive training and demanding competition schedules often lead to stress, weight loss and musculoskeletal problems in athletic horses, negatively affecting performance and welfare. Physiotherapy has gained increasing attention as a valuable tool to enhance recovery and optimize athletic performance in equine sports. Capacitive-Resistive Monopolar Radiofrequency (CRMRF) is a physiotherapy modality that generates an electromagnetic field to induce deep tissue heating, enhance local circulation and stimulate tissue repair. While this modality has been extensively studied in human athletes showing benefits in pain reduction, mobility improvement and faster recovery, scientific data on its application in equine pain management remain limited.

The aim of this study was to evaluate the effect of CRMRF on back pain sensitivity and changes in the mechanical nociceptive threshold (MNT) in athletic horses. In this randomized controlled pilot study, MNT was measured in jumping horses (n = 10) following a standardized physical activity protocol and subsequent CRMRF therapy in trial group. Pressure algometry was used to evaluate MNT before physical activity, immediately after in both groups and following CRMRF treatment. A statistically significant decrease in MNT was observed after physical activity ($p = 0.05$) in both trial (n = 5) and control (n = 5) groups. Further significant changes were recorded after CRMRF application ($p = 0.027$) in the trial group.

These findings support the hypothesis that CRMRF may help lower pain and improve the musculoskeletal condition of the back in equine athletes. This highlights its potential role as a valuable tool in equine rehabilitation and performance optimization.

THE EFFECT OF BIOELECTRONIC TECHNOLOGY APPLICATION ON BOAR SPERM VIABILITY, MOTILITY, AND PH STABILITY

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Innovative bioelectronic technologies that can activate and influence surrounding cells and their processes hold significant promise for improving sperm functionality and preservation. The objective of this study was to evaluate the impact of the Bioelectronic technology prototype on sperm viability, motility, and pH stability incubating diluted boar semen at a temperature of 17 °C for 6 hours. The study used 13 doses of diluted boar semen obtained from a commercial pig farm. Each dose of semen was poured into three equal 30 ml storage tubes. The samples in the tubes were divided into three experimental groups: Control, Bio1short (sample kept on 1 biosensor plate) and Bio4short (sample kept on a 4-biosensor package). All samples were kept in a thermostat maintained at +17 °C. Sperm motility, viability and pH were tested according to the methods used in the lab at two time points: 0 hour (Control sample) and 6 hours (Control, Bio1short and Bio4short). After 6 hours, both experimental groups demonstrated significantly higher motility than the control ($p < 0.05$). The control group showed a statistically significant decrease in sperm motility from 93.90% (SD = 0.85) to 90.95% (SD = 1.34) ($p < 0.05$), whereas motility remained stable in the Bio1short (93.19%, SD = 0.89) and Bio4short (93.70%, SD = 0.89) groups. Sperm viability declined in the control from 94.62% (SD = 0.75) to 92.23% (SD = 1.65) ($p < 0.05$), but remained higher in Bio1short (94.15%) (SD = 1.01) and Bio4short (93.69%) (SD = 1.13) ($p < 0.05$). The results obtained indicate that the use of Bioelectronic technology prototype can have a positive effect on boar semen quality indicators by helping to maintain higher sperm viability, motility, and medium stability during storage.

AGRONOMY

UNLOCKING THE POTENTIAL OF NETTLE (*Urtica dioica* L.): A BIORESOURCE FOR SUSTAINABLE AGRICULTURE

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The increasing global population seriously threatens the ability to ensure food security and agricultural productivity, as demand for food production has resulted in an overreliance on chemical inputs, negatively impacting the ecosystem. Therefore, finding simple and sustainable solutions within the agricultural ecosystem is necessary to improve agricultural productivity and provide better resilience to climate change impacts. Research on utilizing plant biomass as biofertilizers is becoming more attractive since there is a prevailing need to elevate crop yield and soil health while minimizing the detrimental effects of synthetic fertilizers. The use of organic amendments in sustainable agriculture has drawn significant interest due to their potential to enhance soil health and crop productivity. Nettle (*Urtica dioica* L.) has emerged as a promising candidate in sustainable agriculture. Nettle is a perennial plant containing lignified fibers that grows readily in the wild throughout Europe and Asia. It has a rich profile of plant nutrients (carbon, calcium, magnesium, potassium, nitrogen, and phosphorus) and bioactive compounds (flavonoids, phenolic acids, carotenoids, sterols, and coumarins) suitable for enhancing crop productivity and soil health. In this context, nettle-based amendments could pave the way for promising results, positively impacting growth stimulation and leaf promotion. Due to the abundance of bioactive compounds, nettle biomass can exhibit biofertilizing potential, with demonstrated efficacy in improving seed germination, plant vigor, and resistance to biotic and abiotic stresses. Furthermore, incorporating nettle-based amendments into the soil promotes a balanced ecosystem, crucial in nutrient cycling, nutrient uptake, and resilience to plant pests and diseases. In this regard, more in-depth research is required on the multifaceted role of nettle in modern agriculture, emphasizing its contributions to soil health, plant growth, and environmental sustainability. This review highlights the agricultural applications of nettle biomass, identifies knowledge gaps, and suggests future research directions to maximize its potential in organic farming systems.

Keywords: slurry, bioactive compounds, biofertilizer, plant productivity, soil health

COMPARISON OF AGRONOMIC PERFORMANCE AND GRAIN QUALITY IN ANTHOCYANIN-RICH AND COMMON WHEAT BREEDING MATERIAL

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In wheat breeding, increasing attention is given to anthocyanin-rich lines enhancing nutritional value and utilization. Despite higher levels of bioactive compounds, agronomic and technological traits remain key to adaptability and breeding potential (1). The study compared grain quality, agronomic performance, and disease resistance in 67 anthocyanin (11 combinations) and 42 common (9 combinations) winter wheat (*Triticum aestivum* L.) lines grown in 2025 field trials. Following traits were evaluated: grain protein, gluten and starch content, sedimentation index, test weight, grain yield, plant height, lodging, winter hardiness, and resistance to leaf blotch and Fusarium head blight, using ANOVA ($p < 0.05$), PCA, correlation and regression analyses. Anthocyanin lines had significantly higher grain protein content (14.0 ± 0.6%) than common lines (12.9 ± 0.5%) and tended to show higher gluten (24.9 ± 1.1% vs. 24.1 ± 1.8%) and sedimentation values (41.5 ± 4.9 ml vs. 39.2 ± 3.3 ml). Common lines exhibited higher starch content (67.0 ± 0.7% vs. 63.3 ± 0.9%) and grain yield (9.1 ± 0.7 t ha^{-1} vs. 8.1 ± 0.9 t ha^{-1}), while plant height, winter hardiness, and disease resistance did not differ significantly between the groups. In anthocyanin lines, protein content showed a strong positive correlation with gluten ($r = 0.89$) and a moderate negative with starch and yield ($r = –0.39$ and –0.35). In common lines, protein showed a weaker positive correlation with gluten ($r = 0.71$) but stronger negative correlations with starch ($r = –0.67$) and yield ($r = –0.85$). The results indicate that higher accumulation of total and insoluble proteins in anthocyanin wheat lines may be linked to lower yield potential and reduced starch biosynthesis, in agreement with earlier studies (2, 3). Tested lines represent valuable breeding material for improving nutritional quality alongside agronomic performance. Future research should focus on yield stability, heritability and detailed grain quality characterization.

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FUNGAL COMMUNITIES ASSOCIATED WITH SEEDS OF LEGUMES

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Legumes play a vital role in crop rotation, contributing to sustainable crop production and the conservation of soil fertility. Research on legume diseases remains limited, particularly in Europe. Nevertheless, seed infection is widely recognized as a primary source of fungal diseases affecting legumes. The objective of this study was to identify the fungal communities associated with asymptomatic seeds of various legume species. The seeds of Pisum sativum, Vicia faba var. minor, *Trifolium* spp. and *Medicago* spp. were collected in 2023–2025. Pure fungal cultures were obtained from surface-sterilized seeds without disease symptoms using standard mycological techniques. The isolated fungi were identified to the genus level based on morphological characteristics and confirmed using molecular-genetic methods. Fungi representing 22 genera were isolated and identified. Among the isolates, 71% were putative legume pathogens, 18% were possible causal agents of moulds or secondary pathogens, and 11% were soil inhabitants or incidental fungi. Among the pathogenic isolates, *Alternaria* spp. (50%) and *Fusarium* spp. (31%) were dominant across all host species. Fungi from the family Didymellaceae (14%) and *Stemphylium* spp. (15%) also represented a significant portion of the isolates. In addition, *Verticillium* sp. and *Botrytis* spp. were detected. Accurate identification of fungal species is essential for evaluating their roles in plant disease development and for investigating inter- and intraspecific interactions among fungi associated with legumes.

Keywords: *Alternaria, Fusarium, Stemphylium, Botrytis*

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EFFECTIVENESS OF PLANT GROWTH REGULATORS AND PLANT PROTECTION LOAD INDEX UNDER DIFFERENT NITROGEN TOP-DRESSING RATES IN WINTER WHEAT

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A three-year field experiment (2021–2023) was conducted with winter wheat (*Triticum aestivum* L.) cultivar 'Skagen' to evaluate strategies for reducing the Plant Protection Load Index (PLI) associated with plant growth regulator (PGR) use under different nitrogen top-dressing rates (N180, N150, N120), while maintaining effective lodging resistance.

Five PGRs were tested: Cycocel 750 (a.i. chlormequat chloride), Medax Max (a.i. prohexadione-calcium, trinexapac-ethyl), Moddus 250 EC (a.i. trinexapac-ethyl), Terpal (a.i. mepiquat chloride, ethephon), and Moddus Start (a.i. trinexapac-ethyl). Treatments differed in regulator combinations, rates, and application stages. The PLI was calculated from three sub-indicators: human health (PLI.H), ecotoxicology (PLI.ECOTOX), and environmental hazard (PLI.ENV). Plant height, lodging index, and grain yield were recorded.

