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Plant-microbiome Signaling and Holobiont Responses: From Discovery to Farm Trials

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Abstract

Plants and their associated microbiomes have co-evolved for 500 million years, developing holobionts (combined host-microbiome system) that provide ecological services such as nutrient utilization, development, and pathogen defense, while also exhibiting emergent metabolic and adaptive traits. This talk presents three case studies on how (1) a kingdom-wide conserved plant defense signal has been co-opted to induce lifestyle changes in soil microbiomes to form beneficial biofilms that benefit plant growth from long distances in the rhizosphere; (2) a universal antioxidant microbial metabolite acts as a sulfur nutritional stress tolerance signal for plants in a trans-kingdom tradeoff for its partitioning between microbiome members and plants, and (3) an ecology-guided framework that integrates natural microbial interaction structure with metabolic complementarity has been successfully used to rationally predict cooperative resource exchange for designing beneficial consortia to improve growth promotion and protection. Examples of use of integration of genomic, metabolomic, machine learning and field trials will be shared to demonstrate the path from discovery to translation.

Papain-like Cysteine Proteasesduring Barley Development and Leaf Senescence

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Abstract

Leaf senescence is a developmental process that allows nutrients to be remobilized and transported to sink organs. Previously, papain-like cysteine proteases (PLCPs) have been found to be highly expressed during leaf senescence in different plant species. In this study, we analyzed active PLCPs in barley leaves during the terminal stage of natural senescence. Anion exchange chromatography of protein extracts from barley leaves, harvested six weeks after anthesis, followed by activity assays using the substrates Z-FR-AMC and Z-RR-AMC, revealed a single prominent peak corresponding to active PLCPs. This hydrolytic activity was completely inhibited by E-64, a potent and irreversible inhibitor of cysteine proteases. Fractions enriched for PLCP activity were affinity-labeled with DCG-04 and subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis fractionation, separating two major bands at 43 and 38 kDa. These bands were analyzed using tandem mass spectrometry, allowing the identification of eleven PLCPs. Identified enzymes belong to eight PLCP subfamilies, including CTB/cathepsin B-like (HvPap-19 and -20), RD19/cathepsin F-like (HvPap-1), ALP/cathepsin H-like (HvPap-12 or aleurain), SAG12/cathepsin L-like A (HvPap-17), CEP/cathepsin L-like B (HvPap-14), RD21/cathepsin L-like D (HvPap-6 and -7), cathepsin L-like E (HvPap-13 and -16), and XBCP3 (HvPap-8). Among the identified PLCPs, HvPap-6 was the most abundant. Peptides corresponding to HvPap-6 were identified in both the 43 kDa and 38 kDa bands in approximately the same quantity based on total spectral count. Thus, our results indicate that two active HvPap-6 isoforms can be isolated from late-senescence barley leaves.

Plant Growth Regulators and Their Ability to Control Growth on Woody, Ornamental Shrubs

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Abstract

Introduction: Managing vegetative growth in woody, ornamental shrubs present ongoing challenges for landscape professionals. Excessive regrowth following pruning increases maintenance costs and can diminish landscape uniformity. Plant growth

regulators have shown promise in controlling regrowth, but their performance can vary depending on formulation and application rate. This study was conducted to evaluate the growth control efficacy and potential phytotoxicity of various formulations and rates applied to selected ornamental shrub species.

Methods: Experimental sites were established using randomized 5' - 6' hedge sections with buffer strips between treatments, limited to 100 linear feet per species. Foliar applications of different formulations were made following uniform shearing/pruning to ensure consistent plant size and vigor. Treatments were replicated and labeled for identification. Data was collected on regrowth reduction and visual phytotoxicity over the evaluation period.

Results: Significant differences were observed among formulations and dose rates in their ability to suppress vegetative regrowth. Higher concentrations generally achieved greater growth reduction, although species-specific variation was noted. Phytotoxic reactions were observed at certain rates and formulations, highlighting the importance of optimizing treatment combinations for each species.

Conclusion: Findings demonstrate that formulation and rate selection are critical to achieving desired growth control without compromising plant health. The results from this study have been incorporated into best management practices for commercial landscape operations, providing practical guidelines for efficient and sustainable growth regulation in woody ornamentals.

