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12TH INTERNATIONAL CONFERENCE OF YOUNG SCIENTISTS THE YOUNG SCIENTISTS FOR ADVANCE OF AGRICULTURE

ABSTRACTS

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The language of the abstracts has not been edited.

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Vytautas Magnus University Agriculture Academy

PLENARY SESSION

EVALUATION OF FREEZING TOLERANCE IN NORDIC WINTER WHEAT GERMPLASM

Gabija Vaitkevičiūtė, Aakash Chawade, Žilvinas Liatukas, Andrius Aleliūnas, Rita Armonienė Lithuanian Research Centre for Agriculture and Forestry

The growing human population and climate change are both posing an increasing number of challenges to the efforts to meet global food supply demands. The higher productivity of winter wheat in comparison to spring wheat, combined with the gradual shift of its cultivation area towards higher latitudes due to warming temperatures underscore the essential role of winter wheat in food production. Despite the warming climate, winter temperature fluctuations still pose a threat to the survival of winter wheat. Consequently, freezing tolerance (FT) remains an important trait. The collection of Nordic winter wheat cultivars and landraces (NordGen, Sweden) presents a valuable reservoir of genetic diversity, which holds promise for future endeavours in developing new climate-resilient crops. The aims of this study were to 1) assess the FT of 160 Nordic winter wheat genotypes under controlled conditions; 2) identify the single nucleotide polymorphism (SNP) markers and genes, associated with FT via genome-wide association studies (GWAS). The wheats were cold acclimated at 2 °C for 2 weeks and freezing tests were carried out at the target temperatures of -8, -10, -12, -14, and -16 °C for 24 hours. LT50 values (temperature, at which 50% of plants are killed) were determined. Subsequently, GWAS analyses were carried out using BLINK and FarmCPU models with a total of 7401 SNP markers. Our results reveal a high range of FT across the NordGen collection of winter wheat genotypes. Significant differences in FT were detected between genotypes based on country of origin, year of release, and culton type. Moreover, 6 SNP markers were associated with FT under controlled conditions and mapped to chromosomes 2A, 2B, 3A, 5A, 5B, and 7A. This study shows that Nordic winter wheat germplasm can be utilised in the development of novel cultivars with heightened FT.

Acknowledgement: This study was funded by Lithuanian Research Centre for Agriculture and Forestry's long-term research program "Genetics, biotechnology and breeding for plant biodiversity and innovative technologies".

EVOLUTIONARY LINEAGES OF *QUERCUS ROBUR* (L.) OLD GROWTH TREES IN LITHUANIA BASED ON cpDNA MARKERS

Mindaugas Ilčiukas Vytautas Magnus University Agriculture Academy

Pedunculate oak (Quercus robur L.) forests cover only 2.3% of Lithuania's total forests, but the condition (commercial value and viability) of Lithuania's oak forests is not good enough. The aim of the study was to investigate the genetic value of Lithuanian Quercus robur L. old-growth trees by cpDNA markers to identify haplotype lines of high genetic diversity and quality. We used 3 cpSSR markers to identify the evolutionary lineages of 347 natural-origin old-growth Quercus robur trees – the nature monuments. Also, morphotype, skeletal branch angle and bark type determined for each 347 old-growth Quercus robur trees in Lithuania. It was found 5 evolutionary lineages of Lithuanian Quercus robur old-growth trees, that migrates from Eastern and Western Italy, Germany, Balkan and Spain glacial refuge zones. We found that the geographical distribution of haplotypic evolutionary lineages in the Lithuanian territory is not random – the most common haplotypes in the country are the Balkan lineage haplotype H5 BALK (44% of trees) and the German haplotype H4_DE (33% of trees), both of which are distributed in all parts of the country. The German haplotype H4_DE is particularly common in western part of Lithuania (Samogitia region) and rarer in the northern-eastern part of Lithuania. The Eastern Italian H6 EAST IT haplotype is found exclusively in eastern Lithuania. The study shows that there are largely related *Quercus robur* stem quality and bark morphotypic characteristics specific to their evolutionary lineage, as well as a high genetic diversity. The study shows that German haplotype H4_DE has commercially the best single-stemmed morphotype, especially in central Lithuania (about 50% of trees).

Acknowledgement: I am gratefully acknowledged Darius Danusevičius for providing financial support for this study and all help as my supervisor, Rūta Kembrytė-Ilčiukienė for help to conduct works in laboratory. I also would like to thank Virgilijus Baliuckas and Aušra Juškauskaitė for your help with the fieldworks. This study was funded by Ministry of Environment of the Republic of Lithuania, National Scientific project "IDENTIFICATION OF HAPLOTYPES OF HIGH BREEDING VALUE AND DIVERSITY IN LITHUANIAN OAK BASED ON DNR MARKERS" No. VPS-2020-114-SBMŪRP.

MITIGATION OF *ALTERNARIA*-INDUCED CARROT DISEASES WITH PLANT EXTRACTS: A SUSTAINABLE APPROACH TO ENHANCE YIELD AND QUALITY

Simona Chrapačienė Lithuanian Research Centre for Agriculture and Forestry

Carrot diseases caused by Alternaria spp. are a significant concern for carrot growers as they can lead to substantial yield and quality losses. Chemical treatment with fungicides has been a potent and widely used approach for disease control in agriculture, including managing diseases caused by fungi like Alternaria species. While having many advantages, several challenges and concerns are associated with their use, like resistance development, environmental impact, and food security. In response to these challenges, many agricultural systems have shifted toward Integrated Pest Management approaches, with one aiming to minimize the use of chemical pesticides by combining various disease management strategies, including biological control. Recent research has highlighted the effectiveness of alternative approaches, such as plant extracts with antifungal properties. The objective of this research was to assess the impact of plant extracts on mitigating the spread of disease caused by Alternaria spp. under field conditions. Furthermore, the study included an evaluation of the effects on carrot yield. Field experiments were conducted at the experimental fields located within the Institute of Horticulture at the Lithuanian Research Centre for Agriculture and Forestry during 2021 and 2022. Foliar applications included Thymus vulgaris essential oil, Syzygium aromaticum extract, and a mixture of S. aromaticum combined with Laurus nobilis extract. The control group, which did not receive any essential oil or extract treatment, served as a basis for comparing the results. Applied treatments suppressed disease spread in the carrot field and exhibited increased yields when compared to untreated carrots. Notably, the most noteworthy outcomes were observed after combining clove and laurel extracts.

TOWARDS INTEGRATED WEED MANAGEMENT IN LATVIA

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With the Directive 2009/128/EC of the European Parliament and of the Council is dictated that all member states of the European Union implement integrated pest management (IPM) principles in the agriculture already since 1st January 2014. However, there is still a gap in knowledge and lack of scientifically based recommendations to implement IPM principles regarding weed management in field crop production. The aim of this study was to analyse weed distribution in arable fields in regions of Latvia to provide additional information for elaborating recommendations for weed management in economically important crops following the IPM principles. Weed survey in Latvia was conducted in the time period from 2013 to 2017. In total, 50 farms were randomly chosen, where weed counting once per growing period – from 3rd decade of June till 2nd decade of July – in six crop fields was done each year. The method by Rasins and Taurina (1982) was used. Weed identification was done at species or genus level. Plant density was calculated using correlation table based on negative binomial distribution. Field information on crop, crop rotation, soil, crop management, fertilizers, and crop protection were collected. Crop rotation can be used as a tool for weed management. It also affects weed species occurrence. The trends for weed species to increase or decrease their occurrence in crop fields with different cereal proportion in the crop rotation differ among the regions of Latvia. That could be explained by different local environmental conditions and field management practices. This study provided scientific data and results on weed populations and the factors that influence weed population structure and density in Latvia and helped to develop recommendations for weed control under Latvian climatic conditions.

Acknowledgement: The research was funded by two projects: 1) "Integrated pest management for weed control in arable crops for sustainable use of the environment and resources" supported by European Agricultural Fund for Rural Development (EAFRD) (2013–2014) and 2) "Recommendations for effective control of wild oat and other widespread weed species in Latvia" supported by Ministry of Agriculture (2015–2018).

RURAL YOUTH EMPLOYABILITY TENDENCIES AND THE COVID-19 PANDEMIC

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The COVID-19 pandemic makes serious impact on youth employability, especially in rural regions. In rural areas, the system and availability of education, vocational education and training can have a negative impact on a young person's ability to obtain an education and continue to succeed in the labour market. These circumstances can hinder a young person's transition to the labour market. The paper presents a brief analysis of rural youth employment tendencies and the consequences of the Covid-19 pandemic into the labour market in Latvia and an analysis of the youth employability by using dynamic series analysis The research methodology implemented for the present research study is based on the theoretical concepts and statistical data regarding the rural youth employment tendencies and the impact of Covid-19 pandemic. Based on the results of the study, it can be concluded that Covid-19 has contributed to job losses by forcing young people from rural areas to move to a city with better access to employment. The authors have concluded that educated women tend to start their own businesses after graduation, which is positive, especially if it is based in the countryside. Based on the authors' calculations, the forecast of employees in the age group from 25 to 34 in Latvia in 2022 will be 171.9 thousand, in 2023 156.5 thousand and in 2024 138.9 thousand. It must be concluded that the projected number of employees in the 25–34 age group will decrease significantly.