At N120, mean plant height, lodging index, and yield did not differ significantly among treatments. At N150, significantly shorter plants and a trend toward lower lodging were observed with Cycocel 750 (1.0 L ha^{-1}) plus Medax Max (0.5 L ha^{-1}), while the highest yield occurred with Cycocel 750 (1.5 L ha^{-1}) plus Medax Max (0.3 kg ha^{-1}). At N180, all treatments, except Cycocel 750 (1.5 L ha^{-1}) plus Moddus 250 EC (0.4 L ha^{-1}), significantly reduced plant height. Lodging was lower across all treatments, but yield differences were not significant.

The highest PLI (0.79) at N180 occurred with Cycocel 750, Medax Max, and Terpal combined; the lowest (0.02) with Medax Max (0.3 kg ha^{-1}) plus Moddus 250 EC (0.4 L ha^{-1}). Chlormequat chloride contributed most to total load, while prohexadione-calcium showed the lowest PLI.

Overall, integrating low-PLI substances such as prohexadione-calcium and trinexapac-ethyl allows effective lodging control while reducing environmental and health risks. PLI should be considered alongside agronomic efficiency when selecting PGR strategies.

Keywords: PLI, plant growth regulators, plant height, lodging index, *Triticum aestivum*

DETERMINATION OF NITROGEN CONTENT IN POTATO TUBERS USING A NON-DESTRUCTIVE METHOD ACROSS DIFFERENT GROWING SEASONS

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Nitrogen is one of the most essential nutrients required for plant growth, development, and tuber quality in potato (*Solanum tuberosum* L.) cultivation. Precise monitoring of nitrogen levels is crucial for optimizing fertilization practices, improving yield, and reducing environmental impact. Traditional analytical methods for determining nitrogen content are often destructive, time-consuming, and require laboratory conditions. The aim of this study was to determine and compare the nitrogen content in potato tubers grown in different growing seasons using a non-destructive analytical method. Field experiments were conducted at the Institute of Agricultural Resources and Economics (Priekuļi, Latvia) in 2020, 2021, 2023, and 2024, while a pot experiment was carried out at the Latvia University of Life Sciences and Technologies in 2025. Nitrogen fertilizer was applied at a rate of 60 kg N ha^{-1}. The study included three potato varieties: 'Monta', 'Prelma', and 'Jogla'. Nitrogen content was determined using a near-infrared spectrometer. The lowest nitrogen content in potato tubers was found in the pot experiment (Monta — 1.01%, Prelma — 1.06%, Jogla — 0.66%), whereas in field trials it ranged from Monta — 1.12–1.54%, Prelma — 1.17–1.47%, and Jogla — 0.90–1.45%. The nitrogen content in tubers was significantly influenced by the growing year and variety ($p < 0.05$).

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EFFECT OF WINTER WHEAT–LEGUMES CROPPING SYSTEMS ON SOIL MINERAL NITROGEN AND GRAIN YIELD

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Wheat growing under organic farm conditions understood show lower and more variable productivity and grain proteins levels than wheat grown conventionally, primarily because of nitrogen limitations and weed pressure. Sowing legumes as cover crops into wheat rows a practice known as a relay intercropping is considered an effective method to increase N availability in the soil crop system and enhance weed suppression. The aim of the study is to evaluate wheat performance and nitrogen resource competition in relay intercropping systems with legume cover crops under different environmental conditions. During the research year 2023-2024 was measured winter wheat and legumes yield and soil mineral nitrogen content. Experiment were conducted on organic farm conditions located in Akademija, Lithuanian Research Centre for Agriculture and Forestry. Pea (Pisum sativum), lentils (*Vicia lens* L.) egyptian clover (*Trifolium alexandrium*) sown during the wheat tillering stage were compared with pure crop of winter wheat (*Triticum aestivum*). The systems of winter wheat and their mixtures with legumes reduced the amount of mineral nitrogen in the soil (0–60 cm). Although a significant decrease in nitrogen was recorded during the growing season, after the harvest of legumes, a higher amount of mineral nitrogen remained in the soil, indicating their positive effect on the soil nitrogen balance. The results show that winter wheat–legume systems, especially those with peas, complemented the crop without reducing overall yield. The greatest grain yield was achieved in 2023 when winter wheat was cultivated in combination with peas, with the harvested mixture containing 15.3% pea grains and 84.7% wheat grains.

Keywords: grain yield structure, monocrops, relay intercropping, soil mineral nitrogen

OPTIMIZING ROOT BIOMASS AND FUNCTIONS USING BIOSTIMULANTS FOR MOST RECENT OAT VARIETIES

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Roots are the main source of soil organic carbon, sequestering carbon more efficiently than aboveground plant parts, but exploring ways to enhance root systems through different plant varieties and management practices remains limited (Hirte et al., 2021; Heinemann et al., 2025). At the Lithuanian Research Centre for Agriculture and Forestry, field experiments since 2019 have focused on various oat varieties under conventional, extensive, and organic systems. Since 2023, ten top-performing oat varieties, identified for their potential in root carbon sequestration, are being studied for root biomass, architecture, chemical composition, and shoot productivity across soil depths (0–15, 15–30, 30–50 cm). In 2025 trials, 29 biostimulants and biofertilizers are tested for their impact on these varieties, aiming to enhance root development for climate mitigation and adaptation. These findings, part of ongoing PhD research, will be published in Lithuania and are vital for future crop breeding at LAMMC, aligning with climate resilience, soil health, and ecosystem services.

In the multi-year oat variety study, Lithuanian Dotnuva Seeds varieties were used, with 'Delfin' as a control. The 'Simer' and 'Frekula' varieties consistently showed high yields, except in 2022 when 'Svaja' yielded the most. Greenhouse experiments identified 'Simer' as the most productive variety overall. Testing 29 biostimulants revealed only manganese sulfate and a calcium-manganese biostimulant had positive effects; all others underperformed compared to the control.

IN VITRO EVALUATION OF NITROGEN USE EFFICIENCY IN POTATO (*SOLANUM TUBEROSUM* L.) UNDER DIFFERENT NITROGEN LEVELS

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Potato (*Solanum tuberosum* L.) is an important crop for worldwide. Still, it demands large amounts nitrogen (N). Breeding potato varieties with enhanced nitrogen use efficiency (NUE) can sustain optimal yields while lessening environmental impact, aligning with sustainable agricultural practices.

Potato genotypes vary in nitrogen uptake and biomass production across different nitrogen levels. *In vitro* experiments offer controlled conditions to study how potato genotype NUE and morphological traits respond to different N levels, that can be helpful in the breeding and selection process.

The study aimed to evaluate the genotypic-specific characteristics in a two-factorial experiment, analysing microplant responses and NUE depending on nitrogen availability in the growth medium *in vitro*.

The study was carried out in three time-shifted series, where 19 potato genotypes was tested under varying nitrogen levels in an *in vitro* medium. The Murashige and Skoog basal medium used for the experiments included three different N concentrations: 60 mmol L^{-1} (N60), 20 mmol L^{-1} (N20), and 7.5 mmol L^{-1} (N7.5). The potato microplants were evaluated for morphological traits such as plant height, fresh weight (FW) and dry weight (DW) of the whole plant and the shoots and roots. Calculated parameters included the root-to-shoot ratio (R:S ratio), the nitrogen stress tolerance coefficient (NstC), and the nitrogen use efficiency (NUE) of the genotypes.

Reduced nitrogen availability negatively affected the growth of potato plants. The results indicated significant differences in biomass production across various N levels ($p < 0.05$), as well as notable differences in performance among genotypes cultivated at the same N level. NstC varied between genotypes, with some exhibiting lower tolerance to reduced N without any observable changes in morphological traits. This suggests complex interactions among phenotypic characteristics, nitrogen availability, and NUE. Additionally, the R:S ratio and several morphological traits demonstrated strong correlations ($p < 0.05$) with NUE.

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UAV-BASED PHENOTYPING FOR EARLY-GENERATION SELECTION IN SPRING WHEAT: EVALUATING VEGETATION INDICES FOR AGRONOMIC TRAIT PREDICTION

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Early-generation selection in spring wheat is constrained by limited seed availability, making rapid and non-destructive phenotyping essential. The main objective of this study is to determine the most effective vegetation indices (VIs) for predicting key agronomic traits — plant number, spike number, productive tillering, and grain yield, by evaluating the potential of UAV-based remote sensing in early-stage breeding (F_4–F_5 generations). Seventeen breeding lines from three crossing combinations and six parental varieties were sown in three randomized replications using a cassette-type plot seeder at the AREI Stende Research Centre in 2025. Two sowing variants were tested: a calculated seeding rate of 500 seeds m^2 and a fixed row-based seeding of 40 seeds. Plots consisted of three 1 m rows with 33 cm spacing, and the standard variety 'Arabella' was included as a reference control. UAV flights were conducted seven times from the two-leaf stage (GS21) to mid-milk (GS75) using a Matrice 300 equipped with a Sentera AGX710 multispectral camera capturing RGB, red-edge, and NIR bands. Orthomosaics were radiometrically calibrated, and bare soil pixels were excluded using index thresholds and supervised classification. Sixteen vegetation indices (7 RGB, 9 multispectral) and vegetation fraction were extracted per plot, and ground-truth measurements. Prior to correlation analysis, multicollinearity among the 16 indices was assessed, and a subset of non-redundant indices was retained. Pearson correlation analysis revealed that NDRE was consistently identified across all flights, indicating a stable relationship with agronomic traits, while GNDVI, RGBVI, and RDVI were most frequently selected, reflecting sensitivity to canopy density and condition. These indices showed positive correlations with spike number, productive tillering, and grain yield, particularly in mid-to-late growth stages, while correlations with plant number remained weak, suggesting that spectral indices primarily capture canopy development and productivity rather than initial stand density.