The Cost of Re-synchronization in Leaf-cutter Ants

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Abstract

Biological rhythms are essential components of organisms' physiology and behavior. In social insects, biological rhythms can be studied at varying levels of a colony, revealing interesting aspects about how rhythms arise from the individual and collective levels. We developed video-tracking software based on machine learning techniques to investigate the emergent collective rhythms of a leaf-cutter ant colony under laboratory conditions. The colony displayed rhythmic, daily foraging activity, with most of its foraging occurring during the dark phase of the day. The same pattern is found in the leaf-cutting activity. After being exposed to a 6-hour phase shift of the light-dark cycle, the daily rhythm of colony activity resynchronized with the new cycle phase after a few transient days. During these transient days, an increase in its daily leaf intake was measured. Under synchronized conditions, the ratio between foraging and leaf intake of the colony was higher during the light phase and decreased in the transient days after the phase shift, revealing that temporal synchronization plays an important role in the organization of the colony. Our findings illustrate the dynamic aspects of temporal synchronization in complex eusocial systems, with changes in system efficiency due to temporal disturbances, pointing to these systems as exciting new models for comparative research.

Application of Silicon Dioxide Nanoparticles to Address Cadmium Sulfide Nanoparticles Contamination in Spinach

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Abstract

Rising cadmium (Cd) contamination poses significant threats to crop productivity, quality, and human health. To address this, nano-enabled techniques have recently gained attention for their potential to enhance crop yields and remediate contamination due to heavy metals. This study explores the efficacy of silicon dioxide nanoparticles (SiO_2 NPs) in mitigating the effects of Cd sulfide (CdS) NPs in spinach. Field experiments were conducted growing spinach plants subjected to cultivation with 1 mg/L CdS NPs contamination, with foliar application of SiO_2 NPs at concentrations of 1, 20, and 100 mg/L. The phenotypic, biochemical, and metabolic responses of the plants to stress conditions were examined following exposure to CdS and SiO_2 for four weeks. The results showed that SiO_2 NPs increased the fresh and dry weights of both roots and shoots. Furthermore, CdS NPs exposure reduced chlorophyll content by 66.76%, whereas SiO_2 NPs co-exposure increased chlorophyll levels by up to 42% compared to the CdS NPs and control groups. However, elevated malondialdehyde levels were observed in leaves for the CdS-only group and roots for all treatments indicating oxidative stress were most pronounced for the CdS case. Results demonstrated that SiO_2 application significantly reduced Cd accumulation in spinach by up to 34.92%. Also, enhanced mineral accumulations were recorded in both roots and shoots, whereas decreased levels were found in the co-exposure groups, except for zinc. The exposure to SiO_2 resulted in upregulation of metabolites including galactonic acid, d-aspartic acid and others, and uridine 5′-diphosphogalactose was downregulated in the group exposed only to CdS NPs. The upregulation of these metabolites by SiO_2 NPs demonstrates their mitigating effect against CdS NPs induced stress. This work enhances understanding of phenotypic and metabolic alterations induced in spinach by CdS and SiO_2 NPs, and independently and through their co-exposure.

Overall, our findings indicate that Cd contamination can be reduced in spinach using SiO_2 NPs when applied at low levels, and the mechanisms are discussed.

Palm Tree Fertilization by Injection: Benefits, Limitations and Practical Considerations

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Abstract

Palm species in Florida frequently exhibit nutrient deficiencies due to soil characterized by low cation exchange capacity, limited water-holding capacity, and elevated pH. Compounding this issue, state-mandated fertilizer blackout periods during the rainy season (November through June) restrict the application of nitrogen and phosphorus. This regulatory constraint coincides with peak root growth activity in palms, potentially exacerbating nutrient limitations and negatively impacting plant health overall. Trunk injections have emerged as an alternative nutrient delivery method, involving the drilling of a small hole into the trunk to install a semi- permanent, self-sealing injection port. This approach targets nutrient application while minimizing environmental losses. Interest in trunk injections has increased in recent years due to evolving fertilizer regulations and the need to address disorders such as lethal bronzing. The objective of these trials is to provide evidence-based guidance for the use of trunk injections as a supplemental fertilization strategy for managed landscapes. Research studies were conducted on a variety of palm trees to ascertain nutrient uptake, palm tree health via drone imagery as well as issues associated with palm tree injection. The studies presented here synthesize findings from multiple research trials evaluating nutrient injection in palms with an emphasis on efficacy, limitations and practical implantation.