Acknowledgement: The research was supported by the National Research Programme "Latvian Heritage and Future Challenges for the Sustainability of the State", project "Challenges for the Latvian State and Society and the Solutions in International Context (INTERFRAME-LV)", grant number VPP-IZM-2018/1-0005.

I SECTION. Horticulture

GREEN SYNTHESIS, CHARACTERIZATION AND ANTIMICROBIAL ACTIVITY OF SILVER NANOPARTICLES SYNTHESIZED BY SYMPHYTI RADIX

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Nanosized materials have unique chemical, optical, physical properties, and antimicrobial activity. Various types of nano materials like gold, copper, zinc, magnesium, titanium, and silver were used for antimicrobial activity against pathogenic microorganisms. Green synthesis provides advancement over chemical and physical methods as it is cost effective, environment friendly, and no need to use high pressure, temperature, and toxic chemicals. Many studies reported synthesis of silver nanoparticles using leaf, flowers, seeds, stems, and other extracts of various plants. Phytochemical elements have been used as green reductants to reduce Ag ions to AgNPs. Symphytum radix (S. radix) is a medicinal plant, the effects of which were already known in ancient times. Allantoin and rosmarinic acid are probably of central importance for its pharmacodynamic effects. The aim of this study was to synthesized silver nanoparticles (AgNPs) using aqueous extract of Symphyti radix. The morphology and size of the synthesized AgNPs were carried out by using SEM microscope. Phytochemical and antioxidant activity analysis was performed for the pure and AgNPs S.radix extracts. Samples was tested by different methods such as ABTS, DPPH and FRAP assays. The antimicrobial activity was investigated against gram-negative and gram-positive bacteria cultures. The agar disk diffusion test was used to analysed the activity of green AgNPs and pure S. radix extract. and minimal inhibitory concentration. The pure extracts and S. radix/AgNPs contain hydroxycinnamic acid, flavonoids and phenolic acid derivates that provide antimicrobial and antioxidant activity. The AgNPs assisted by S. radix were spherical shaped with a size of about 35 nm. S. radix/AgNPs inhibit the viability of Gram-positives and Gram-negative bacteria strains. The inhibition zone diameter increased from 0 to about 15 mm in tested pathogenic opportunistic microorganisms. Significant antibacterial activity was observed against S. aureus with zone of inhibition to 13.3–18.3 mm of AgNPs synthesized in tested extracts.

Acknowledgement: This project has received funding from the Research Council of Lithuania, agreement No. S-PD-22-13.

THE ANTAGONISTIC ABILITY OF THE BACTERIAL ISOLATES FROM PLUM RHIZOSPHERE AGAINST MONILINIA FRUCTIGENA

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Some microorganisms in the environment of plants have natural antagonistic properties. The rhizosphere contains the most microorganisms of any zone of a plant's environment. This is because of relatively consistent environmental factors, such as temperature, humidity, nutrients, and soil pH. Applied agricultural practices highly affect the diversity and composition of the microbiota. Usually, conventional and organic practices are compared together, and noticeable shifts in microbial communities are seen. Moreover, the host also determines the colonizing microbial communities. To make it clear, microbes might be beneficial or harmful to the plant host. One of the most destructive pathogens in pome and stone fruit orchards is *Monilinia fructigena*. This is a fungal species that causes blossom and twig blight, twig canker, and brown rot on fruits. On the other hand, beneficial microbes can help plant hosts fight against such pathogens through various pathways. Additionally, we can harness such microorganisms to play an antagonistic role against another non-desirable microorganism, inhibit its growth, and use it as an ecological biocontrol agent. In this study, the rhizosphere bacteria were isolated, and the diversity, composition, and antagonistic properties were compared to bacterial communities of plum buds.

PREPARATION OF ADSORBENT USING PLANT RESIDUE AND ITS APPLICATION IN Cr6+ REMOVAL

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Plants are the best source of every nutrient; they are called the "Lungs of the Earth" [1]. Plants combat climate change, absorbing carbon dioxide and mitigating its impact, reminding us that they are not just part of the solution but our greatest allies in the fight against global warming. If they are used in a sustainable manner, even their waste can be used as the most beneficial source to reduce water pollution [2]. An adsorption mechanism can play a vital role in removing heavy metal pollution. It can lead to sustainable development and growth of any country [3]. This study investigates comparative assessment using Sugarcane Bagasse Powder (SBP) and Peanut Shell Powder (PSP) for the preparation of absorbent and their application in removal of Cr6+ from self-synthetic polluted water. Temperature was low during pyrolysis process and was prepared using Bench Scale Fixed Bed Reactor in application for water treatment, specifically for Chromium. Resultant biochar was characterized by SEM-EDX, FTIR, and BET. The Colorimetric method was used for estimation of Chromium. The best possible results after experimentation were obtained with Fe Modified PSP with a 99.97 removal percentage, upon Cr6+ conc 20 mg/L, adsorbent dosage = 0.3 g, shaking time 180 mints and pH 2. Modified SBP gives removal percent of 98.96% with the same conditions as Cr6+ conc 20 mg/L, adsorbent dosage = 0.3 g, shaking time 180 mints and pH 2. Pseudo 1st and 2nd order kinetic models were implemented for calculation of efficiencies. This study reveals that highest efficiency was obtained with iron modifies peanut shell powder and it's the most economical way for removal of Chromium from water.

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SOLID GRAIN WASTE DIGESTATE IMPACT ON THE BIOMETRIC PARAMETERS OF DIFFERENT TYPES VEGETABLE SEEDLINGS

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Lithuanian Research Centre for Agriculture and Forestry

Recent studies have shown that high-quality greenhouse vegetable seedling production significantly impacts vegetable yield. The development of resourceful and efficient fertilizers for vegetable crops is an important step toward. Biomass from the biogas production process, also known as solid grain waste digestate has been widely used for the cultivation of various crops, but there is a lack of research on the use of greenhouse vegetable seedlings. The main objective of this research was to investigate the influence of different rates of solid grain waste digestate inserted in the peat substrate on vegetable seedling quality. The research was carried out in a greenhouse covered with double polymeric film at the Institute of Horticulture, Lithuanian Research Centre for Agriculture and Forestry. Different ratios of digestate were investigated: control (peat), peat +5% digestate, peat +10% digestate, peat +15% digestate and peat +20% digestate with 3 repetitions by using a completely randomized design. The biometrical parameters of the vegetable seedlings were evaluated. The results showed that +5%, +10%, and +15% of digestate inserted in peat had a significantly higher for tomato seedlings in plant height, leaf area, leaf fresh, and all plant fresh masses compared with the control variant. Pepper seedlings improved in all biometrical parameters with an additional insertion of +10% of digestate in peat compared with the control variant. The use of +5% digestate inserted in peat increased the biometrical parameters of cucumber seedlings compared with other variants. All types of vegetable seedlings had lower biometrical parameters by using +20% digestate mixture with peat. This research showed that cucumber seedlings need a smaller amount of digestate to get an effective growth result. For pepper seedlings the most effective was +10% of peat-digestate, and for tomato seedlings - +15% of digestate.