Keywords: *Triticum aestivum* L., early-generation breeding, UAV phenotyping, vegetation indices, grain yield prediction, field emergence, multispectral imaging

SOLAR-BATTERY POWERED SELF-PROPELLED DRUM SEEDER FOR LOW-CARBON PADDY CULTIVATION IN CLIMATE-RESILIENT URBAN-PERIURBAN FARMING SYSTEMS

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The increasing demand for sustainable and energy-efficient mechanization in agriculture has driven the development of decentralized, low-emission field equipment. This study presents the design and performance evaluation of a self-propelled solar and battery-operated sitting type drum seeder tailored for direct paddy sowing. The machine integrates a 500 W brushless DC motor powered by four 12 V, 26 Ah lead-acid batteries (total 48 V, 26 Ah), supplemented by a 550–650 W solar photovoltaic (PV) panel for off-grid recharging. Charging trials showed that the battery could be fully recharged from 44 V to 51.5 V within 2.4 hours under optimal sunlight. Without solar input, the system operates continuously for 2.5 hours, confirming the essential role of solar integration. Discharging tests revealed an average voltage drop of 2.6 V/h under load, and simultaneous charging-discharging trials demonstrated voltage stability between 50–51 V, indicating near-equilibrium energy exchange between solar input and motor demand. Field trials conducted at three forward speeds (2.0, 2.5, and 3.0 km/h) showed increasing theoretical field capacity (0.36 to 0.54 ha/h) and actual field capacity (0.31 to 0.48 ha/h), with field efficiencies ranging from 84% to 88%. The results confirm the machine's high efficiency, operational reliability, and adaptability to field conditions. The findings highlight the viability of integrated solar-battery systems for smallholder mechanization, reducing dependence on fossil fuels and grid power. The developed seeder exemplifies a climate-resilient, net-zero energy solution for rural agriculture, contributing to sustainable food production and supporting the broader framework of decentralized energy systems for climate-resilient and net-zero cities.

LEGACY EFFECTS OF SIXTY YEARS OF FARMYARD MANURE AND LIME APPLICATION ON SOIL AGGREGATION AND CARBON-NUTRIENT RETENTION

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Soil acidification is a major constraint to soil structure and fertility in northern Europe. This study examined the effects of farmyard manure (FYM), lime, and their combination on soil aggregate distribution, stability, and associated carbon (C), nitrogen (N), and phosphorus (P) fractions in an acidic loam soil of Lithuania. Four treatments were applied: naturally acidic soil (control), FYM at 60 t ha^{-1}, lime at 3.5 t ha^{-1}, and a combined application of FYM and lime. Soil samples collected from 0–10 and 10–20 cm depths were analysed for aggregate size fractions, mean weight diameter (MWD), geometric mean diameter (GMD), fractal dimension (FD), and structural stability index (SSI). The combined treatment (FYM + lime) significantly increased macroaggregate (52.9–62.4%) formation, MWD (3.08–3.72 mm), and SSI (4.81–4.94%), indicating improved aggregate stability compared with the control. In parallel, the same treatment enhanced soil organic carbon (SOC), permanganate-oxidizable carbon (POXC), and water-extractable organic carbon (WEOC) in all aggregate fractions. Total N and P concentrations were also greater in macroaggregates and the silt–clay fraction, suggesting improved nutrient retention. Overall, the integration of FYM and lime effectively restored aggregate stability and nutrient-enriched structure in acidic soils, offering a practical approach to enhance soil health and fertility under acid soil conditions.

Keywords: soil aggregate stability, soil carbon fraction, acid soil remediation, integrated management, sustainable restoration

AGRICULTURE, AGROBIOLOGY, AGROECOLOGY

NON-INVASIVE MONITORING OF PLANT WATER STATUS USING PORTABLE AIR-COUPLED ULTRASONICS FOR PRECISION AGRICULTURE

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Efficient water management is one of the most critical challenges in modern agriculture. Traditional techniques for assessing crop water status, such as pressure chambers or gravimetric methods, are invasive, time-consuming, and labor-intensive. This research introduces a portable, non-invasive air-coupled ultrasonic system designed to support precision agriculture practices by enabling rapid in-field evaluation of plant water status.

The system utilizes ultrasonic waves transmitted through air to measure leaf thickness, ultrasound velocity, attenuation, and density—key biophysical parameters strongly correlated with relative water content and water potential. Compact, field-portable design ensures usability under variable environmental conditions, while advanced signal processing enhances accuracy and repeatability of measurements.

By integrating cloud-based data analytics, the device provides actionable insights to farmers, supporting real-time irrigation decision-making, reducing water wastage, and improving crop yield predictions. This non-destructive approach contributes to sustainable resource management and aligns with the global need for environmentally responsible farming strategies.

The results highlight the potential of portable air-coupled ultrasonic technology as a powerful tool for agronomy, agroecology, and agricultural engineering, paving the way for next-generation precision agriculture practices.

IMPACT OF VERTICAL TILLAGE ON SOIL QUALITY AND ENVIRONMENT

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The choice of tillage technology has a significant impact on soil quality and environmental pollution. This study evaluated the effects of four different tillage methods (minimum tillage, vertical tillage, vertical tillage with seeding and direct seeding) on soil aeration porosity, moisture, mechanical resistance and nitrogen oxides (NO_x) emissions from a mobile source of pollution during seeding.

NO_x emissions were lowest during direct seeding. In other technologies, emissions increased during seeding, respectively: minimum tillage — 38.5%, vertical tillage — 28.2%, vertical tillage with seeding — 26.7%. This shows a clear relationship between the intensity of soil movement and NO_x emissions. Aeration porosity significantly improved with direct seeding (32.99 ± 1.95%) and vertical tillage with seeding (32.87 ± 2.98%) compared to minimal tillage (21.11 ± 3.58%). This parameter is extremely important for oxygen circulation and microbial activity in the soil. Soil moisture ranged from 15.93 ± 2.31% (minimal tillage) to 17.08 ± 2.35% (vertical tillage with seeding), which is important for plant growth, especially in drier periods. Soil hardness distribution showed that in minimally tilled soil at a depth of 10 cm, the hardness of the soil at a depth of 20–50 cm was higher than after other technologies — this may limit root development during later growth stages or at harvest. Meanwhile, direct sowing resulted in a more uniform hardness profile and reduced mechanical resistance at a depth of 30–50 cm, providing more favorable conditions for root penetration and better infiltration.

REDUCING AMMONIA EMISSIONS FROM MANURE BY MANAGING SURFACE AND BULK MOISTURE LEVELS

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Ammonia (NH_3) is released to the atmosphere primarily through convective mass transfer across the manure–air interface. Mitigating NH_3 air pollution, therefore, requires suppressing the physicochemical pathway whereby nitrogenous species in manure are converted to gaseous ammonia and transported from the surface to ambient air. Controlled laboratory experiments were conducted using a GME 700 laser-spectroscopy analyser and fresh cattle manure to test two moisture-management strategies. (i) Surface-only control: the moisture of the manure layer directly exposed to ambient air was regulated using various biocovers, targeting the interface without altering deeper layers. (ii) Bulk-to-surface control: the surface moisture in contact with air was modulated indirectly by adjusting the moisture content of the entire manure volume (e.g., by mechanical separation). In both approaches, we observed a linear relationship between manure surface moisture and NH_3 emission intensity: drier surfaces yielded lower emissions. Quantitatively, decreasing the surface moisture from 94.61% to 67.14% reduced mean air contamination in test vessels by 61.71%, indicating a commensurate decline in emission intensity. These findings demonstrate that managing the hydrological state of the manure surface—either directly with biocovers or indirectly via bulk moisture reduction—is an effective lever for NH_3 mitigation. Practical implementation of moisture management can thus complement existing manure handling practices to reduce agricultural ammonia emissions at source.

INOCULATION EFFICIENCY IN TWO VARIETIES OF SOYBEAN

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Soybean (Glycine max) in symbiosis with nitrogen-fixing bacteria can fix atmospheric nitrogen and enrich soil through its biomass. However, in regions with specific climatic conditions, achieving significant soybean production requires developing adapted cultivars.

The aim of this study was to assess two varieties of soybean (Laulema and Merlin) inoculated with different commercially available inoculants containing *Bradyrhizobium japonicum* strains and to identify the most effective pairs in terms of biological nitrogen fixation and other biological parameters.

The experiment was conducted in organic fields at the Lithuanian Research Centre for Agriculture and Forestry in Akademija (55°24′ N, 23°51′ E). The stable isotope ratio method, along with nitrogen content measurements, was used to determine nitrogen sources and utilization efficiency. Various biological parameters were measured to evaluate their correlation with applied treatments.

The study showed that most biological parameters were higher with inoculation. Nodulating bacteria appeared only in inoculated treatments, and nitrogen derived from the atmosphere (NDFA) in shoots ranged from 30% to almost 78%. Meanwhile, NDFA in beans was even higher, exceeding 88% and reaching up to 134 kg/ha. Inoculation with selected bacterial strains significantly increased protein content to 41%, with effects being both strain- and variety-specific. Biomass in Laulema was double that of the control.

Our results demonstrate that establishing effective soybean–microbe interactions by selecting suitable soybean varieties and microbial strains is crucial for optimizing agricultural practices and improving crop performance, especially in sustainable and environmentally conscious farming systems under the cool climatic conditions of Europe.