Development of a Specific Primer to Detect the Papaya Ringspot Virus Gene in Genetically Modified Organism

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Abstract

Genetically modified organisms improve crop quality by providing resistance to insects and plant diseases. Transgenic papaya that provides resistance to papaya ringspot virus (PRSV), which is transmitted by aphids, requires reliable diagnostic methods to confirm the presence of this trait. This research entailed developing a pair of primers that specifically identify the coat protein (cp) part of the PRSV gene in papayas using polymerase chain reaction (PCR). A total of thirty-five different primers were designed using primer-basic local alignment search tool, which were screened for use by OligoEvaluator, of which three fulfilled all inclusion criteria (hairpin: pass; self-annealing: pass; dimers: very weak/no dimers were found). Genomic DNA from transgenic and organic samples of papayas was then isolated for PCR analysis, with which the performance of primers would be analyzed using agarose gel electrophoresis. Papain and carboxypeptidase A1 (CPA-1) were used as experimental controls, in which papaya DNA would inherently be a resultant marker. The primers for the cp of the PRSV gene produced a rate of CP4 F/R: 6/8 (75%, of which 3 organic, 3 transgenic), 12.5% for CP6 F/R: 1/8 in transgenics only, while those of CP7 F/R were also 12.5% in transgenics only; in which the former, named as lead primers, showed greatest efficiency in detecting papayas produced in Puerto Rico. This represents a project with a comprehensive design that aims for developing the cheapest, simplest, and most reproducible PCR strategy for isolation of PRSV in papayas produced in Puerto Rico.

De Novo Transcriptomic Assembly of the Native Species *Allophylus Edulis* for Atlantic Forest Conservation

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Abstract

The Atlantic Forest is a biodiversity-rich biome, and its severe degradation has transformed it into a "restoration hotspot." In recent years, genomic research has enabled major advances in the study of forest ecosystems. Thus, understanding the genetic and molecular diversity of forest ecosystems is crucial for informed decision-making in the conservation and sustainable management of plant species. In this study, we performed a de novo transcriptome assembly of *Allophylus edulis*, a native Atlantic Forest species with potential for the regeneration of degraded areas. Leaf samples from four individuals of *A. edulis* were subjected to RNA extraction using a commercial Zymo research kit. Sequencing of the four samples was carried out on the NextSeq 2000

platform (Illumina, USA), generating RNA-seq libraries with approximately 15 million paired 100 base pair reads per sample. Since no reference genome is available for the species under study, a de novo assembly was performed. Raw sequencing data were assessed using FastQC, and sequence filtering was conducted with Trimmomatic. Transcriptome assembly was performed using Trinity 2.8.5. Completeness was evaluated with Benchmarking Universal Single-copy Orthologs. We obtained 850 complete genes (52.7% completeness), including 35.1% single-copy, 17.6% duplicated, 21.1% fragmented, and 26.2% missing. The transcriptomic dataset generated here will serve as a reference source for gene identification and functional annotation, as well as for the detection of molecular markers such as single nucleotide polymorphisms, enabling future assessments of intraspecific genetic diversity in *A. edulis*.

De novo Transcriptome Assembly of *Pera glabrata*, An Endemic Species of the Atlantic Forest, based on RNA Sequencing

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Abstract

The Atlantic Forest is recognized as a global hotspot for tropical forest restoration. In recent years, the growing availability of genomic resources has enabled significant advances in the study of forest ecosystems. In this study, we performed de novo genome assembly of Pera glabrata, a native species of the Atlantic Forest with high potential for regenerating degraded areas. Leaf samples from five individuals were subjected to RNA extraction using the Quick-RNA Miniprep kit (Zymo research) and sequenced on the NextSeq2000 platform (Illumina, USA). We evaluated the raw sequencing data using FastQC and filtered the sequences using Trimmomatic on the galaxy platform. De novo transcriptome assembly was conducted using Trinity 2.8.5, and assembly completeness was assessed with Benchmarking Universal Single-copy Orthologs. We obtained 1,433 complete genes (88.8% completeness), of which 18.4% were single-copy, 70.4% duplicated, 5.8% fragmented, and 5.5% missing. Our current strategy focuses on removing redundant contigs using CD-HIT and the tr2aacds.pl pipeline from EvidentialGene. The genomic data generated in this study will serve as a reference for gene identification and annotation, as well as for the detection of molecular markers such as single nucleotide polymorphisms, supporting future assessments of intraspecific genetic diversity in Pera glabrata.