Acknowledgement: To my Supervisor Dr Julė Jankauskienė, Scientific Consultant Dr Kristina Laužikė and Senior Technician Roma Starkutė

THE VARIATION OF RED-LEAF LETTUCE PIGMENTS AFTER GREY MOLD INFECTION UNDER HPS AND LEDS RADIATION

Asta Kupčinskienė, Aušra Brazaitytė, Alma Valiuškaitė, Neringa Rasiukevičiūtė Lithuanian Research Centre for Agriculture and Forestry

The aim of study was to determine the impact of grey mold infection (B. cinerea) on red-leaf lettuce coloration pigments. Experiment was maintained in growth chambers under high pressure sodium (HPS) lighting with photosynthetic photon flux density (PPFD) 200 µmol m⁻² s⁻¹ and the photoperiod was 16-h. The day/night temperature was $21 \pm 2/16 \pm 2$ °C and the relative humidity of air was 70 ± 10 %. Lettuces were infected by 7-day-old fungus BC isolate (LT13B_FRA_76) maintained on PDA at 22 °C in the thermostat. Infected and noninfected lettuce was grown using HPS and LEDs (PPFD = 12 - of far-red, 108 - of red, 24 - of orange, 14 - of green, 40 – of blue, 2 μ mol m⁻² s⁻¹ of purple) lamps. The leaves of lettuce were measured non-destructively each day during the 7 days lasting experiment. Spectral indices ARI2=R800×(1/R550)-1/R700, CRI2 = (1/R515)-(1/R770), FRI = 1/R410-1/R460)×R500, SIPI = (R800-R445)/ (R800-R680), NDVI = (R800-R650)/(R800-R650), R = R700/R670, G2 = R570/R670, B = R450/R490, BGI2 = R450/R550, BRI2 = R450/R690 were selected to measure coloration pigments. The results showed that FRI of infected lettuce significantly increased under HPS (from 0.076 to 0.311) and LEDs (from 0.052 to 0.360) on the second day of experiment. R of infected lettuce significantly increased under LEDs on the fourth day. G2 of infected lettuce significantly decreased (from 1.54 to 1.410) under HPS lighting on the first day of experiment. B of infected plants had trend significantly decrease under HPS the first (from 1.149 to 1.124) and the second (from 1.163 to 1.110) days after infection. BGI2 and BRI2 of infected lettuce tended to decrease under LED on the third and seventh days. In summary, FRI tended to increase after infection independently of lighting. R of infected lettuce increased under LEDs. Meanwhile G2, B, BGI2 and BRI2 decreased every day after infection.

TWIG SCAB IN PEAR IN LATVIA

Regīna Rancāne

Lithuanian Research Centre for Agriculture and Forestry

The ascomycete Venturia pyrina, the cause of pear scab, has a biology very similar to the causal agent of apple scab, V. inaequalis. Both pathogens overwinter as pseudothecia in old, infected leaves on the ground, but they may also overwinter as mycelium and conidia in the bark of young shoots. This phenomenon is named twig or shoot scab and is very common in pear, especially in orchards with infrequent fungicide applications, but it is rarely found in apple orchards. Conidia from twig lesions establish primary infections more easily than ascospores because of their short distance to new emerging tissue within the trees. The aim of this study was to investigate the epidemiology of V. pyrina, with an emphasis on conidial inoculum from wood infections. Observations were carried out in an organic orchard on two pear cultivars from 2022 to 2023. Second year shoots were collected bi-weekly, starting from early March, and were examined through August for presence of conidia of V. pyrina. The dissemination of conidia began ca. 2 months earlier than the ascospores started to be released from leaves on the ground, and formation of conidia continued during the summer, after ascospore release had ceased. From the moment when scab symptoms appeared, disease incidence and severity was assessed on pear leaves, fruit, and shoots. On young, actively growing shoots, new infections were observed as velvety scab spots in early June in 2022, and as the season progressed, they changed to corky, canker-like areas. Depending on the cultivar, the severity of scab on the shoots reached 7–25% in early August. Disease symptoms on young shoots were not observed in 2023 due to dry weather conditions.

THE DISTRIBUTION OF FUNGAL PATHOGENS IN WEEDS AND ALTERNARIA SPP. CONTROL

Vytautas Bunevičius, Simona Chrapačienė, Neringa Rasiukevičiūtė, Alma Valiuškaitė Lithuanian Research Centre for Agriculture and Forestry

Pathogenic fungi can cause various plant diseases, resulting in yield losses. Plant protection relies on chemical pesticides, but pesticides contribute to environmental pollution, adversely affect human health, and can remain in the soil for years. Therefore, it is essential to look for alternative biocontrol methods. One of them could be the use of plant extracts (PE). PE contains many valuable secondary metabolites, many of which can be used safely and effectively to control fungal diseases. It is no longer necessary to show the negative impact of weeds on agriculture and its ecosystems. In addition, weeds could play an important role as reservoirs for plant pathogens. This study aimed to obtain the distribution of pathogens in weeds and evaluate clove (Syzygium aromaticum L.) plant extract inhibition to Alternaria spp. The experiment was carried out at the LAMMC Institute of Horticulture in Lithuania. Samples collected in 2020 to evaluate the fungi contamination levels of prevailing weeds in carrot crops. The Alternaria spp. inhibition was evaluated by 75 μ l/l, 150 μ l/l and 300 µl/l concentrations of clove plant extract (PE), obtained by subcritical CO₂ extraction. The results showed that Penicillium spp. and Alternaria spp. prevailed most in Galinsoga parviflora and Equisetum arvense. Besides Fusarium spp., Aspergillus spp. and Phytophthora spp. were also detected. The clove PE concentrations inhibited variously Alternaria alternata and Alternaria consortialis. Studies have shown that more significant inhibition of mycelial growth is achieved with a higher concentration of PE. A PE concentration of 300 μ l/l achieved the best inhibition of mycelial growth. Our findings show that weeds play a reservoir host for plant pathogens and should be monitored and controlled. In addition, clove PE potentially could control Alternaria spp., however, the imbibitional effect is relatively short-term. Therefore, we should work on higher concentration and formulation.

BIODIVERSITY AND ADAPTABILITY IN THE PERENNIAL ALLIUM SPECIES

Vaida Čepulienė

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Allium genus species belong to the family Amaryllidaceae. They are native to the Northern Hemisphere and species grow widely in various regions. Some species, such as Allium fistulosum L., was historically the main Allium vegetable of China and Japan, where it has been cultivated for more than 2000 years. Nevertheless, Allium fistulosum L. is originally from Romania and remains very important in China and Japan. Among Lithuania's perennial Allium plant species, the most well-known and cultivated are Allium schoenoprasum L., Allium angulosum L., Allium nutans L., Allium fistulosum L. Cold hardiness and resistance in winter are the main factors determining the geographical distribution of garlic. Perennial Allium species adapt well to their growing environment, but yields remain constant or may increase when the bulbs are transplanted under conditions like those in which they were grown in their original location. Locations differ in soil type, fertility, water availability, temperatures, day length, solar radiation, and management practices. However, it has been found that the optimal growing conditions for perennial plants are moist, humus-loamy soil. Moreover, plants are resistant to drought, especially in summer. Winter temperature fluctuations disrupt the natural seasonal rhythm, which is significant for the vegetation of these plants. Winter frost damage to plants is a big problem for garlic in our country, even for local cultivars. In addition, the susceptibility of garlic to pests and pathogens also poses a serious threat to genetic resources stored in uncontrolled field collections. However, most research on perennial plants of the Allium genus is preliminary and under-analysed. The possibilities of adaptation of plants to changing climatic and environmental conditions and the biochemical mechanisms that determine them have been little studied in Lithuania and foreign countries. Thus, more detailed studies and a comprehensive assessment of environmental factors are needed. The research aims to introduce the biodiversity and adaptability of the investigated species of perennial plants of the genus Allium.

THE DIVERSITY OF POME FRUITS IN THE OLD ORCHARDS OF LITHUANIA FROM A PHYTOPATHOLOGICAL POINT OF VIEW

Aurelijus Starkus

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The aim of this study was to collect as many apple and pear genotypes as possible from old orchards in different regions of Lithuania and to preserve these old varieties in the germplasm collection of institute horticulture at Lithuanian research centre of agriculture and forestry (LAMMC), as the loss of old varieties is threatened by the age of the plants and the loss of gardens and homesteads. During the period 2015–2022 in total 2300 genotypes were found in 88 old gardens, including 26 gardens planted in parks, beside museums, and in existing or former estates. By vegetative propagation the varieties of apple have survived several centuries. This is apparently due to their adaptability and the high value and demand for fruit. The most common and abundant apple varieties found in old Lithuanian orchards are 'Popierinis', 'Rudeninis strižuotasis', 'Lietuvos pepinas', 'Paprastasis antaninis', 'Sierinka'. In total 300 genotypes of apples were grown in Central Lithuania in collection of institute horticulture at LAMMC and evaluated against fungal pathogens *Venturia inaequalis, Phyllosticta mali* and *Podosphaera leucotricha* by the same phytopathological background. In total 34 genotypes of apple were selected as donors of fungal disease resistance for the development of new varieties.