INVESTIGATING THE INFLUENCE OF FEEDSTOCK TYPE AND PYROLYSIS TEMPERATURE ON BIOCHAR SUITABILITY FOR SOIL APPLICATIONS

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Biowaste, such as food waste, garden residues, paper, and cardboard, can be converted into biochar – a sustainable and eco-friendly material which can be used as soil remediation product. Biochar is thermally and chemically stable, with a large surface area capable of trapping pollutants from contaminated soils. Producing biochar from organic waste supports long-term sustainability, as biowaste represents about 30–40% of municipal waste in many countries, much of which still ends up in landfills or the environment. Converting this waste into biochar helps reduce pollution and contributes to more sustainable waste management practices. Research shows that biochar derived from biowaste can significantly improve soil quality, especially in degraded soils affected by erosion, pollution, or nutrient loss. However, because the properties of biochar depend on both the type of biowaste and the pyrolysis temperature, it is crucial to analyze its characteristics to determine the most effective production conditions.

In this study, biochar was produced via pyrolysis from six primary feedstocks: hemp leaves, stems, seed husks, sewage sludge, sawdust, and pig manure digestate, at five different temperatures (400–800 °C). Various physicochemical properties were analyzed, such as yield, ash content, bulk density, pH and concentrations of nutrients.

The findings of this study aim to identify the optimal pyrolysis temperature and the most suitable biowaste source for producing biochar which could be used for soil applications.

THE IMPACT OF CLIMATE CHANGE ON SPRING BARLEY (*HORDEUM VULGARE* L.) PHENOLOGY IN PRIEKUĻI, LATVIA IN THE 20TH AND 21ST CENTURIES

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Long-term phenological records provide valuable insight into both climate variability and the long-term impacts of climate change on crop development. This study analyzes a unique dataset from Priekuļi, Latvia, documenting the sowing, heading, and full ripening dates of spring barley (*Hordeum vulgare* L.) from 1928 to 2024. Sowing time is primarily determined by weather conditions preceding sowing, while other growing factors and varietal characteristics play a smaller role. The optimal sowing period for spring barley is from the second decade of April to the first decade of May; however, in several years sowing has been delayed until the third decade of May due to late spring onset or excessive precipitation. The earliest recorded sowing date was April 14 (1990), and the latest was May 24 (1928), one of the wettest years in Latvian meteorological history. Over the past century, the sowing time has advanced by approximately two weeks. The duration from sowing to full maturity has remained relatively stable, although in years with extreme heat or drought, heading and ripening occur considerably earlier. Late sowing has been shown to negatively affect crop development and yield, demonstrating a clear negative correlation (–0.56) between sowing date and productivity. It should also be noted that during the study period, barley varieties and agrotechnical practices have changed substantially. These long-term observations highlight the influence of changing climatic conditions on crop phenology and underline the need for adaptive management strategies in cereal production under a warming climate.

MANAGEMENT RECOMMENDATIONS FOR MAINTAINING HIGH BIOLOGICAL VALUE GRASSLANDS BASED ON FUNGAL BIOINDICATORS

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Natural and semi-natural grasslands are vital for biodiversity and sustainable farming across Europe. These globally threatened habitats support diverse plant and fungal communities and provide key ecosystem services. The EU Habitats Directive (92/43/EEC) protects priority grasslands, linking agriculture with biodiversity goals. Fungi, especially CHEGD taxa (Clavariaceae, Hygrophoraceae, Entolomataceae, Geoglossaceae, *Dermoloma* spp.), serve as indicators of ecological stability, with waxcap-rich grasslands recognized as globally important for fungal diversity and conservation.

Fieldwork at nine grassland sites under different management regimes involved collecting fungal specimens using the transect method, recording surface cover of grasses, mosses, and lichens, and analyzing soil pH, carbon, nitrogen.

Study revealed that the highest number of CHEGD species was recorded in the rotationally sheep-grazed meadow (7 species) and in the grassland grazed by horses and cattle (6 species). *Hygrocybe acutoconica* and *Entoloma chalybeum* were found in both grazed and regularly mown meadows, where cut biomass was removed. In contrast, no CHEGD fungi were found in sites grazed by a large herd of cattle without rotational management or in unmown or mown grasslands where biomass is left after cutting.

The results showed that well-managed grasslands support the highest fungal diversity, particularly of Hygrocybe and Entoloma species typical of well-preserved sites. These findings highlight the close link between fungal diversity and sustainable land use and allow the development of recommendations:

- Implement short rotational grazing cycles for vegetation recovery.
- Reduce stocking density if rotation isn’t possible to prevent overgrazing and soil compaction.
- Mow two times a year and remove biomass to keep nutrient levels low for CHEGD fungi.
- Avoid intensive grazing and prolonged abandonment to preserve fungal diversity and ecological value.

INTEGRATING UAV MULTISPECTRAL DATA AND MACHINE LEARNING FOR MAIZE YIELD PREDICTION UNDER CONTRASTING SOIL AND FERTILIZATION SYSTEMS

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Maize (*Zea mays* L.) is one of the most important cereal crops globally, and its cultivation in Northern Europe has expanded due to the introduction of earlier-maturing hybrids and climate change. However, achieving high and sustainable yields under contrasting soil fertility conditions remains challenging. Efficient nutrient management—particularly nitrogen—is essential to maintain productivity while reducing environmental impacts. This study aimed to evaluate how different mineral, organic, and integrated fertilization systems affect maize productivity and nitrogen use efficiency under contrasting soil conditions, and to assess the potential of combining multispectral UAV data with ground-truth measurements for accurate yield prediction. Field experiments were conducted at two Lithuanian sites (Akademija and Ruoščiai) in 2023–2024, encompassing thirteen fertilization treatments combining ammonium nitrate, pelleted cattle manure, hydrogel, and silicon amendments. Measurements included total aboveground biomass (TAB), grain yield, and nitrogen uptake. UAV-based multispectral data, vegetation indices, and field measurements were integrated using machine learning models (Random Forest) to predict grain yield at different maize growth stages. Results showed that maize yields were consistently higher at Akademija (~20–30%) than at Ruoščiai, primarily due to more favorable soil conditions. The highest yields and nitrogen uptake were achieved under high-rate mineral fertilization (AN2), while pelleted manure (PCM) treatments produced up to 35% lower yields. Integrated fertilization (AN1+PCM) often matched or exceeded medium-rate mineral treatments (AN1). Model simulations demonstrated that combining spectral bands, vegetation indices, and field measurements significantly improved yield prediction accuracy (R^2 up to 0.67; NRMSE < 10%). The milk growth stage (R3) was identified as the most suitable time for yield estimation. The integrated framework demonstrates a promising approach for precision agriculture, enabling timely and spatially detailed assessment of maize performance under varying nutrient management and soil conditions.

ANALYSIS OF COMPARISON BETWEEN ZINC SOIL AND FOLIAR APPLICATION TO IMPROVE ZINC BIOFORTIFICATION OF RICE

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Zinc (Zn) is an essential micronutrient; its deficiency causes complicated health problems. Among different strategies to tackle Zn deficiency, biofortification of the rice crop is considered an easy and environmentally safe method. Thereby, this study aimed to compare the potential of two agronomic biofortification methods: soil and foliar application in rice under field conditions during the year 2021 in the kharif season. The experiment consists of a total of four treatments: T1 control, T2 Zn soil supplementation at a rate of 10 kg ha-1, T3 Zn foliar spray at the booting stage at the rate of 0.25%, and T4 Zn foliar spray at the booting + flowering stage at a rate of 0.25%. Each treatment was replicated thrice following a randomized complete block design (RCBD). At harvest, crop growth, physiology, yield, and Zn concentration in paddy grain straw, Zn uptake parameters were analyzed. The findings revealed maximum growth (5.6%), number of tillers (90.9%), panicle length (48.5%), weight of panicle (54.7%), and number of grains (32.7%), at T4 from their respective control. The highest value of Chlorophyll a (42.9%) at T3, T4, Chlorophyll b (100%) at T2, T3, T4, Total chlorophyll (62.5%) at T4, carotenoid (33.3%) at T2 in compared to the control. Yield parameters obtained, such as grain yield (56.3%), straw yield (8.2%), and biological yield (13.7%), to than their control. Maximum Zn concentration in paddy grain and uptake were 400 and 300-fold at T4, T3, respectively. While Zn concentration in rice straw is 300-fold at T4, and uptake in paddy straw is also 300-fold at T4, in comparison to their control. In conclusion above results Zn dose at flowering time at the rate of 0.25% suitable for the desirable increment in paddy grain straw and their uptake as well; however gap in the study suggests further investigation at the cellular level of the plant is needed.

Keywords: Micronutrient, Growth, physiology, Chlorophyll, Zinc concentration

QUINOA (*CHENOPODIUM QUINOA* WILLD.): A PROMISING SOURCE OF BIOACTIVE COMPOUNDS FOR FUNCTIONAL FOOD DEVELOPMENT

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Introduction: Quinoa, known as the "mother of all grains," is an ancient Andean crop that has recently gained worldwide attention due to its exceptional nutritional and functional qualities. In addition to being a rich source of proteins, essential amino acids, and minerals, quinoa contains various bioactive compounds such as phenolic acids, flavonoids, saponins, and phytosterols. These substances contribute to its antioxidant, anti-inflammatory, and metabolic health-promoting effects.

Methodology: A literature-based synthesis was conducted using scientific databases to identify and summarize recent studies on quinoa bioactive components. Data were analyzed according to the type of compounds, extraction methods, and their reported biological activities. Particular attention was given to studies linking quinoa genotype, environmental conditions, and processing effects on bioactive compound content.

Results: Findings show that quinoa seeds and by-products possess high levels of phenolic compounds and flavonoids, which exhibit strong antioxidant activity. Saponins and phytosterols also play significant roles in reducing cholesterol and supporting immune defense. The concentration of these compounds varies with cultivar, altitude, and processing techniques such as germination or fermentation.