Establishing Cannabis sativa Bio-factories for the Production of Added-value Compounds

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Abstract

Cannabis sativa produces a diverse array of high-value secondary metabolites, including phenolic compounds with established and emerging potential for pharmaceutical and cosmetic applications. Whole-plant cultivation is still the dominant source of these compounds, but it is resource-intensive as it depends on land and water. It is also highly sensitive to climate and pests, with consequences on both biomass quality and quantity, and it must comply with agricultural and regulatory standards. Plant cell suspension cultures, instead, provide a standardized, scalable and fully controlled alternative, offering uniform growth conditions and the possibility of optimizations. Their metabolite yield, however, can remain modest compared to that obtained from whole plants, unless specifically improved. In this study, a vigorously growing cell suspension culture of Cannabis sativa was established and the impact of elicitation on the production of phenolic compounds was investigated using omics. To pave the way to scalability, the cell suspension culture was transferred from flask to stirred-tank bioreactors and the cultivation optimized at the multi-liter scale. This work establishes a foundation for optimizing Cannabis cell suspension cultures as bio-factories, enabling consistent biomass production and improved production of added-value compounds with industrial applications.

Anthracnose *Phaseolus vulgaris* L. and Resistance Phenotyping in Greenhouse Conditions

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Abstract

Bean anthracnose, caused by the fungus *Colletotrichum lindemuthianum*, is one of the most destructive diseases of common bean (*Phaseolus vulgaris* L.), significantly limiting crop productivity and seed quality. The pathogen exhibits high genetic and pathogenic (race) variability, which complicates the breeding of resistant cultivars and undermines the durability of single-gene

resistance. This review summarizes current knowledge on the biology of the pathogen, its epidemiological features, and race diversity, as well as the genetic mechanisms of resistance in common bean, including major co-series resistance genes and loci underlying quantitative resistance. Particular attention is given to methodological approaches for phenotyping resistance under controlled greenhouse inoculation conditions. Published artificial inoculation protocols are discussed, including the use of standardized inoculum, incubation under high relative humidity for 48 h, and disease assessment using the International Center for Tropical Agriculture 1 - 9 disease severity scales. Evidence indicates that combining traditional visual scoring with quantitative image-based lesion measurements improves the accuracy and reproducibility of genotype classification for anthracnose resistance. Prepared at the initial stage of the author's research internship at Michigan State University, this review provides a theoretical and methodological basis for planning greenhouse experiments aimed at resistance phenotyping. The materials presented are of practical value for monitoring pathogen races, selecting resistant genotypes, and supporting breeding programs focused on durable resistance to bean anthracnose.

Isothermal Nucleic Acid Amplification for In-field Identification of Fungal Pathogens

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Abstract

Present plant pest management relies on a mixture of specific, data-driven interventions (e.g., spraying for insect pests found while scouting) and a probabilistic, risk-based approach (e.g., pathogen-resistant variety selection). While some decisions regarding specific interventions could be better informed with timely data regarding, current field-portable plant pathogen diagnostic tests are complicated to conduct and not trusted, due to high false positive rates. SHARP Diagnostics is commercializing the single-stranded DNA-binding protein-helicase assisted with rapid polymerase chain reaction (SHARP) methodology for isothermal DNA amplification, offering the same quality and workflow as polymerase chain reaction without the required training or thermocycler use. In this presentation, we will describe some potential use cases for SHARP in the development of in-field detection of plant fungal pathogens, such as *Phytophthora*, *Macrophomina*, and *Fusarium* species affecting strawberry growers in California.