II SECTION. Agronomy, Agrobiology and agroecology

ANTIOXIDANT ACTIVITY ALTERATIONS IN MICROGREENS UNDER VARYING LIGHT INTENSITY

leva Gudžinskaitė

Lithuanian Research Centre for Agriculture and Forestry

Light is one of the most important growing environmental factors, which can influence plants nutritional value, visual appearance, and overall taste. Our research aims to show that lighting intensity may have an impact on microgreens antioxidant activity. The experiments were conducted in a greenhouse (Lat 55°). Brassica juncea, Amaranthus tricolor, Brassica oleracea var. italica, Brassica oleracea microgreens were grown in peat substrate with supplemental light-emitting diodes (LEDs) lighting, the total PPFD of 100, 150, 200 and 250 µmol m⁻² s⁻¹ was maintained for 16h photoperiod with 20 ± 3 °C temperature. For supplemental light was used white LED lamps. Results showed that for mustard microgreens on harvest day the highest FRAP antioxidant activity was determent under 150 µmol m⁻² s⁻¹, but during the 3 postharvest storage days the differences lost significance. For amaranth during harvest and after 1 day of storage the highest ABTS antioxidant activity was determent under 250 µmol m⁻² s⁻¹, and after 3 days of storage, significantly higher activity was found to be under 200 and 250 µmol m⁻² s⁻¹. For Broccoli, on harvest day there was no significant differences between antioxidant activity, but during postharvest storage it was determined 100 and 150 µmol m^{-2} s⁻¹ to result in higher FRAP and DDPH activity. For kale on harvest day the highest DPPH activity was determined under 250 µmol m⁻² s⁻¹, but during postharvest storage it seemed to be under 100 and 150 µmol m⁻² s⁻¹ PPFD. To conclude, in this study investigated microgreens showed species dependant response to the same growing conditions and light intensity alterations. Mustard, broccoli, and kale showed to exhibit higher antioxidant activity when grown under 100–150 μ mol m⁻² s⁻¹ and amaranth under 200–250 μ mol m⁻² s⁻¹.

EXOGENOUS PHYTOHORMONES: IMPACT OF KINETIN AND ABSCISIC ACID ON ANTIOXIDANT GENE EXPRESSION AND PRODUCTIVITY IN LETTUCE

Martynas Urbutis

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Phytohormones such as kinetin and abscisic acid because of their unique properties and impact on plant developmental processes can be considered as plant biostimulants. Plant biostimulants foster plant growth and development throughout the crop life cycle from seed germination to plant maturity in several ways: improving the efficiency on the plant's metabolism to increase yield and improve crop quality. It has been shown that biostimulants could also be used as stress tolerance boosters or abiotic stress recovery promoters, mainly through facilitating nutrient assimilation, translocation and use, improving quality attributes of produce, including sugar content, colour, rendering water use more efficient. Moreover, they are derived from natural or biological sources and can enhance plant growth and development, help improve the efficiency of plant nutrients, provoke biochemical and molecular plant response. In the coming few years, it is expected that plant bioregulators will significantly contribute to fulfilling the EU Green Deal goals for ecologically and economically sustainable crop production systems within more resilient agroecosystems and lay the cornerstone for a future large-scale sustainable agriculture catalysed by the bio-based industry. Although plant bioregulators appear to be a novel category with high community to elucidate the molecular and physiological mechanisms which will facilitate the promotion and broader use of these bio-products in the agricultural sector. Hormone-based bioregulators can positively affect plant growth and help plants change yield losses. Several scientific studies have demonstrated the potential of various categories of bioregulators to improve crop production and ameliorate abiotic stresses such as drought. Lettuce (Lactuca sativa L.) cv. Green Cos Lobjoits was grown in a greenhouse with 16-hour photoperiod, 70% humidity and average temperature of 21-22° C during the day and 15-17° C at night was maintained. In this study, both single phytohormone treatments with lower concentrations of kinetin and abscisic acid and a mixture of these two resulted an increased antioxidant gene expression. These findings suggest a potential avenue for enhancing the antioxidant capacity of lettuce plants through targeted phytohormonal treatments.

EFFECT OF SOWING TIME AND CULTIVAR ON *MICRODOCHIUM* SP. CAUSED ROOT ROT INTENSITY AND YIELD IN WINTER WHEAT

Aurimas Sabeckis

Lithuanian Research Centre for Agriculture and Forestry

Seed-borne pathogens such as Microdochium nivale and Microdochium majus are causing agents various wheat diseases and not controlled can do a considerable impact on quantity and quality of yield. It is well documented that these pathogens cause root rot and in favourable conditions proliferate in tissues of winter cereals causing pink snow mould. M. nivale and M. majus infect plants in late autumn – early spring period in low positive temperatures under humid snow cover. Apart from fungicide treatment, the possible solutions to mitigate winter damage would be appropriate sowing time and the usage of pathogen-resistant cultivars. As if for this study – Aim was to evaluate sowing time and cultivar influence on root rot intensity and yield. Two-year field experiment was carried-out during 2021–2023. Untreated seeds of four cultivars: 'Ada', 'KWS Emil', 'Skagen' and 'Patras' were sown at optimal and late sowing time. Infection levels of root rot were assessed in early spring in each plot. Seedling base segments were gathered from each plot in early spring and were placed on PDA media in controlled conditions for pathogen identification. Results of this study suggested that disease intensity was generally lower in year 2022 at both sowing times compared to that of 2023. Lower disease intensity resulted in similar yields regarding sowing times. In contrast, in spring of 2023 winter wheat seedlings, especially later sown, were more infected by root rots thus yield quantity coincided with the intensity level in each variety. Cv. 'Ada' and 'KWS Emil' were more susceptible and that resulted in significant yield loses compared to lower infected optimal sown plots of mentioned cultivars. Data from laboratory analysis coincided with data of root rot assessment as later sown winter wheat were more infected by Microdochium sp. in 2023.

AUXIN: BIOSYNTHESIS, TRANSPORT AND INVOLVEMENT IN PLANT PHYSIOLOGICAL FUNCTION

Sulaiman Khan, Muhammad Ayaz, Monika Toleikienė Lithuanian Research Centre for Agriculture and Forestry

Plant hormones study have been at the core of plant physiology for over a century. Phytohormones play a role in every stage of plant development, from seedling through maturity. Auxin is a plant hormone with morphogen-like properties that plays a larger part in the life cycle of plants than other phytohormones. When a plant cell is exposed to auxin, it undergoes substantial changes in gene expression, with numerous genes being up- or down-regulated. The specific processes by which this occurs are still not being studied, although there is now widespread agreement on at least two auxin signalling pathways. Literature reported that, auxin hormone is involved in cell wall extension, cell elongation, stem growth, root growth, flowering, and seed development, etc. The molecular and genetic study of auxin has led to the important visions that have invigorated the field of phytohormones. Thus, the literature review of 97 articles has been done and the systematic analysis to evaluate the influence of auxin in the plant life cycle and its biosynthesis, transport and its effect on cell and physiology of plants. A dimension of auxin role in phototropism, apical dominance, cell elongation of coleoptile, root development and is important for plant improvement and managing diverse functions in plants will be stated using most recent literature. Most scientists only study the effect of auxin on root and cell development, in the future, we should also explore the auxin produced in the plant can be transported by different transporter proteins which distribute it for various physiological functions, the effect of auxin on the stem, sex expression and their response under different environmental stresses.

Keywords: phytohormones, auxin, biosynthesis, transport, cell elongation.

Acknowledgement: I would like to express my sincere gratitude to all those who have contributed to the preparation and submission of this Abstract. First and foremost, we extend our heartfelt appreciation to our co-authors Muhammad Ayaz and Dr Monika Toleikienė for their invaluable collaboration, insightful discussions, and dedicated efforts in conducting the review presented in this Abstract.

THE IMPACT OF WINTER WHEAT CULTIVARS MIXTURES ON DISEASES AND YIELD AFTER DIFFERENT PRE-CROPS

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Winter wheat cultivar mixtures have gained significant attention in recent years due to their potential to influence disease management and crop yield. This innovative approach involves planting different wheat varieties together in the same field, as opposed to monoculture farming, where a single cultivar is grown. The impact of these mixtures on diseases and yield has been a subject of research and experimentation. One of the key benefits of cultivar mixtures is their potential to reduce the prevalence and severity of diseases in winter wheat crops. This is because different cultivars possess varying resistance and susceptibility to specific diseases, which makes it more challenging for pathogens to adapt and spread. By sowing mixtures, the overall disease pressure can be lowered, thus decreasing the need for chemical interventions. Additionally, the diversity within mixtures can enhance the overall resilience of the crop to environmental stress, further reducing disease incidence. Furthermore, cultivar mixtures can positively impact yield. By choosing varieties that complement each other in terms of growth patterns, maturity, and stress tolerance, farmers can potentially maximize their overall yield. This is especially important in variable climates, where the combination of various cultivars can ensure that some will thrive even in adverse conditions. However, the success of cultivar mixtures depends on careful selection of the component cultivars and their proportions. Improper choices can lead to reduced yield or other unforeseen issues. It also requires a more complex management approach, as the mixing of cultivars can complicate harvest and marketing. Nonetheless, as research continues and as growers gain experience, winter wheat cultivar mixtures hold promise for enhancing disease resistance and ultimately improving yields, contributing to more sustainable and resilient agricultural practices. Based on a series of studies, the majority of 67% cultivar mixtures had the potential to reduce the number of fungicide applications compared with mono-crop.

