

2021
Dr. Donald L. Sparks & Dr. Bill Witt
Integrated Plant and Soil Sciences
Graduate Student Symposium



January 22, 2021

Zoom



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Symposium Sponsors

Dr. Donald L. Sparks

Current Position: S. Hallock du Pont Chair of Soil and Environmental Chemistry, Francis Alison Professor, and Chairperson, Department of Plant and Soil Sciences at the University of Delaware

Degrees:

- Ph.D. – Soil Science – Virginia Polytechnic Institute and State University Dissertation: Potassium Adsorption and Desorption Kinetics in a Soil System and Its Relation to Plant Uptake
- M.S. – Soil Science – University of Kentucky Thesis: Physical, Mineralogical, and Chemical Properties, Including Ammonium Distribution, in the Shrouds Soils of Kentucky
- B.S. – Agronomy – University of Kentucky

Dr. Sparks researches the environmental soil chemistry of contaminants such as As, Zn and Ni, and nutrients such as S and P. He investigates their binding to soil under varied environmental and biological conditions. He is known for his use of synchrotron-based X-ray spectroscopy to understand the molecular basis of contaminant and nutrient interactions with soil and his emphasis on kinetics. His research helps to predict the leaching of contaminants and nutrients into water supplies and subsequent bioavailability and toxicity to plants, animals, and humans. He is a Fellow of the American Society of Agronomy, the Soil Science Society of America, and the American Association for the Advancement of Science. He has served as President of the Soil Science Society of America and the International Union of Soil Sciences. Prof. Sparks is also Recipient of the 2007 - UK Department of Plant and Soil Sciences Graduate Program Distinguished Alumni Award.

Professor Emeritus Bill Witt, Department of Plant & Soil Sciences

Dr. Bill Witt received his Ph.D. in weed science from North Carolina State University. He was a faculty member in the Department of Plant and Soil Sciences at the University of Kentucky for 38 years, retiring in 2012. During those years, he dedicated much of his time to graduate student advising. He advised 40+ M.S. and Ph.D. graduate students, as well as serving on many other graduate student committees. He received the College's George Mitchell Award for Service to Graduate Education in 2002 and the Outstanding Teaching Award, the Distinguished Achievement Award in Education, and the Distinguished Service Award - Academia from the Weed Science Society of America, the North Central Weed Science Society, and the Southern Weed Science Society, respectively.

Acknowledgements

The graduate students extend their deepest gratitude to Professor Donald L. Sparks, Professor Emeritus Bill Witt, and the University of Kentucky Graduate School Block Grant program for providing the funding for this symposium. We would also like to thank our faculty and postdoctoral judges for their time and consideration: Dr. Dave Van Sanford, Dr. Ray Smith, Dr. Hanna Poffenbarger, Dr. Wei Ren, Dr. Travis Legleiter, Dr. Tim Phillips, Dr. Kritika Kothari, Dr. Yawen Huang, Dr. David Hildebrand, Dr. Steve McBride, Dr. Andy Bailey, Dr. Chris Shepard, Dr. Montse Salmeron, Dr. Ole Wendroth, Dr. Rebecca McCulley, and Dr. Jason Unrine.

**2021
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Friday, January 22, 2021**

9:00-9:15 am Welcome and opening remarks

Session I - Moderator: Jarad Cochran

Time	Presenter	Advisor
9:15-9:30 am	Virginia Verges	Dr. Van Sanford
9:30-9:45 am	Elzbieta Szuleta	Dr. Phillips
9:45-10:00 am	Amber Herman	Dr. Legleiter
10:00-10:15 am	Dan Quinn	Dr. C. Lee
10:15-10:30 am	Andrea Keeney	Dr. Bailey

10:30-10:45 am Break

Session II - Moderator: Kent Pham

Time	Presenter	Advisor
10:45-11:00 am	Rebecca McGrail	Dr. McNear
11:00-11:15 am	Brian Rinehart	Drs. Poffenbarger & McNear
11:15-11:30 am	Alayna Jacobs	Dr. McCulley
11:30-11:45 am	Sam Leuthold	Dr. Poffenbarger
11:45-12:00 pm	Jason Simmons	Dr. Ritchey

12:00-1:00 pm Lunch and virtual posters

Session III - Moderator: Ela Szuleta

Time	Presenter	Advisor
1:00-1:15 pm	Travis Banet	Dr. Poffenbarger
1:15-1:30 pm	MD Anik Mahmud	Dr. D'Angelo
1:30-1:45 pm	Jarad Cochran	Dr. Tsyusko
1:45-2:00 pm	Tim Shull	Dr. Smalle
2:00-2:15 pm	Jia Tan	Drs. Geneve & Rodriguez Lopez