Effect of Some Plant Extracts on Controlling Soft Rot Disease in Some Economic Plants Associated with Molecular Studies

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Abstract

Pectobacterium carotovorum strains were isolated from carrot, onion, and pepper to evaluate their molecular identity, pathogenic variability, and response to plant extracts, nanoparticles, and biological control agents. Molecular analysis confirmed that the three isolates—PB-1 (carrot), PB-2 (onion), and PB-3 (pepper)—belong to *P. carotovorum*. Phylogenetic reconstruction showed that all strains clustered tightly within the *P. carotovorum* group, and genome sequencing further supported these results. Pathogenicity tests indicated clear differences in virulence, with PB-1 identified as the most aggressive strain compared with PB-2 and PB-3. Antibacterial screening of fourteen plant extracts showed that *Tamarindus indica* (fruit) produced the largest inhibition zone against the carrot isolate (17.5 mm), followed by *Hibiscus sabdariffa* (16 mm), *Rhus coriaria* (15.8 mm), *Punica granatum* (13.6 mm), *Citrus paradisi* (11.6 mm), *Psidium guajava* (11.6 mm), Citrus sinensis (7.1 mm), and *Citrus limon* (6.6 mm). For the onion and pepper isolates, *P. granatum* peel extract exhibited the strongest inhibitory effect, followed by *H. sabdariffa* (14.25 and 13.75 mm) and *R. coriaria* (11.8 and 11.05 mm), outperforming the chemical control (streptomycin 150 ppm). Nanoparticles also showed strong antibacterial activity. Nano-copper produced inhibition zones of 15.12, 7.6, and 14 mm against the carrot, onion, and pepper strains respectively, whereas nano-silver yielded 10.5, 10.7, and 9.75 mm. Among the tested bioagents, *Bacillus subtilis* exhibited the highest antagonistic activity, recording inhibition zones of 13.6 mm (carrot) and 13 mm (onion), surpassing *Streptomyces*, *Trichoderma*, and *Saccharomyces*.

Sustainable Weed Management: The Effects of Applying Pre and Post-emergence Herbicides to *Medicago Ruthenica*

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Abstract

Medicago ruthenica is a forage legume crop that is widely used as fodder and for ecological restoration in arid and semi-arid areas in Northcentral Asia. During the seedling stage, weeds challenge the growth and development of *M. ruthenica*, especially in fields sown for seed production. However, strategies to effectively control weeds in crops of *M. ruthenica* using herbicides have not been investigated. We evaluate the efficacy of different herbicides that control pre- and post-emergence of weeds in *M. ruthenic a*. The results indicated that the most effective pre-emergence herbicides, imazethapyr (1530 mL ha^{-1}) and flumetsulam (120 mL ha^{-1}), resulted in crop safety and soil microbial community equivalent to a weed-free check. The most effective post-emergence herbicides are imazethapyr + haloxyfop-P (1800 + 600 mL ha^{-1}) and 2,4-DB + haloxyfop-P (2250 + 600 mL ha^{-1}). These herbicide treatments demonstrate effective control of most weeds (*Amaranthus retroflexus*, *Chenopodium album*, and grasses) while ensuring crop safety. Application of these herbicides to control weeds in *M. ruthenica* prior to or after their emergence represents a viable strategy for their control and improve agricultural viability and crop yield and quality. Our research contributes to sustainable agriculture and ecological restoration in arid regions.

Rice Yield Response to Changing Rainfall Regimes in China

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Abstract

The impact of rainfall on crop yields is highly heterogeneous, depending on its timing, intensity, and duration. However, existing studies have primarily focused on seasonal total rainfall, providing limited evidence on sub-seasonal (event-based) rainfall impacts on crop yields. This study combines nationwide site-level datasets (1999-2012) to assess rice yields response to sub-seasonal rainfall across China. The results reveal that the regional variation in rice yield sensitivity to rainfall (43%) is primarily driven by the changes in the number of effective panicles per plant (PN, 28%) and the total number of grains (TG, 12%). These regional differences are linked to sub-seasonal rainfall impacts: reduced sunshine during the vegetative period affects PN, and pre-rainfall vapor pressure deficit during the reproductive period affects TG. Under a medium-range emission scenario (SSP2 - 4.5), projected rainfall changes are likely to cause an additional 7.3 ± 0.4% decrease in national rice yields by the end of the century (2086 - 2100), compared to the historical baseline (1999 - 2012). This impact is particularly pronounced in southern China, where single and late rice yields are expected to decline by 9.3% and 14.6%, respectively. This contrasts with the previous projections (+1.3 ± 0.1%) involving rainfall changes as the seasonal total. These findings underscore the necessity of incorporating sub-seasonal rainfall changes into site-specific rice production adaptation strategies.