GREEN SYNTHESIS, CHARACTERIZATION, AND ANTIMICROBIAL ACTIVITY OF SILVER NANOPARTICLES SYNTHESIZED BY VIBURNUM OPULUS PLANT BY-PRODUCTS

Vaidė Sakalauskienė Lithuanian Research Centre for Agriculture and Forestry

Various types of nanomaterials like gold, copper, zinc, magnesium, titanium, and silver were used for antimicrobial activity against pathogenic microorganisms. Green synthesis provides advancement over chemical and physical methods as it is cost effective, environment friendly, and there is no need to use high pressure, temperature, and toxic chemicals. It has been reported that plant metabolites such as terpenoids, phenolics, tannins, flavonoids, terpenoids, alkaloids, and polysaccharides contribute to the reduction of Ag ions to AgNPs. The novelty of studies is the secondary use of by-products from the processing of fruit and vegetables. After extraction and use of biologically active compounds, the remaining substance will be used as a raw material to produce organic NPs. Extracts of plant by-products of Viburnum opulus are used in the work. The aim of this study was to synthesize AgNPs using an aqueous extract of Viburnum opulus. The morphology of the synthesized AgNPs was carried out by using SEM/EDS and TEM microscopy. Antioxidant activity analysis was performed for the raw and Viburnum opulus/AgNPs extracts by methods: ABTS'+, DPPH•, CUPRAC, and FRAP assays. The antimicrobial activity was an investigation against Gram-negative and Grampositive bacteria cultures by the agar diffusion test for the evaluation of an antibacterial activity. The raw and Viburnum opulus/AgNPs aqua extracts contain hydroxycinnamic acid, flavonoids, and phenolic acid derivates that provide antimicrobial and antioxidant activity. Viburnum opulus/AgNPs particles were spherical at approximately 45 nm, Total polyphenolic content is 3396,90 mg GAE/100 g and 3016,83 mg GAE/100 g. It's concluded that AgNPs synthesised in extracts have a wide variety of biological uses, activity and can be used as an organic substance without adverse effects.

SUSTAINABLE USE OF SOLID BIOFUEL ASH FOR THE PRODUCTION OF FERTILIZERS AND THEIR APPLICATION IN AGRICULTURE

Gabija Žilytė, Donata Drapanauskaitė Lithuanian Research Centre for Agriculture and Forestry

The growing demand for renewable energy sources has increased the production of biofuels, which has led to a large amount of by-product – biofuel ash. Biofuel ash is alkaline waste (pH about 13), which is rich in minerals and can meet the urgent need to increase soil fertility. The usage of biofuel ash to create fertilizers can help to solve the waste management challenges associated with increased amounts of biofuel ashes in landfills. The objective of this study was to investigate the effect of biofuel ash extracts for spring wheat germination in controlled climate conditions. For the experiment we used three ashes from three different combustion plants, spent coffee grounds and two granulated ash products. Chemical composition of ashes and spent coffee grounds were analysed by using inductively coupled plasma mass spectrometer. The spring wheat germination rate was determined after 3, 6, 8 and 10 days. Early seedling growth parameters, such as shoot length, root length was measured to gain a comprehensive understanding of the impact of biofuel ash on seedling vigour and stress tolerance. Extracts for germination test were prepared by shaking ashes for 2, 4 and 24 h with deionized water. Solid – liquid ratio for preparing extracts was 1:4. The studies showed that the highest germination rate after 10 days was after using spent coffee ground extract, which was shaken for 2 hours. Also, it is important to mention that extracts made from biofuel ashes have different impact.

Acknowledgement: This work was undertaken with the financial support of Research Council of Lithuania project No. S-REP-22-2 according to State-commissioned research, the program of required research and Lithuanian Research Centre for Agriculture and Forestry program Student summer internship.

ASSESSING THE IMPACT OF DIGESTATE AND ITS DERIVED BIOCHAR ON SANDY SOILS PHYSICOCHEMICAL AND BIOLOGICAL PROPERTIES

Zeineb Louati CERTE

Improving soil quality is essential for healthy ecosystems and sustainable agriculture. This study aimed to evaluate the impact of solid digestate and biochar amendments on the physicochemical and biological characteristics of sandy soils. Over six months period, a controlled incubation test was conducted to investigate the impact of different doses of solid digestate (SD) and derived biochar (DB) (0, 50, 75, and 100 T/ha) on sandy soil properties. We assessed important soil characteristics such as pH, organic matter content, nutrient availability, microbial activity, and enzymatic reactions. The physicochemical and biological characteristics of sandy soils were significantly enhanced by the addition of solid digestate (SD) and derived biochar (DB) amendments. First, an alkalizing effect was evident as the pH values increased from 7.98 (at 0T/ha) to 8.8 for SD and 9.1 for DB (at 100 T/ha). Additionally, the levels of the total organic carbon (TOC) content increased from 0.37% (at 0 T/ha) to 1.68% for SD and 2.31% for DB (at 100 T/ha) which will improve the soil's structure and its ability to hold water, and nutrients. In addition to increasing the soil organic content, the addition of biochar reduced the CO₂ emissions as compared to digestate. Microbial respiration measured in soil amended with solid digestate was about 5368 mg C/kg against only 1770 mg C/kg in soil amended with biochar. Overall, the study highlights the potential of biochar derived from solid digestate in sandy soil properties enhancement and carbon sequestration. Implementing this strategy can improve soil fertility, water management, and ecosystem resilience, benefiting sustainable agriculture and reduce the negative impact of the application of chemical fertilizer on the environment.

Acknowledgement: This research study was financially supported by the Ministry of Higher Education and Scientific Research of Tunisia.

NITROGEN FIXATION EFFICIENCY OF SYMBIOTIC AND ASSOCIATIVE BACTERIA IN GREENHOUSE AND FIELD CONDITIONS

Yasha Jamil

Lithuanian Research Centre for Agriculture and Forestry

Soybean, also known as Glycine max (L.), is one of the most essential grain legumes crops globally due to its high protein and oil content. To achieve optimal growth and yield, soybeans form a symbiotic relationship with rhizobia bacteria that resides in root nodules and convert atmospheric nitrogen into a usable form for the plant. Our study aim is to select locally isolated and commercial symbiotic, associative microorganism and bio stimulants which effectively promoting nitrogen fixation in soybean plant. For this purpose, natural occurring endophytic and exophytic bacteria screening was done for soybean plants growing at LAMMC fields in 2022. Ten endophytes out of 130 were selected as promising for nitrogen fixation increase in soybean plants. A greenhouse experiment GE1 was conducted to test the effects of these endophytes on 2022–2023. To investigate nitrogen derived from the air, the soil was fertilized with ammonium nitrate (NH₄NO₃⁻). solution containing labelled 95 percents stable 14N isotope. Our results showed that 4 endophytes Arthrobacter pascens, Serrartia inhibens, Bacillus velezensis, and Serratia plymuthica had higher leaf chlorophyll content and fluorescence parameters and net photosynthesis rates compared to the control at different stages of crop growth. Based on the analysis of fresh and dry roots and shoots length and dry biomass of soybean plants, it has been found that microorganisms Arthrobacter pascens, Serrartia inhibens, Bacillus velezensis, and Serratia plymuthica shown the best effect on soybean productivity. However, comparing the effect of endophytes, none of these had the effect as symbiotic nodules forming bacteria Bradyrhizobium japonicum. The effect of endophytes was from 34 to 76 percent part of the effect exposed by B. japonicum. Based on these results the field experiment FE1 was established to compare the effect of our selected endophytes with the commercial ones from all the Europe. These data will be very important for farmers and also the scientists, since in Lithuania, under cool climate conditions there was no soybean endophytes screened yet.

Acknowledgement: Supervisor Dr Monika Toleikienė.