Discussion and Conclusion: Quinoa's bioactive compounds make it an excellent candidate for developing functional foods and nutraceuticals. In the context of Algeria, promoting quinoa cultivation and valorizing its bioactive molecules could enhance national strategies for healthy and sustainable food innovation. Further local studies are recommended to evaluate the composition of Algerian quinoa varieties under different growing conditions.

Keywords: quinoa, bioactive compounds, phenolics, antioxidants, saponins, functional food

AGROECOLOGICAL APPROACH TO ENVIRONMENTALLY FRIENDLY INNOVATIONS IN SUSTAINABLE FARMING SYSTEMS OF LATVIA

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Achieving climate neutrality in agriculture requires a shift toward agroecological practices that balance productivity with environmental responsibility. This study presents research from Latvia evaluating eco-innovative bioproducts as part of sustainable crop management strategies. Field trials were conducted in Viļāni (Latgale region) on winter wheat (*Triticum aestivum L.*) and winter rapeseed (*Brassica napus L.*), where biologically active, environmentally friendly plant growth regulators (PGRs) were tested as alternatives to synthetic ones. The results demonstrated that bio-based treatments improved crop resilience and achieved comparable or higher yields under variable climatic conditions. These outcomes suggest that partial replacement of chemical inputs with biologically active substances can effectively contribute to sustainable and competitive farming systems. From an agroecological perspective, the findings highlight how eco-friendly innovations can support the transition toward climate-smart and resource-efficient agriculture in Latvia and the Baltic region. This research provides practical evidence for integrating bio-based and microbiological products into crop management, strengthening both environmental and economic sustainability. The results also align with the objectives of the European Green Deal, offering insights for policies that promote reduced chemical dependency and greater resilience in regional agriculture.

Keywords: agroecology, sustainable agriculture, bio-based products, environmentally friendly innovations, plant growth regulators, climate neutrality

AGRICULTURE, AGROECOLOGY AND AGRICULTURAL ENGINEERING

DIAGNOSTIC OF PLANT PATHOGENS IN THE EARLY STAGE BY USING DEEP LEARNING ALGORITHMS FOR DIFFERENT IMAGE TYPES

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Apple scab, caused by *Venturia inaequalis*, poses a significant threat to apple production. This study presents a resource-efficient diagnostic method using deep learning. We developed a MobileNetV2-based CNN, optimized with a custom dataset and a multi-stage retraining approach. Notably, our model is highly efficient, with a compact size of 1.9 MB and a processing time of 64 ms. It outperformed a rapid-prototyping model in accuracy and speed, validating our domain-specific training. The resulting model is suitable for mobile applications, providing a robust tool to assist specialists in monitoring and managing apple scab in the field.

Keywords: precision farming, object detection, *Venturia inaequalis*, artificial intelligence, Malus

MAPPING MULTIRESISTANCE: ANTIBIOTIC-RESISTANT BACTERIA IN LITHUANIAN AGRICULTURAL ECOSYSTEMS

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Antibiotic-resistant bacteria (ARB) represent an increasing concern within agricultural ecosystems, where farming practices can significantly influence both microbial diversity and the development of antibiotic resistance. The present study examined the occurrence and distribution of ARB under ecological farming conditions in pastoral farmlands of Lithuania, with particular emphasis on soil, feed, and freshwater environments.

Forty-eight bacterial strains resistant to ampicillin, streptomycin, tetracycline, and chloramphenicol were isolated from three pastoral dairy farmlands' soil, feed, and freshwater. ARB are identified by restriction fragment and 16S rRNA sequencing. Statistical assessments included relative frequency distribution, Chi-square test, correspondence analysis, and correlation analysis. Minimum inhibitory concentration (MIC) test was conducted to determine resistance levels for each antibiotic across all strains.

The isolates represented 12 bacterial genera, with *Bacillus* and *Enterobacter* being the most prevalent. The highest abundance of ARB was observed in soil, and lowest in freshwater. A significant association between ARB genera and environmental sources was observed (Chi-square = 42.759). Correspondence analysis showed that *Solibacillus* sp. and *Providencia* sp. were most associated with soil, *Escherichia* sp. with feed, *Klebsiella* sp. and *Enterococcus* sp. with freshwater. Correlation analysis showed the strongest antibiotic resistance pattern relationship between *Enterobacter* sp. and *Lysinbacillus* sp.; *Klebsiella* sp. and *Aeromonas* sp. ($r \geq 0.85$), suggesting potential co-occurrence and co-resistance mechanisms. The MIC tests of each strain revealed that the highest resistance rate was detected against ampicillin and streptomycin, followed by chloramphenicol, then tetracycline. Our results suggested that about 75% of bacteria exhibit resistance to more than one antibiotic.

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OPTIMIZATION OF HORTICULTURE RESIDUES BIOCONVERSION USING BY-PRODUCTS OF ANIMAL ORIGIN AND BIOEFFECTORS

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The agricultural horticulture sector is becoming an important source of biodegradable waste. Large amounts of waste are generated due to mechanical damage, pest infestations, plant diseases and primary processing operations. The bioconversion of plant-based waste into higher-value soil improvement products is recognized as an economically viable and environmentally friendly waste management strategy.

The use of animal by-products such as meat and bone meal (MBM) and biological origin stimulants (BIO) can contribute to the optimization of process parameters, ensuring lower variability of the observed indicators.

The aim of this study was to determine the effect of different MBM and BIO additive rates on the composting process parameters of cabbage waste (CW) and wheat straw (WS) mixtures during the mesophilic phase, by evaluating temperature and pH dynamics as well as carbon dioxide (CO_2) emissions.

During the short-term experimental study, five mixture variants were prepared and analyzed, each with three replicates: a control mixture (CWWS) and control mixtures treated with 5 and 15% MBM and 5 and 15% MBM+BIO additives.

The results of the study showed that the variants with different additives and their rates maintained slightly alkaline pH (the median values (Me) are given below: 5% MBM – 8.05 ± 0.12; 5% MBM+BIO – 8.10 ± 0.08) or alkaline pH values (15% MBM – 8.96 ± 0.08; 15% MBM+BIO – 8.87 ± 0.06) throughout the experiment, compared to the control (Me 7.48 ± 0.17). At the end of the experiment, when evaluating the stabilizing effect of additives on pH changes, it was found that a 15% MBM+BIO (8.86 ± 0.03) additive rate ensured the lowest pH fluctuation in the medium compared to the control (6.71 ± 0.17).

The observed temperature dynamics showed a positive effect of 5 and 15% MBM+BIO additives on faster temperature rise – the highest temperature values were recorded on the third day of the study. In the control variant and mixtures with MBM – after seven days. However, throughout the study, both variants with a 15% additive rate were distinguished by higher and longer-lasting temperature values. At the beginning of the study, increased CO_2 emissions were recorded in variants with 5 and 15% MBM additive rates. During and at the end of the experiment, the lowest CO_2 values were found in the 15% MBM+BIO (0.37%) and 5% MBM+BIO (0.21%) variants, compared to the control (0.1%).

A positive effect of the 15% additive was observed both with and without BIO, ensuring pH stability, faster temperature rise, and lower CO_2 emissions.

HOUSEHOLD FOOD WASTE RECYCLING TO PRODUCE ECO-FRIENDLY FERTILIZERS ENHANCING SOIL QUALITY AND IMPROVING MASS YIELD

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Household food waste recycling represents a constructive and effective approach to sustainable food waste management. Currently, the majority of household food waste is collected as general waste, which is often incinerated or sent to landfills, posing a significant challenge globally. However, there is a valuable opportunity to transform this food waste into organic fertilizers through innovative methods such as anaerobic digestion (AD) and pyrolysis, effectively linking ecological sustainability with enhanced agricultural productivity. By diverting food waste from landfills, where it generates methane (CH4), a potent greenhouse gas, we can create nutrient-rich organic fertilizers. These fertilizers greatly improve soil quality by replenishing organic matter, enhancing water retention, and restoring essential microbial biodiversity, all of which are vital for resilient agroecosystems. This study is dedicated to recycling household food waste to mitigate its negative impacts. The main aim of this research is to collect household waste to produce solid and liquid organic fertilizers, investigate their effects on soil quality indicators such as pH, ECe, organic matter, organic carbon, total nitrogen, and available NPK, and evaluate mass yield under greenhouse conditions. By turning waste into a valuable resource for soil regeneration, we can foster sustainable food systems that prioritize environmental protection and amplify agricultural productivity.

Keywords: food wastes, soil quality, organic, green, yield, fertilizer

RESEARCH ON THE POTENTIAL OF FOUR FUNGI OF THE FAMILY HYMENOCHAETACEAE FOR SAFE AND TECHNOLOGICALLY RELIABLE USE IN THE PRODUCTION OF BIOCOMPOSITE MATERIALS

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The Hymenochaetaceae family includes around 893 fungal species important in wood decay and forest ecosystems. Genera such as *Phellinus* and *Fomitiporia* possess ligninolytic enzymes enabling the conversion of lignocellulosic substrates into renewable mycelium-based biocomposites. These materials are biodegradable, lightweight, and energy-efficient but remain poorly studied in terms of safety and volatile organic compound (VOC) emissions. This research investigated *Fomitiporia* robusta, *Phellinus igniarius*, *Phellinus tremulae* and *Phellinus pomaceus* to evaluate their growth, biocomposite-forming ability, and VOC profiles.

Fruiting bodies were collected from Lithuanian forests and isolated on malt extract agar (MEA). Identification was confirmed by ITS rDNA sequencing. Mycelial growth rates were tested on agar, rye grain, and hemp shive substrates. Biocomposites were produced from hemp shives colonized by selected fungi, dried at 50 °C, and analyzed for density, moisture content, and mechanical strength. VOCs were assessed using headspace sampling and chromatographic analysis.