Nuclear Lamina Phase Separation Orchestrates Stress-induced Transcriptional Responses in Plants

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Abstract

The nuclear lamina (NL), a meshwork of nucleoskeleon and inner nuclear membrane (INM) proteins, orchestrates peripheral chromatin architecture and gene regulation in eukaryotes. While central to transcriptional control, NL-mediated regulation remains poorly characterized in plants, which lack canonical animal lamins. Here, we identified plant INM protein plant nuclear envelope transmembrane (PNET2) as a central regulator that couples phase separation to transcription factor sequestration within the NL. We found that PNET2 interacts with membrane-bound NAC transcription factors (NTLs) via intrinsically disordered regions, promoting their liquid-liquid phase separation at the nuclear periphery. This condensate formation effectively sequesters NTLs and suppresses their transcriptional activity. Conversely, loss of PNET2 deregulates NTLs, leading to ectopic, broad-spectrum stress responses. Importantly, we found this mechanism is directly responsive to environmental signals. External stimuli such as heat shock dissolve PNET2-NTL condensates, releasing NTLs for target gene activation. Our study unveils a dynamic, phase separation- based regulatory hub within the plant NL that gates the activity of membrane-tethered transcription factors. This mechanism integrates spatial compartmentalization with environmental sensing, providing a rapid and reversible switch for stress-responsive gene expression. These findings establish a paradigm for transcriptional control at the nuclear periphery in plants and highlight the conserved logic of using biomolecular condensates to regulate gene expression in response to external cues.

Plant Phenomics: From Unseen to Seen

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Abstract

Dissecting the dynamics of maize plant architecture will be beneficial for ideotype-based maize breeding and prediction, as the genetic basis controlling plant height (PH) in maize remains largely unknown. High-throughput phenomenology technology can lay a solid foundation for correlation analysis and intelligent prediction of complex traits and multi omics, providing reliable data support and decision-making tools for intelligent design and breeding of crops. We developed an automated high-throughput phenotyping platform to systematically and non-invasively quantify 77 image-based traits (i-traits) and 20 field traits (f-traits) for a maize inbred population across all developmental stages. An i-trait-based genome-wide association study identified 4945 trait-associated single nucleotide polymorphisms, 2603 genetic loci, and 1974 corresponding candidate genes. By integrating the PH-association network with the transcriptome profiles of specific internodes, we revealed 13 hub genes that may play vital roles during rapid growth. The candidate genes and novel i-traits identified at multiple growth stages may be used as potential indicators for final PH in maize. One candidate gene, ZmVATE, was functionally validated and shown to regulate PH-related traits in maize using genetic mutation. Furthermore, machine learning was used to build predictive models for final PH based on i-traits, and their performance was assessed across developmental stages. Collectively, our study provides a valuable tool for dissecting the spatiotemporal formation of specific internodes and the genetic architecture of PH, as well as resources and predictive models that are useful for molecular design breeding and predicting maize varieties with ideal plant architectures.

Applied Ecology of Environmental Tritium: Rates and Parameters of Its Transfer in the Environment

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Abstract

The rapid development of AI-technologies and their implementation in everyday life can be determined as a digital explosion. To power AI-datacenters it is required to supply more and more energy. Due to the actions to prevent global warming and necessity to reduce carbon emissions one can see growing demand for the green energy sources. Thanks to the reliability and consistency of nuclear energy production by fission reactors as well as future fusion reactors, these are in the focus of attention, and such projects are under development in many countries worldwide. Basing on previous operational experience we can expect that deployment of many new nuclear power plants, and fusion reactors will cause ingress of radioactive hydrogen isotope – tritium – in the environment. Tritium will be distributed among environmental media, up taken by plants, including crops, and will increase risk of extra dose irradiation of humans. Tritium behavior in the environment has been studied since sixties of the last century. Despite that there are still lacunas and white spots in the knowledge of key transfer processes and rates of the processes, in particular from the point of applied ecology. This paper presents the research results of tritium transfer in the environment, including rates and parameters of the processes, in vicinity of a long-term emission source. The results are tritium dry and wet deposition, hydrogen tritium oxide washout from atmosphere with rain, tritium uptake by soil, lichens plants and crops as well as build-up of organically bound tritium. The results can be used by applied ecologists at further safe development of nuclear fission as well as fusion power sources.