III SECTION. Plant genetics and crop breeding

PROTEIN NETWORKS DURING DROUGHT STRESS IN DIPLOID AND TETRAPLOID DAYLILIES

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Drought is a significant growth-limiting factor in the changing climate and is vital for perennial ornamental plants' survival, productivity, and attractiveness. Chromosome doubling in perennial plants may improve abiotic stress tolerance. Understanding and elucidating the molecular mechanisms that determine plant response to abiotic stress is essential. De novo transcriptome assembly of diploid and autotetraploid Hemerocallis spp. cv. Trahlyta was done under artificially induced stress to elucidate molecular mechanisms related to plant response to drought. The protein network of daylily plants indicates key hubs and modules associated with differentially expressed genes, providing insights into protein-protein interactions (PPI) and regulatory networks. These interactions act as regulatory points in cellular processes, showing the protein function and its roles in polyploidization. Different PPI networks were observed in diploid and autotetraploid daylily plants during stress. Diploid plants activate more PPI networks than tetraploids (137 and 92, respectively), resulting in greater destructive use of plant resources and vitality. Specific networks of heat shock protein (HSP) and cellulose synthase (CESA) are essential in both types of daylilies. WRKY22 and WRKY33 transcription factors played an important role in upregulating the mitogen-activated protein kinase (MAPK) pathway in both ploidy groups that participate in the primary immune response of plants. Tetraploid daylily cv. Trahlyta has a broader potential for adaptation to abiotic stresses by inducing lipoxygenase 4 (LOX4), nitrogen assimilation control (NAC) and early responsive to dehydration 9 (ERD9) by triggering a defence response. Summarizing the data, it was found that autotetraploid plants of daylily have a broader potential for adaptation to drought stress. Understanding essential proteins, transcription factors, and signalling pathways involved in the PPI network can aid in developing strategies for enhancing drought tolerance in daylily plants. Therefore, autotetraploid adapt faster and better to adverse drought conditions by activating alternative signalling pathways.

THE STUDY OF TOTAL PHENOLIC CONTENT, ASCORBIC ACID AND REDUCING ACTIVITY VARIATION OF BEE POLLEN *IN VITRO* IN IMPACT OF DIFFERENT STORAGE CONDITIONS AND BEE POLLEN BOTANICAL ORIGIN DETECTION

Rosita Stebuliauskaitė Lithuanian University of Health Sciences

Background. Bee pollen has been gaining prominence as a functional food. Chemical composition is determined by the botanical origin and the pharmacological activities are mainly attributed to the presence of polyphenolic compounds and vitamins variation. In order to preserve it biological activity, preparation and storage conditions of bee pollen is of great importance, as they can lose their biological activity over time.

Aim. To evaluate the influence of storage conditions and duration of bee pollen on the total phenolic content, ascorbic acid and reducing activity and to detect the botanical origin of bee pollen.

Methods. The samples of bee pollen were collected in May, in Pasvalio district, Lithuania. One part of pollen was dried, another part was fresh-frozen in a freezer (at –20 °C and –80 °C). The phenolic compounds were determined using Folin-Ciocâlteu method. Antioxidant activity was tested by CUPRAC. Ascorbic acid values were evaluated by titrimetric analysis. Botanical origin was detected by melissopalynological analysis.

Results. Total phenolic content in bee pollen samples in the start point was in range of 23.61±0.27 mg GAE/g to 24.5±0.3 mg GAE/g. There was no statistically significant decrease of total phenolic content in fresh-frozen bee pollen after 3 months storage. The reducing activity was decreased by 18% (CUPRAC assay) in dried pollen after 6 months as compared to control. Ascorbic acid amount in dried bee pollen samples after 6 months storage was decreased by 32%, respectively. Fresh-frozen bee pollen samples were much less affected. After melissopalynological detection, pollen from the *Salix* spp., *Taraxacum officinale* L., *Aesculus hippocastanum* L., *Brassica napus* L. and *Pinus sylvestris* was detected.

Conclusion. According to obtained results, storage conditions and duration had no significant impact on total phenolic content after 3 months duration, however, decreases the ascorbic acid content and reducing activity in dried bee pollen samples whereas fresh-frozen bee pollen samples are less affected.

Acknowledgement: Sonata Trumbeckaitė, Mindaugas Liaudanskas, Neringa Sutkevičienė

TOTAL PHENOLIC COMPOUNDS OF *GERANIUM PALUSTRE* (L.) IN ABOVE-GROUND PARTS DURING VEGETATION PERIOD

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Background. *Geranium* (cranesbills) is the largest genus of the *Geraniaceae* family and contains about 400 species. One of the most common *Geraniums* is *Geranium palsutre* (L.). According to literature data, *Geranium palustre* contain flavonoids: catechin, quercetine, kaempferol, luteolin; flavonoid glycosides: rutin, hyperoside, quercitrin; gallic acid, bergenin, cinnamic acid and its derivatives; 7 free organic acids (malic, citric, oxalic, succinic, tartaric, pyruvic and ascorbic) and 15 amino acids and other compounds, due to which plant possesses a wide range of properties, important for treatment: anti-inflammatory, antiviral, antioxidant, and antimicrobal.

Aim. The aim of the current study was to investigate the quantitative composition of Marsh Cranes'bill (*Geranium palustre* L.) from naturally growing in Lithuania different cenopopulations raw materials phenolic compounds of their extracts.

Methods. The samples of the research was above-ground raw materials of Marsh Crane's-bill plants collected from 21 different cenopopulations naturally growing in Lithuania during the plant's vegetation period of June–August. Extracts were prepared using 0.1 g of dry matter and 10 mL of 70% ethanol. Folin-Ciocalteu method was used to determine the total content of phenolic compounds, the results were expressed as gallic acid equivalents (GRE) (mg/g).

Results. In different vegetation periods the total phenolic content in above-ground was in a range of 88.48 GAE mg/g to 149.06 GAE mg/g. Evaluating individual above-ground parts the highest levels of phenolic compounds (71.72±7.76 GAE mg/g) were found in the leaves which were collected at the beginning of vegetation. The lowest levels of phenolic compounds (18.67±3.39 GAE mg/g) were found in the stems which were collected at the beginning of vegetation.

Conclusion. The study revealed that Marsh Crane's-bill raw materials accumulate significant amounts of phenolic compounds of variation depend directly on the morphological part of the plant and the cenopopulation.

Acknowledgement: Raimondas Bents.

VARIATION IN *PYRUS* RESISTANCE TO EUROPEAN PEAR RUST CAUSAL AGENT *GYMNOSPORANGIUM* SABINAE

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European pear rust, whose causal agent is the rust fungus Gymnosporangium sabinae, is an economically significant pear disease. Infection mainly affects leaves, decreasing the photosynthetically active surface and causing premature fall, thus negatively affecting the tree's potential fruit yield and overall health. European pear rust control is complicated due to the lack of cultivars with complete resistance. The study aims to assess the severity of European pear rust on commercial cultivars and local landrace 'Kazraušu bumbiere' seedlings and to evaluate leaf morphological traits that characterize resistant and susceptible genotypes. Doing so would provide insight into possible pear resistance mechanisms against European pear rust and set a basis for more in-depth studies and developing methodology for selecting genotypes for breeding purposes. Preliminary research took place during two periods: the first period was from 2008 to 2015, when the initial disease severity evaluation of 271 cultivars and 35 seedlings occurred both in the field and in a greenhouse. The second period of evaluations took place from 2018 to 2020. Twenty-six seedlings showing resistance to European pear rust were selected for more in-depth evaluation, including disease severity assessment on the field. Leaf samples were gathered to measure leaf water content, wet and dry mass, dry mass and leaf area ratio. Light microscopy was used to measure anatomical structures: leaf epidermis, mesophyll and vascular tissue width, and stomatal density. The first evaluation provided a baseline for a systematic study of European pear rust symptoms in the field. In contrast, the second evaluation provided evidence of 12 genotypes with stable resistance to European pear and gave insight into morphological differences between resistant and susceptible cultivars. A third evaluation period of commercial cultivars and 'Kazraušu bumbiere' was started in 2023 to expand the data on pear resistance to European pear rust.

USE OF LOW COVERAGE WHOLE GENOME SEQUENCING FOR CLARIFICATION OF FLANKING SEQUENCES OF DISEASE RESISTANCE-LINKED CANDIDATE GENES IN SCOTS PINE

Vilnis Šķipars

Latvian State Forest Research Institute "Silava"

For many non-model organisms, reference genomes are not available, but transcriptome data exist or can be generated more easily. This is also the case for *Pinus sylvestris* L., a species of high economic and ecological importance. We present a follow-up investigation related to our previous study about transcriptome dynamics in Scots pine in response to inoculation with the root rot causing fungus *Heterobasidion annosum*. To clarify mechanism of regulation of disease resistance-linked genes, we decided to clarify flanking sequences of Scots pine candidate genes for resistance against root rot. We presume that these sequences contain regulatory regions (distal enhancers and silencers) influencing and coordinating gene expression. Initially, linear DNA amplification in combination with high throughput sequencing was used with very limited success. To clarify the reasons behind the problems encountered using this approach, it was decided to attempt whole genome sequencing using long-read sequencing. Given the large size of the Scots pine genome (~24 Gbp), very low genome sequence coverage was expected. After analysis of a part of the obtained data – only the best and longest reads (L≥30 kb, q≥10, n~867 k) we obtained 72% of the targeted flanking sequences. Criteria for read selection for flanking sequence harvesting and principal steps for automated analysis have been defined. Our results demonstrate the usefulness of low coverage long read sequencing for the analysis of plant species with limited genomic resources.