Phellinus igniarius grew fastest (2.8 mm/day), followed by *Phellinus pomaceus* (2.2 mm/day), *Fomitiporia robusta* (2.1 mm/day) and *Phellinus tremulae* (1.8 mm/day). *Fomitiporia robusta* produced dense, well-structured biocomposites with densities of 91–108 kg/m³ and moderate compressive and bending strength. VOC analysis revealed a wide diversity of volatile compounds among all species, including the hazardous compound 2-ethylhexanol.

Among the four tested species, *Fomitiporia robusta* showed the most favorable characteristics for biocomposite production—stable substrate colonization, uniform structure, and adequate mechanical performance. However, the detection of 2-ethylhexanol highlights the need for further research on health and environmental safety before industrial application.

MICROWAVE-ASSISTED SYNTHESIS OF ANTIMICROBIAL SILVER NANOPARTICLES USING PROPOLIS EXTRACTS

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Silver nanoparticles (AgNPs) biosynthesis using propolis extracts as capping and reducing agents presents multiple opportunities for solving many biological challenges. This study demonstrates sustainable, low toxicity and high production cost phytochemical synthesis of AgNPs using propolis extracts and microwaves. Biosynthesized with propolis AgNPs are analyzed by various methods– phytochemical, physicochemical, and morphological, such as TEM. The determined antimicrobial and antioxidant activity of propolis extracts is compared with the activity of green synthesized AgNPs with propolis. The green synthesized AgNPs are spherical shaped with an average size ranging from 6 to 40 nm. The biosynthesized AgNPs demonstrate potential antibacterial activity on tested microorganism strains by two folds higher than pure propolis extracts.

Keywords: green synthesis, silver nanoparticles, propolis, antimicrobial activity, phytochemical analysis, antioxidant activity

HMDS-SILYLATION IMPROVES COMPATIBILITY OF PIGMENT-RICH AGRO-WASTE FILLERS IN PDMS COMPOSITES

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Lithuanian Research Centre for Agriculture and Forestry Agro-industrial by-products abundant in natural pigments are potential bio-fillers; however, their hydrophilic nature restricts compatibility with hydrophobic polydimethylsiloxane (PDMS). This study explores the vapor-phase silylation of pigment-rich powders, including seabuckthorn, shadbush, beetroot, and raspberry, using hexamethyldisilazane (HMDS), followed by their integration into PDMS at concentrations of 5 and 20 wt%. surface modification confirmed by FTIR analysis, evidenced by the decrease in O–H/C = O bands and the enhancement of Si–C/Si–CH_3 signals, which aligns with a reduction in surface polarity. SEM/EDS demonstrates enhanced filler dispersion and a reduction in interfacial voids following HMDS treatment, particularly noticeable at 5 wt% loading. The colorimetric analysis indicates an increase in lightness (L*) and yellowness (b*) in HMDS-treated seabuckthorn and raspberry systems compared to the untreated powders. Sessile-drop tests reveal elevated water contact angles for HMDS-treated composites, with peak values noted for 20 wt% formulations (reaching approximately 94.6°), indicating reduced surface energy. At a loading of 5 wt%, HMDS-treated fillers, specifically seabuckthorn and raspberry, demonstrate an improvement in elasticity and puncture force relative to their untreated analogue. However, increased loadings may lead to agglomeration. In summary, a simple, catalyst-free HMDS vapour treatment proficiently modifies the filler–matrix interphase, resulting in enhanced brightness and hydrophobicity in PDMS composites derived from low-value agro-wastes, thereby promoting sustainable pathways for silicone-based functional materials.

UNVEILING TRAIT ASSOCIATIONS FOR YIELD IMPROVEMENT IN RICE (*ORYZA SATIVA* L.) GENOTYPES

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Correlation analysis serves as an effective approach to elucidate the interrelationships among yield and its component traits in rice (*Oryza sativa* L.), thereby aiding in the formulation of efficient selection strategies in breeding programmes. The present investigation aimed to estimate the correlation coefficients among ten quantitative traits in rice genotypes. Grain yield per plant exhibited a strong positive association with the number of productive tillers ($r = 0.46$), spikelet fertility ($r = 0.40$), and total tillers ($r = 0.27$), underscoring their importance in enhancing yield. Conversely, days to 50% flowering showed a significant negative correlation with yield ($r = –0.39$), suggesting that early flowering genotypes are advantageous for higher productivity. Panicle weight demonstrated a positive association with the number of filled grains ($r = 0.36$), while test weight revealed weak and non-significant correlations with most traits. These results highlight the potential of selecting for productive tillers, total tillers, and spikelet fertility to achieve genetic improvement for yield in rice.

Keywords: rice, correlation, productive tillers, spikelet fertility and yield

PREDICTIVE MODELING OF GRAFT COMPATIBILITY IN CHERRY USING GENOMIC MARKERS AND MACHINE LEARNING APPROACHES

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Graft compatibility between rootstock and scion is a key determinant of success in cherry production, influencing plant vigor, yield, and orchard longevity. Traditional assessment of compatibility relies on prolonged field evaluations, which are time-consuming and often influenced by environmental variability. Advancements in molecular biology and computation modelling will help in predicting, screening of graft compatibility at an earlier stage. This study aims to develop an integrative framework based on machine-learning algorithms and molecular marker data to predict compatibility outcome at the graft interface between cherry scions and rootstocks. Physiological and biochemical markers, including phenolic accumulation, antioxidant enzyme activities, and isozyme patterns—serve as early indicators of incompatibility. A diverse panel of compatible and incompatible scion–rootstock combinations will be genotyped using high-throughput SNP markers, and key genomic regions associated with graft success identified through genome-wide association analysis (GWAS). Machine learning algorithms, including Random Forest, Support Vector Machine, and Gradient Boosting, will be trained to predict compatibility based on marker profiles and validated using cross-validation techniques. The integration of genomic data with machine learning provides a rapid and reliable framework for screening compatible combinations, reducing breeding time, and supporting precision rootstock selection in cherry improvement programs.

Keywords: graft compatibility, cherry (*Prunus* spp.), molecular markers, machine learning, predictive modelling

ADVANCING DNA-FREE PLANT GENOME EDITING THROUGH NANOCARRIER-MEDIATED DELIVERY SYSTEMS

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In 2050, almost 10 billion people will need food production technologies to increase crop yields and withstand unpredictable climate events. Nanotechnology is a new platform for plant biotechnology that offers control at the range of 1–100 nm. Nanoparticles (NPs) have distinct optical, electrochemical, and mechanical properties; thus, they are used for targeted delivery, sensing in real time, and digital monitoring of plants, soil, and water systems. Methods like Agrobacterium-mediated transformation or biolistics used for gene delivery are fairly ineffective for many species and may damage host cells or insert the transgene randomly. On the other hand, the delivery mediated by nanocarrier is a DNA-free, transgene-free alternative that enhances the efficiency of CRISPR/Cas-based genome editing. Recent investigations reveal that nanomaterials (NMs), including mesoporous silica nanoparticles, carbon nanotubes, and layered double hydroxides, can effectively assist in the transport of biomolecules through non-porous plant cell walls with minimal toxicity and high transformation efficiency (>60%). Nanocarriers can deliver proteins, RNA, or the RNP to the nucleus to realize precise genome modification without stable DNA integration. Furthermore, optimizing the uptake and localization of nanomaterials by plants requires understanding plant–nanomaterial interactions regulated by size, charge, and surface chemistry. Nanotechnology-assisted genome editing has made enormous progress recently. Meanwhile, DNA-free approaches are being sought to overcome biosafety, regulatory, and public acceptance issues with genetically modified organisms (GMOs). If we incorporate responsible research and innovation (RRI) in nanobiotech R&D, it will allow us to deploy this technology sustainably and responsibly. Using nanocarriers to edit genes may result in next-generation crops that do not carry transgenes but tolerate stress, are productive, and are advantageous for the environment.

PHYSIOLOGICAL AND YIELD RESPONSES OF STOCK (*MATTHIOLA INCANA*) TO DIFFERENT BIOSTIMULANT TREATMENTS

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Stock (*Matthiola incana*) is a flowering plant belonging to the family of Brassicaceae. In Pakistan, stock flowers are mostly used in garden borders and container planting. A variety of flower shapes which can be used as fresh and dried cut flowers. The present research was conducted to investigate the effect of different biostimulants (T1 = Quantis @4ppm, T2= Quantis @2ppm, T3 = Pilatus @4ppm, T4 = Pilatus @2ppm, T5 (control) = water) on the productivity of stock (*Matthiola incana*). The experiment was conducted using a randomized complete block design (RCBD) with three replications of four treatments each, along with a control. The data was collected on various morphological, reproductive, and photosynthetic parameters. Results indicated a significant difference among all treatments compared with control. Pilatus @2ppm showed maximum plant height, raceme length, leaf area, number of florets, stem diameter, root length, total chlorophyll content, stomatal conductance, fresh weight of raceme, dry weight of raceme, fresh weight of plant, dry weight of plant, bloom period (days). Pilatus @4ppm showed a maximum stem length, and number of leaves. Quantis @4ppm showed a maximum flower diameter. Quantis @2ppm showed a maximum number of days to first flowering. Pilatus @2ppm perform better in reproductive and vegetative production and produces high-quality flowers. This research study provided valuable insight into enhancing the output and productivity of stock (*Matthiola incana*), promoting eco-friendly practices for a sustainable floral industry.