Predicting Spotted-wing Drosophila (*Drosophila suzukii*) Seasonal Activity and Infestation Risk in U-pick Blueberry Orchards

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Abstract

Spotted-wing drosophila (SWD), *Drosophila suzukii* (Matsumura), is an economically important pest of small fruits worldwide and was first detected in Indiana in 2012. Currently, there is limited knowledge of seasonal SWD activity and corresponding risk of infestation for blueberry varieties grown in Indiana. In collaboration with U-pick blueberry growers in North Judson and West Lafayette, Indiana a three-year study was conducted to model SWD activity and infestation risk in 'Bluecrop', 'Blueray', and 'Elliott' blueberry varieties using cumulative degree days (CDD), adult trap counts, and number of infested blueberries

from May - August 2021 - 2023. First detection of adult SWD in monitoring traps occurred during the month of June at both locations and across all three years of the study. The three-year combined degree-day model estimated 5%, 25%, and 50% of cumulative adult SWD trap catch to occur at 865 (± 112), 1,175 (± 53), and 1,659 (± 39) CDD base 7.2 °C, respectively. Among blueberry varieties, late season 'Elliott' berries were most susceptible to infestation by SWD, and firmer blueberries (measured as amount of penetration force) had lower rates of infestation, no matter the variety. Interestingly, SWD adults were consistently detected first in the U-pick orchard surrounded by wooded habitat. These results improve our ability to predict SWD activity and management in U-pick blueberry orchards in the Midwest.

Automated Detection of Tomato Diseases in Controlled Environments Agriculture Using Machine Learning Processed Hyperspectral Data

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Abstract

Greenhouse tomato production is highly valuable but remains vulnerable to rapid disease outbreaks. Controlled environments favor both plant growth and pathogen development. Although nondestructive disease detection methods are preferred, current practices still rely heavily on manual scouting. Hyperspectral sensing has shown strong potential for plant disease detection. However, most studies are limited to tightly controlled conditions and focus on leaf-scale analysis. This leaves a critical gap in real greenhouse applications. This study proposes a canopy-scale approach for automated detection of tomato bacterial spots. The feasibility of canopy-scale hyperspectral detection was first validated in a growth chamber, where a machine learning model using a small set of selected spectral features achieved an accuracy of 89%. Building on this foundation, an automated hyperspectral data collection system was developed for Greenhouse. The system addresses key challenges associated with dynamic greenhouse environments. A preprocessing workflow was implemented to enhance spectral data quality, resulting in improved consistency and a 5.7% increase in classification accuracy compared to models trained on raw data. To further improve robustness under changing environmental conditions, a continual learning framework was introduced to adapt to shifts in data distribution across experiments. The proposed model outperformed a conventional neural network by approximately 7% when evaluated on unseen data, indicating improved generalization. Overall, this work demonstrates that integrating automated canopy-scale data acquisition with adaptive learning strategies enables more reliable and scalable hyperspectral disease detection in greenhouse environments. This provides a practical pathway toward real-world implementation.

Inducing Potential Mutants in Industrial Hemp (*Cannabis sativa* L.) via Chemical Mutagenesis

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Abstract

Cannabis sativa is a multi-use crop with applications in food, fiber, construction, and medicinal industries. In the US, Cannabis plants with low **tetrahydrocannabinol** (THC) concentrations (hemp) have recently been decriminalized according to the 2018 farm bill but farmers are still hesitant about its legality. To avert the risk and constant regulatory pressures due to potential THC contents, we aim to develop a compliant hemp variety using chemical mutagenesis. We selected ethyl methanesulfonate as the chemical mutagen and identified the LD50 doses for two hemp varieties. Hemp seeds were treated with the LD50 dosage of the mutagen to produce mutant M1 populations. The M1 plants displayed a wide array of mutant phenotypes and were tested for their trichome profiles. Selection of M1 plants was done based on mutant phenotypic traits and trichome production, followed by self-hybridizations to produce M2 seeds. The obtained lines are expected to be 100% compliant with all regulations. These promising lines present a new, versatile, and sustainable crop with applications in food, fiber, and construction industries, addressing the growing needs of the nation.

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