Acknowledgement: Funding was provided by European Regional Development Fund, post-doctoral research aid, project ID 1.1.1.2/VIAA/3/19/510. I express gratitude to Adam Vivian-Smith from Norwegian Institute of Bioeconomy Research (NIBIO) for assistance in data analysis and collaboration.

ASSESSING *BRASSICA OLERACEA* THROUGH AGRONOMIC TRAITS: INSIGHTS INTO THE ALIPHATIC GLUCOSINOLATE PATHWAY FOR BREEDING ADVANCEMENTS

Hajer Ben Ammar UNICT

Quantitative Polymerase Chain Reaction (qPCR) has emerged as a powerful molecular technique for the precise quantification of gene expression. In this study, we employed qPCR to investigate the expression levels of a carefully selected panel of 12 genes related to various biological processes in Brassica oleracea. Our research aims to shed light on the aliphatic glucosinolate pathway, a critical component in Brassica species, with implications for crop breeding and genetic improvement. Brassica oleracea, commonly known as cabbage, broccoli, or kale, belongs to the Cruciferae family and is renowned for its nutritional value and diverse culinary uses. Glucosinolates, secondary metabolites present in Brassica species, contribute to the characteristic flavors and health benefits of these vegetables. The aliphatic glucosinolate pathway plays a pivotal role in determining the glucosinolate profile, thereby influencing the plant's defense mechanisms and nutritional properties. In this study, we utilized qPCR to quantify the expression levels of 12 genes associated with the aliphatic glucosinolate pathway. These genes encompass a range of functions, from biosynthesis to regulation, in this complex metabolic network. By examining their expression patterns, we aimed to gain insights into the key regulatory nodes governing glucosinolate biosynthesis. Our results reveal dynamic gene expression patterns across different developmental stages and plant tissues. Notably, we observed differential gene expression profiles associated with glucosinolate accumulation in specific tissues, indicating tissuespecific regulation of the pathway. Additionally, our findings suggest potential candidate genes for targeted manipulation in breeding programs aimed at enhancing glucosinolate content for improved nutritional quality or pest resistance. Furthermore, the study underscores the importance of understanding the molecular basis of the aliphatic glucosinolate pathway in Brassica oleracea. This knowledge can inform breeding strategies to tailor Brassica varieties to specific agricultural and dietary needs. Ultimately, our research contributes to the broader goal of sustainable agriculture and healthier food choices by harnessing the power of molecular techniques like qPCR to elucidate complex metabolic pathways in important crop species. In conclusion, our investigation leveraged qPCR and a set of 12 genes to unravel the intricacies of the aliphatic glucosinolate pathway in Brassica oleracea. Our findings provide valuable insights into the regulation of glucosinolate biosynthesis, with implications for crop breeding and genetic improvement, paving the way for the development of Brassica varieties with enhanced nutritional and agronomic traits.

IV SECTION. Forestry, Agricultural economics and rural sociology, Veterinary medicine and animal sciences

EARLY INFECTION STAGE-SPECIFIC TRANSCRIPT PROFILE OF HETEROBASIDION ANNOSUM IN SCOTS PINE

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Transcriptomes form stem-inoculated Scots pine saplings at four time points post inoculation were obtained to reveal early infection stage-specific *H. annosum* transcripts. To be able to harvest reasonable quantity of *H. annosum* transcripts, high sequencing depth was necessary (as the vast majority of transcripts come from Scots pine). To achieve this, MGI Tech sequencing platform was used. Statistical characterization of the *H. annosum* was limited due to low H. annosum transcript quantity. Still, insights were obtained based on differentially expressed genes with p values ≤ 0.01 . Our data support previous findings about Norway spruce – *Hetersobasidion annosum* s.l. pathosystem indicating role of carbohydrate- and lignin degradation genes in pathogenesis at different timepoints post inoculation. Additionally, role of lipid metabolism genes starting from week two post inoculation is proposed.

Acknowledgement: Funding was provided by European Regional Development Fund, post-doctoral research aid, project ID 1.1.1.2/VIAA/4/20/686. I express gratitude to Vilnis Šķipars from LSFRI Silava for assistance in data analysis and NGS.

FUNGAL DIVERSITY AND POTENTIAL PATHOGENS ASSOCIATED WITH FROST CRACK AFFECTED HYBRID ASPEN TREES IN LATVIA

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Hybrid aspen Populus tremula L. × Populus tremuloides Michx. is a fast-growing and prospective tree for Europe as a potential source of biomass for bioenergy production. However, the knowledge about the phytopathological risks of hybrid aspen clones, in particular relation to frost crack damages as a possible infection gateway of fungal infections, is scarce. In total, five clones represented by 205 trees from three trials in Latvia were studied; two wood samples (at root collar and 1.3 m height) were obtained per tree. Woodinhabiting fungi were isolated and detected by their morphology and sequencing of ITS region with fungal specific primers; their communities were compared using PERMANOVA. Fungal communities representing trees with stem cracks were richer in species, especially pathogens, and there was a vertical gradient. Plant pathogens were isolated from 52% of all samples. Soft rot-causing Alternaria and Fusarium were dominant; Alternaria was more common at the height of 1.3 m, while Fusarium – at the root collar. White rot fungi were isolated from less than 2% of all samples, indicating a low degree of tree infection in 15- to 16-year-old plantations. Clonal differences were no significant for fungal communities in general; nevertheless, for occurrence of genus Cladosporium clonal differences were observed. In conclusion, the estimated differences in fungal communities according to stem cracks implied only indirect clonal effects on phytopathological risks, emphasising the resistance of stem cracking as a crucial trait for the sustainability of hybrid aspen plantations. Keywords: hybrid aspen, frost cracks, wood-inhabiting fungi, soft-rot, Alternaria; Fusarium.

Acknowledgement: Research was funded by JSC Latvia's State Forests, project "Assessment of future phytopathological risks" no. 5–5.9.1_007f_101_21_69.

BIOCONTROL POTENTIAL OF DIFFERENT BASDIOMYCETES AGAINST *HETEROBASIDION* SPP. PRIMARY INFECTIONS

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One of the most efficient methods to control *Heterobasidion* root and butt rots is based on treatments of freshly cut coniferous stumps with biological or chemical products. Biological preparations based on the fungus *Phlebiopsis gigantea* are widely used in Europe as stump treatments against *Heterobasidion* spp., but these are more effective on pine stumps than on Norway spruce stumps. In the present study, we tested different Latvian isolates of *Bjerkandera adusta* and *Sistotrema brinkmanii* in combinations with *P. gigantea* for their ingrowth in the wood and antagonistic potential against both *H. annosum sensu stricto* and *H. parviporum*. As controls native isolates of *P. gigantea* and Finnish Rotstop[®] were used. We analysed their persistence in the wood after an inoculation and impact on other wood inhabiting fungi of *Picea abies* and *Pinus sylvestris* stumps. Wood samples for treated and control stumps were used for DNA extraction and fungal community analysis using sequencing of fungal ITS region by PacBio. Additionally, we have initiated to test isolates representing *Hypholoma, Resinicium* and *Trichaptum* genera for the same purpose – to reduce *Heterobasidion* infection of freshly cut conifer stumps and to increase stump decomposition rate.

Acknowledgement: This study was funded by ERDF project Nr. 1.1.1.1/20/A/095 "Biological control of *Heterobasidion* root rot using Latvian fungal strains" and the ERDF within the framework of the project 'Forest Sector Competence Centre of Latvia' (Contract No. 5.1.1.2.i.0/1/22/A/CFLA/007 "Cord-forming basidiomycetes: possibilities of their use in limiting root rot in forests on peat soils").

ARMILLARIA SPP. NATURAL OCCURENCE OF IN FORESTS ON PEAT SOILS AND ITS INTERACTION WITH OTHER BASIDIOMYCETES IN PEAT SUBTRATE IN VITRO

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Climate change intensifies environmental stress and as a result, pests and diseases increasingly threaten forests. *Heterobasidion* and *Armillaria* spp. are the most important root-rot-causing pathogens of conifers. *Armillaria* species primarily spread by rhizomorphs and occasionally can cause severe economic losses in spruce stands. High incidence of *Heterobasidion* root rot has been observed in some spruce stands on peat soils in Latvia whereas the prevalence of *Armillaria* sp. in peat soils is largely unknown. The aim of the current study is to evaluate occurrence of *Armillaria* rhizomorphs in six Norway spruce stands on peat soils infected with *Heterobasidion* and to test several *Armillaria* isolate growth on peat substrate in vitro in combination with cord-forming basidiomycetes of genera *Resinicium* and *Hypholoma*. *Armillaria* rhizomorphs were found in 60 out of 90 soil samples. The total length of rhizomorphs per sample (volume – 2355 cm3) ranged from 5.2 to 763.9 cm (49.6 cm on average). *Armillaria* rhizomorphs per square meter of soil at a 30 cm depth was on average 6.2 m. Obtained data indicates that peat favours development of *Armillaria* rhizomorphs.