Keywords: stock (*Matthiola incana*), biostimulants, reproductive, morphological, yield

HORTICULTURE

MICROBIOLOGICAL FERMENTATION FOR FLAVOUR COMPOUND GENERATION FROM FRUIT SEEDS

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Oil extraction and protein extraction are the most popular proposed valorization strategies for fruit seeds, a by-product of fruit processing. The study explored the feasibility of producing a soy sauce analogue using Japanese quince (Chaenomeles japonica) seeds (JQS) as a partial or complete replacement for soy beans under project (No.10.9.1-11/25/1191-e).

Mixtures of soybeans+wheat (SW), soybeans+JQS+wheat (SJW), and JQS+wheat (JW) were inoculated with Aspergillus sojae, solid-state fermented for 48 hours at 30°C, and afterwards liquid-state fermented in a 15% brine for 6 months at ambient temperature, monitoring soluble solids and pH. The finished product was pasteurized at 90°C for 15 minutes. Free amino acids, sugars and organic acids were analysed using HPLC-MS and HPLC-RID. Commercial soy sauces were used for comparison to compare fermentation versus substrate efficiency.

The pH and soluble solids were lower in the brine with JQS. The pH of the produced sauces was similar to commercial products—4.4 – 4.6 (JW and SJW – SW), compared to 4.5 – 4.8, but soluble solids were much lower—22.6 – 24.3 (JW – SW), compared to 32.3 – 35.5%Brix. SW had the highest and JW had the lowest free amino acid content (total, sweet, bitter, and umami amino acids), the main constituents being glutamic and aspartic acid, and leucine, and most of the free amino acids providing bitter flavours. Free amino acid contents were much lower than in commercial products. The main sugars in the sauces were glucose and galactose, and the main acids were acetic acid and lactic acid. While other constituents were similar, sucrose and lactic acid content was much higher in commercial products.

Initial results suggest that JQS are a suitable substrate for microbiological fermentation and umami production, but process optimization may be advisable.

POSTHARVEST QUALITY OF HIGHBUSH BLUEBERRIES USING SUSTAINABLE PACKAGING

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Rising global blueberry production demands sustainable postharvest solutions to reduce plastic waste and food losses. Previous studies have shown that packaging type can influence postharvest quality attributes of fresh fruit. However, evidence on sustainable packaging for blueberries under real storage conditions remains limited.

To address this gap, we investigated how biodegradable and conventional packaging materials affect the postharvest quality of highbush blueberry cultivar 'Draper' fruits during one-week cold storage. Four packaging types were compared: polypropylene (PP, control), cardboard (CB), cardboard with cellulose lid (CBC) and rice-straw punnet with polylactic acid lid (RPLA). Fruit quality attributes—including weight loss, firmness, colour (Chroma), total soluble solid content, total organic acid content, and total phenol content—were analysed.

During one week of storage, weight loss of blueberry cultivar 'Draper' fruits differed significantly between packaging types. The smallest weight loss occurred in polypropylene (PP, 4.3%), whereas it was significantly higher in cardboard (CB, 10.6%). Firmness declined in all packaging types compared to the initial value (1.75 N), reaching 1.20–1.40 N after storage, with no significant differences between packages. Chroma increased during storage regardless of packaging type. Total soluble solids content increased from the initial 10.3 °Brix to 11.0 °Brix in PP and CBC, 12.2 °Brix in CB, and peaked at 12.9 °Brix in RPLA. Total phenol and total organic acid content also varied depending on packaging, suggesting that biodegradable materials (CB, CBC, RPLA) may differently influence the metabolic composition of berries compared to the PP control.

CBC and RPLA showed overall quality attributes comparable to plastic, with significant differences limited to total soluble solids, total organic acid and total polyphenol content.

APPLE PATHOGENIC FUNGI CONTROL USING ALTERNATIVE MEANS

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Pathogenic species of pathogenic fungi can infect various parts of plants, including leaves, flowers, stems, trunks, fruits and roots, often causing significant pre-harvest and post-harvest losses. Their presence in the soil can suppress plant growth, reduce yield and may also contribute to a higher incidence of replant disease. Although chemical pesticides are commonly used for plant protection, the European Union is limiting their use because of adverse effects on human health and the environment, even though effective alternatives to chemicals are still lacking. This highlights the need to explore alternative biocontrol strategies. One promising approach involves the use of plant extracts (PE), which are rich in valuable secondary metabolites that can be safely and effectively used to manage fungal diseases. This study aimed to evaluate the inhibitory effect of clove (*Syzygium aromaticum* L.) and rosemary (*Rosmarinus officinalis* L.) plant extracts against *Fusarium* spp. and *Colletotrichum* spp. plant pathogens as alternative plant protection means. The experiment was carried out at the LAMMC Institute of Horticulture (IH). The pathogen isolates used in this study were obtained from the LAMMC IH Laboratory of Plant Protection collection. The inhibition of pathogens was evaluated using different extracts at concentrations of 2400 µl/l, 2800 µl/l, and 3000 µl/l, obtained by subcritical CO_2 extraction. Inhibition results indicated that clove PE completely inhibited both pathogens at all tested concentrations. Rosemary PE showed inhibitory effects against both pathogens. In the case of *Fusarium* spp., at a concentration of 3000 µl/l inhibition reached 70% seven days after inoculation. Meanwhile, under the same conditions, the inhibition of *Colletotrichum* spp. reached only 56%. It was also observed that all tested concentrations of rosemary PE showed no significant differences in their effects on the two pathogens. The impact of the measures investigated for managing pathogens requires more detailed examination.

ASPECTS OF CORRELATION ANALYSIS AMONG 44 ACCESSIONS OF OREGANO IN THE *EX SITU* COLLECTION

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During long-term investigations (2012–2020), plant material of 44 oregano (*Origanum vulgare* L.) accessions from the *ex situ* collection of aromatic and medicinal plants (N 56º39´45.3´´; E 23º45´15.2´´), located at the Latvia University of Life Sciences and Technologies, was analysed. Using Draft Descriptor List, plants were described by more than 60 traits, including morphological indicies, fresh and air-dry biomass, winter hardiness, severity of fungal diseases, insects and physiological lesions, content and composition of essential oils, ascorbic acid content etc. Initially samples were collected from local natural habitats in different places of Latvia — around Aizkraukle, Cēsis, Jelgava, Madona, Pļaviņas, Talsi, Tukums, Valmiera and Rīga.

Correlation analysis showed that a moderate correlation (correlation coefficient (r) is in the range from 0.4 to 0.7) exists between traits. For plant height, between it and branching density r = 0.524, density of foliage r = 0.465, density of flowers r = 0.401, fresh biomass r = 0.499 as well as air-dry biomass r = 0.420. For branching density, between it and density of foliage r = 0.419, fresh biomass r = 0.480 and air-dry biomass r = 0.503. Between density of flowers and density of foliage r = 0.439.

Correlation coefficients showed that the taller plant is, the more intensive branching density, density of foliage, density of flowers as well as the highest fresh biomass observed for oregano accessions. More intensive branching density means higher density of foliage as well as bigger fresh and air-dry biomass. In addition, the effect of branching density on air-dry mass is slightly greater than on fresh biomass. The correlation between density of flowers and density of foliage means that increasing of one indicator positively affects the result of the second indicator.

Grouping accessions according to traits with a moderate correlation as well as performing cluster analysis, the obtained dendrogram showed that clustering was influenced by the origin of the accessions. This means that the place of plants' collection has a significant impact on observed traits.

ANTAGONISTIC EFFICIENCY OF *BACILLUS SUBTILIS* AGAINST *ALTERNARIA* SPP. UNDER *IN VITRO* CONDITIONS

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Potato early blight is caused by species of the genus Alternaria and occurs annually. Biologically based plant protection products, containing various beneficial fungi and/or bacteria, may offer a promising alternative to chemical products. This study investigated the antagonistic interaction between a *Bacillus* subtilis-based microbiological preparation and two Alternaria isolates (obtained from the collection of the Institute of Soil and Plant Sciences) under *in vitro* conditions. The B. subtilis strain used in this research is a newly isolated strain originating from Latvian soils and provided by the Latvian State Institute of Wood Chemistry. Antagonistic activity was assessed under different setups: when both organisms were placed on the plate simultaneously; when *Bacillus* was introduced first and the Alternaria isolates added later; when plates were rinsed with the *Bacillus* preparation before placing the Alternaria mycelial discs. Each treatment was conducted in five replicates, with appropriate positive and negative controls.

Results revealed that the antagonistic effect was strongly depended on the application method. The most pronounced inhibition of *Alternaria* spp. growth was observed when the PDA surface was rinsed with the B. subtilis preparation before fungal inoculation. In this treatment, fungal mycelial expansion was almost completely suppressed, and the colonies remained compact with limited radial growth.

These findings confirm that B. subtilis can effectively suppress *Alternaria* spp. growth under controlled conditions, particularly when the bacterium is allowed to colonize the substrate prior to fungal establishment. The study highlights the importance of application timing and technique in maximizing the biocontrol efficiency of B. subtilis preparations, supporting their potential as sustainable and environmentally friendly agents for managing *Alternaria* spp. induced plant diseases.