Keywords: peat soils, Armillaria, rhizomorphs, root rot, Norway spruce, Resinicium, Hypholoma.

Acknowledgement: This study was supported from the by JSC Latvian State Forests project No. 5– 5.9.1_007q_101_21_79, "Investigation of the impact of root rot and reducing risks caused by root rot" and ERDF within the framework of the project 'Forest Sector Competence Centre of Latvia' (Contract No. 5.1.1.2.i.0/1/22/A/CFLA/007 "Cord-forming basidiomycetes: possibilities of their use in limiting root rot in forests on peat soils").

A WAY TO ATTRACT FARMERS TO AGRI-ENVIRONMENTAL SUBSIDY SCHEMES – ANALYSIS OF FACTORS USING MACHINE LEARNING ALGORITHM

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As the human population grows, tensions arise regarding food security, environmental quality, provision of raw materials or opportunities to experience the diversity of ecosystems. In this regard, agriculture is a unique economic sector that is itself part of an ecosystem. With a greater need for agricultural production, intensified activities have negative consequences for the environment due to land, water, air and food pollution. Agrienvironmental subsidies (AES) are targeted to reduce harmful effects of agriculture on environment pollution of soil, water, air and food, and to promote environmentally friendly farming. The AES are implemented through the Common Agricultural Policy of the European Union, so analysis of factors that attracts farmers to involve in AES is relevant, as the effectiveness of new CAP 2023–2027 depends on uptake of adjusted and redesigned AES schemes. The aim of the research – to analyse the factors that attract farmers to participate in AES and examine its importance. To address the objectives of the research the analysis of scientific literature, comparative analysis, systematic analysis, and summary analysis was used to select variables used in the research. The methodology includes descriptive and inferential statistics of the data as well as using machine learning algorithms of multilayer perceptron. It is a first attempt to examine the Lithuanian family farms participation in AES and to identify the affecting factors and their importance, using machine learning algorithms. The results reveal that Lithuanian farmers prioritize decisions related to maintaining the farm's production level. It indicates importance of agricultural output and farmers' education, other factors, such as farmer age and farm size, were not as important. We assume that influencing factors may change over time due to other actions and policies, so such research conducted periodically could help with selecting appropriate measures and adapt at the right time.

ROYAL JELLY AS A FOOD SUPPLEMENT EFFECTS ON DOG'S SEMEN QUALITY

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Royal jelly, a substance produced by worker honeybees, has garnered interest for its potential effects on canine reproduction. Previous studies suggest that royal jelly, rich in essential nutrients and antioxidants, can enhance dog fertility and reproductive performance. The aim of our study was to investigate the effect of royal jelly as a food supplement on dog's semen quality. This study involved six German Dwarf Spitz dogs (2.5-3 years old). During the study, the dogs were divided into two groups: a control (N = 3) and an experimental (N = 3). For a period of ten days, the control group dogs received glucose (100 mg/day), whereas the experimental group dogs were given royal jelly (100 mg/day). Both products were manufactured by Medicata Filia and used as a dog food supplement. Semen samples were collected before the study, after ten days of receiving the supplements and two months after the start of the study. In total, 18 canine semen samples were collected manually and analysed for semen volume, subjective sperm motility, sperm viability, concentration, and morphology. The analysis of our research results revealed that dog food supplementation with royal jelly had a positive effect on dog semen quality parameters. After ten days of the study, the experimental dog group demonstrated higher values in semen volume, subjective sperm motility, and the total number of intact spermatozoa, with respective differences of 0.73 mL (SD = 0.26), 11.67% (SD = 2.11), and 26.67% (SD = 15.3), compared to the control dog group's semen (P < 0.05). Subjective sperm motility and the total number of intact spermatozoa in the control group after two months of the experiment were 11.67% (SD = 2.89) and 16.33% (SD = 12.65) lower than in the experimental dog group (P < 0.05). The research underline royal jelly's promising significance in veterinary science and animal breeding, as a natural and accessible dietary supplement to positively influence various aspects of canine reproduction.

Keywords: royal jelly, canine, semen quality.

Acknowledgement: I would like to express my sincere gratitude to Tauro Kenell for generously providing opportunity to conduct our research with their dogs. Their cooperation and support were essential in the successful completion of this study. I would also like to extend my heartfelt thanks to Medicata Filia for providing the supplements that were crucial to this research.

ACCESSING ORAL MICROBIOTA AND ANTIMICROBIAL RESISTANCE FACTORS IN DOGS AND OWNERS

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Antimicrobial resistance (AMR) has emerged as one of the most aggressive public health problems of this century and understanding of emerging zoonotic diseases become crucial for environmental, human and animal health. The aim of this study was to compare oral microbiomes and resistomes in healthy dogs and their owners. Samples from oral cavity were taken from six dogs and their owners and extracted DNA was analysed by shotgun metagenomic sequencing using Illumina HiSeq. All dogs with the range of age from 6 months to 15 years were clinically healthy and presented to veterinary clinic for a dental prophylaxis. Biochemical and morphological blood analysis confirmed their status. Additionally, oral cavities were observed by periodontal pocket probing and full mouth radiography was initiated to evaluate the level of possible periodontitis under general anaesthesia. Dog owners who volunteered to provide their oral samples to be investigated together with the samples of dogs were healthy adults who had a close daily contact with dogs including sharing of their sleeping space. In total 70 and 229 bacterial species were detected in dogs and their owners respectively. There were no similar species of bacteria shared by the dogs and their owners demonstrating different microbial populations in oral cavities of humans and dogs, in spite of their close contact. Low numbers of similar AMR genes that can be transferred from dogs to humans and vice versa were detected. Although this pilot study demonstrated unique oral microbiomes in healthy dogs and owners' further studies using higher numbers of dogs and owners need to be performed with the aim to prove the low risk of oral microbiota and AMR genes transfer from dogs to humans. Moreover, oral microbiome of dogs with different stages of periodontal disease should be investigated as their microbial composition can significantly differ from healthy individuals.

APPLICATION OF MICRO AND NANO BUBBLE TECHNOLOGY IN IRRIGATION: IMPACT ON WATER USE EFFICIENCY AND THE ENVIRONMENT

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The research presented in this dissertation explores the innovative application of Micro and Nano Bubble Technology in irrigation, with a particular focus on its implications for water use efficiency and environmental sustainability. The study encompasses two fundamental dimensions: the development of research methodology and the setup of a lab-scale experiment that closely simulates real-world conditions. The research methodology development phase involved defining research objectives, which encompassed an extensive investigation into the effects of micro-nano bubble water-based irrigation on various facets, including root zone soil characteristics, soil respiration, soil moisture retention, nutrient uptake, nutrient leaching, water use efficiency, and crop yield. To ensure the reliability of the findings, data requirements were identified, and relevant data were meticulously collected. Appropriate statistical analysis methods will be employed to interpret the collected data. In the lab-scale experiment, which commenced on January 23, 2023, we examined the effects of nanobubbles aerated water on soil conditions, water retention, water leaching, and nutrient uptake using various soil types. The experimental setup included six silty loam buckets, nine silty loam buckets characterized by a higher clay particle content (with three of them amended by biochar), and nine sandy loam buckets (with three amended by biochar). Samples were subjected to irrigation with either regular water or nano bubble saturated water. Furthermore, three buckets of each soil type, amended with biochar, received nanobubble water. The water inflow and outflow from each bucket were carefully monitored, with chemical analysis of both incoming and outgoing water performed to assess parameters such as soil moisture, electrical conductivity, pH, various nutrient concentrations, COD (Chemical Oxygen Demand), TDS (Total Dissolved Solids), and various elements. The experimental focus centers on understanding the influence of nano bubbles on soil characteristics, particularly emphasizing water retention, which is crucial for efficient irrigation practices. To observe the impact of these irrigation methods and soil types on plant growth, "California pepper" plants were cultivated in each bucket during the spring season. Various plant-related parameters were measured, including chlorophyll concentration, stomatal conductance, and the number of leaves, providing valuable insights into the plants' response to different irrigation techniques and soil conditions. This comprehensive research contributes to our understanding of the potential of micro and nano bubble technology in agriculture, with implications for sustainable water use and environmental conservation.