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CONTROLLED ENVIRONMENT CULTIVATION FOR VALUABLE MEDICINAL AND AROMATIC LAMIACEAE SPECIES

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Medicinal and aromatic plants are valuable for their crucial roles in everyday life. Conventional cultivation is insufficient to meet the needs of customers. Growing them in a controlled environment system is an efficient approach to fulfill customer demand and produce high-quality plants. This study aimed to evaluate the growing potential of some well-known medicinal and aromatic species in controlled conditions to improve the phytochemical contents. Familiar species of Lamiaceae family, including *Salvia nemorosa*, *Salvia officinallis*, *Dracocephalum kotschyi*, *Dracocephalum maldavica*, *Provskia arbotonoides*, *Provskia atriplicfolia*, *Thymus daenensis*, *Thymus vulgaris*, *Thymus serpyllum*, *Zataria multiflora*, *Ziziphora tenuior*, and *Satureja hortensis* were selected. Seedlings grown in rockwool were transferred to a deep water culture system in a chamber at 23/19°C day/night (16/8 h photoperiod). Light-emitting diode (LED) spectra consisting of 15% blue (455 nm), 15% white, and 70% red (660 nm) light (250 µmol m^{-2} s^{-1}) were used as a light source. The results showed that all plants developed and grew normally under controlled conditions, and the growth of some of them was more compatible and in harmony with controlled conditions. However, antioxidant activity and chlorophyll content between species were different; so that some species like *Thymus serpyllum*, *Dracocephalum maldavica*, *Thymus vulgaris*, *Provskia arbotonoides*, and *Thymus daenensis* had higher antioxidant activity. Generally, the controlled environment system is appropriate for growing selected medicinal and aromatic plants, and plant species make a significant impact on optimizing biomass and bioactive compounds in controlled conditions.

Keywords: antioxidant activity, hydroponic system, morphological traits

MINERAL COMPOSITION IN LEAVES AND INFLORESCENCES OF *ALLIUM* SPECIES

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The genus *Allium* comprises a wide range of species valued for their nutritional and functional properties. While biochemical characteristics such as vitamins, sugars, and phenolic compounds have been widely studied, less attention has been paid to the mineral composition of different plant parts. The present study aimed to compare the concentrations of essential macroelements—carbon (C), nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), sodium (Na), and magnesium (Mg) — in the leaves and inflorescences of five perennial *Allium* species: *A. schoenoprasum* L., *A. angulosum* L., *A. nutans* L., *A. fistulosum* L., and *A. ursinum* L. Nutrient contents were determined using the Tyurin (C) and Kjeldahl (N) methods, spectrophotometry for P after H_2SO_4 mineralization, and flame atomic absorption spectroscopy (AAS) for K, Ca, Na, and Mg following wet digestion with HNO_3 + H_2O_2. The results showed a different distribution of mineral substances in leaves and inflorescences. Leaves contained higher levels of potassium (3.6–4.3% DW) and calcium (up to 1.7% DW), indicating their nutritional importance as sources of mineral elements. Inflorescences accumulated more nitrogen (2.3–3.4% DW), reflecting their active metabolic status during flowering. Among species, *A. fistulosum* L. showed particularly high K concentrations in leaves, while *A. angulosum* L. exhibited elevated N in inflorescences.

These findings emphasize the nutritional, physiological, and functional potential of perennial *Allium* species, providing valuable insights for breeding, selection, and sustainable cultivation.

Keywords: *allium* species, inflorescences, leaves, mineral elements, nutrition

EFFECT OF LIGHT INTENSITY ON GROWTH PERFORMANCE OF TOMATO ROOTSTOCKS IN CONTROLLED ENVIRONMENTS

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Light intensity plays a vital role in regulating growth and biomass partitioning of tomato rootstocks during early development. This study aimed to evaluate the effect of different light intensities on the growth characteristics and root system development of two tomato rootstocks, Goldrake and TOR23901 under controlled environmental conditions. The plants were grown under three light intensities: 150, 250, and 350 µmol $m^{-2}s^{-1}$ Biometric parameters including plant height, stem diameter, leaf area, root length and total biomass were measured and analyzed statistically. Results revealed that light intensity had a significant effect ($p < 0.05$) on all evaluated traits. Goldrake exhibited the most vigorous shoot growth at 250 µmol $m^{-2}s^{-1}$ with leaf area increasing nearly threefold (from 20 to 65 cm^2) and shoot biomass rising from 0.57 to 1.99 g compared with the low-light treatment (150 µmol $m^{-2}s^{-1}$). Conversely, TOR23901 responded more positively at 350 µmol m-2s-1 with root length increasing from 13.9 to 20.7 cm and root dry mass rising from 0.008 to 0.030 g. The findings demonstrate that moderate irradiance enhances balanced shoot growth in Goldrake, while elevated light intensity promotes vigorous root development in TOR23901. These results contribute to optimizing light management strategies for diverse tomato rootstocks, improving seedling quality and resource-efficient tomato production under controlled environments.

Keywords: tomato rootstock, light intensity, seedling growth, controlled environment horticulture

INFLUENCE OF CALCIUM CONCENTRATIONS IN HYDROPONIC SOLUTION ON FUNGAL PATHOGENS IN ROCKET

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Fungal pathogens such as *Alternaria* spp. and *Botrytis* spp. are among the main causes of yield loss and post-harvest deterioration in leafy vegetables. Calcium (Ca) plays a critical role in maintaining cell wall integrity and regulating plant resistance to pathogens; however, its quantitative effect in plants cultivated in nutrient solution remains insufficiently characterized.

This study investigated the effect of three calcium concentrations (40, 80, and 120 ppm) in nutrient solutions on the development of *Alternaria alternata* and *Botrytis cinerea* in rocket (*Eruca sativa*). Leaves were inoculated with 6 mm fungal discs and incubated at 22 °C. Disease incidence per leaf area was evaluated at 2, 4-, and 7-days post-inoculation (DPI).

The obtained results showed that the response to calcium levels was pathogen-specific. *A. alternata* infection intensity did not differ significantly between treatments at any stage of evaluation, although slightly lower infection was observed at 80 ppm Ca. In contrast, *B. cinerea* exhibited a clear inhibitory response at 7 DPI, with disease severity decreasing from 84.7% at 40 ppm to 60.9% at 120 ppm Ca. This indicates that higher calcium concentrations effectively limited lesion expansion during the later infection stage.

Microbiological evaluation revealed that *Trichoderma* and *Fusarium* dominated in nutrient solutions, while *Penicillium*, *Pythium*, and *Cladosporium* were the most prevalent on leaf surfaces, particularly under moderate Ca levels (80 ppm). These results suggest that moderate Ca enrichment can influence both pathogen development and microbial balance in the phyllosphere.

Keywords: *Alternaria spp.*, *Botrytis spp.*, *Eruca sativa*, microbial diversity

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SALINITY TOLERANCE AND GROWTH PERFORMANCE OF SEVEN *AMARANTHACEAE HALOPHYTES* UNDER CONTROLLED ENVIRONMENTAL CONDITIONS

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Amaranthaceae halophytes comprise diverse salt-tolerant species that hold unique agronomic and nutritional significance due to their high content of proteins, minerals, and phytochemicals with antioxidant potential. Their exceptional ability to maintain proper growth and productivity under varying saline conditions makes them a significant candidate for hydroponic cultivation. The current study examined the growth responses of seven Amaranthaceae halophytes, including *Amaranthus lividus*, *A. passion*, *A. red Aztec*, *Chenopodium giganteum*, *Ch. quinoa*, *Salsola komarovii*, and *Artiplex hortensis* under various hydroponic solution salinity (0, 150, and 300 mM NaCl) to determine species with superior biomass production and adaptability. The environmental conditions, including a Blue: Red: Far-Red LED spectrum at 22:65:13 with an intensity of 250 µmol m^{-2} s^{-1} and a temperature of 18/22 ± 2 °C, were maintained in a walk-in growth chamber throughout the experiment. A strong negative correlation between hydroponic solution salinity and survival rate, height, fresh and dry weight, root length, leaf area, relative growth rate, leaf area ratio, and specific leaf area in all tested Amaranthaceae species was detected, except for a strong positive correlation between salinity, dry weight per leaf area, and leaf weight ratio in all tested species. A strong positive correlation was found between the salinity of the hydroponic solution and the survival rate in *Salsola komarovii*. The 300 mM hydroponic solution salinity resulted in a significant decrease in the survival rate and biomass accumulation of all tested species, as well as a reduction in root length. Consistent performance of these species under 150 mM NaCl hydroponic solution salinity demonstrates their potential as resilient crops for sustainable food production and controlled environment agriculture.

DETERMINATION OF HEAT STRESS TOLERANCE MECHANISMS IN STRAWBERRY THROUGH TRANSCRIPTOMICS AND MACHINE LEARNING APPROACHES

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Heat stress is one of the most detrimental abiotic factors limiting strawberry (*Fragaria* × *ananassa*) growth, productivity, and fruit quality. Understanding the molecular mechanisms underlying thermotolerance is crucial for developing resilient cultivars. Recent advances in transcriptomics and machine learning (ML) have provided powerful tools to explore and predict complex stress responses in plants. Transcriptomic analyses using RNA sequencing have revealed that heat stress induces extensive reprogramming of gene expression in strawberries. Key heat shock proteins (HSPs) and heat shock transcription factors (HSFs) play vital roles in protein folding, stabilization, and cellular protection under thermal stress. Genes associated with antioxidant defense, cell wall reinforcement, and lncRNA-mediated regulation show enhanced expression in heat-tolerant cultivars, supporting cellular homeostasis and thermotolerance. In contrast, heat-sensitive cultivars exhibit downregulation of GDSL esterase/lipase (GELP) genes, leading to weakened cuticle structure and greater susceptibility to heat stress. Machine learning approaches, including Random Forest, Support Vector Machine, and Extreme Gradient Boosting, have emerged as effective tools for analyzing complex transcriptomic datasets. ML models can identify key regulatory genes and classify genotypes based on their heat tolerance profiles. Feature importance and interpretability analyses further help pinpoint biomarker genes predictive of thermotolerance, providing valuable insights for marker-assisted breeding and genomic prediction. The integration of transcriptomics with ML represents a promising frontier for unraveling the genetic architecture of heat tolerance in strawberry. This combined strategy enhances our understanding of stress-responsive gene networks and accelerates the development of climate-resilient strawberry cultivars through data-driven breeding and precision genomics.