2:15-2:30 pm Break

Session IV - Moderator: Amber Herman

Time	Presenter	Advisor
2:30-2:45 pm	Sanjay Joshi	Dr. Perry
2:45-3:00 pm	Mohammad Foteh Ali	Dr. Kawashima
3:00-3:15 pm	Lakshay Anand	Dr. Rodriguez Lopez
3:15-3:30 pm	Joshua James Singleton	Dr. Yuan
3:30-3:45 pm	Tajbir Raihan	Dr. Rodriguez Lopez

3:45-3:50 pm Closing remarks

Platform Presentations

Session I

Title: Genomic Selection for Fusarium Head Blight Resistance in wheat

Presenter: Virginia Verges, Ph.D. candidate

Advisor(s): Dr. Dave Van Sanford

Abstract

Genomic Selection (GS) is a form of marker-assisted selection (MAS) that simultaneously estimates all locus, haplotype or marker effects across the entire genome to calculate genomic estimated breeding values (GEBVs). In wheat, Fusarium head blight (FHB) resistance is a challenging breeding target due to the combination of quantitatively inherited resistance and a challenging phenotype that is not easy to reproduce artificially. GS could become an excellent tool to improve and accelerate breeding for FHB resistance. In a first study, we evaluated the effect of training population size (TP) and TP optimization method on prediction accuracy (PA) under cross validation and forward GS when predicting FHB traits in breeding lines belonging to the University of Kentucky wheat breeding program. We used data from the Uniform Northern and Uniform Southern Soft Red Winter Wheat Scab Nurseries (NUSN and SUSN respectively) to comprise the Training Population (TP). The selection candidates were a total of 306 lines evaluated in a FHB screening nursery, at Lexington, KY, in 2017. In a second study, we evaluated the effect of marker set size and TP size on PA, when predicting two scab traits, deoxynivalenol (DON) content and DSK, an index of DON, Fusarium damaged kernels, and FHB rating, under cross validation and forward GS schemes. The same TPs from the first study were used, and the selection candidates were a total of 306, 281 and 198 lines that were evaluated in 2017, 2018 and 2019 respectively at Lexington, KY. Results of both studies showed moderate (0.4-0.6) and consistent PA with cross validation and moderate PA (0.4-0.5) with some forward GS scenarios. This is promising news for breeders looking to make more efficient the breeding process reducing the breeding cycle (time) and phenotyping costs.

Presentation Type: Research Results

Title: Evaluation of Winter Rye (*Secale cereale* L.) for Adaptation to Kentucky

Presenter: Elzbieta Szuleta, Ph.D. student

Advisor(s): Dr. Tim Phillips

Abstract

Winter Rye (*Secale cereale* L.) is a grain crop well known for its outstanding tolerance to unfavorable weather and soil conditions. A sequence of historical events in the United States caused a decline in rye demand and decline in support for rye research, which resulted in very little work done on rye breeding over 50 years. At present, interest in this crop in the United States is increasing because of its wide range of possible uses (e.g., cover crop, feed for livestock, bread, cookies, distilling industry), pro-health properties and its unique flavor, impossible to replace by other grains. Unfortunately, rye production in the country is not high enough to meet the demand. In the 2019/2020 season United States imported 280 thousand metric tons of rye grain, which is over 58% of worldwide imported rye. To increase rye production in Kentucky, we need to encourage farmers by presenting them a high yielding rye variety that will suit Kentucky's environment and bring them benefits. We conducted a winter rye planting date experiment in two seasons (2018/2019 and 2019/2020) at two locations in Kentucky (Lexington and Adairville). Each season, we tested 24 winter rye varieties that were available in the US at 3 planting dates: early, middle, and late. The aims of this study were to 1) find a variety suitable for Kentucky's environment, 2) establish an optimal planting date of winter rye in Kentucky and provide this information to the growers, and 3) identify promising parents for rye breeding. In both locations and both growing seasons the best performing entries were European hybrids (Serafino, Daniello, Bono and Brasetto), and the best yielding population varieties were Hazlet and Dylan. The differences in yield between planting dates were statistically different both seasons. Different varieties performed better at different planting dates. In general, the 2018/2019 growing season showed that rye performed better when planted early, but in 2019/2020, a severe May freeze caused extensive damage in early planted rye, and the best planting date was the late one.

Presentation Type: Research Proposal

Title: Evaluation of Italian Ryegrass (*Lolium perenne* spp. multiflorum) Seed Retention and Distribution in Wheat at Harvest

Presenter: Amber Herman, M.S. student

Advisor(s): Dr. Travis Legleiter

Abstract

There is a growing concern over herbicide resistance in Italian ryegrass (*Lolium perenne* spp. multiflorum) in the state of Kentucky and new ways to control this weed in wheat are needed. One possible method of control is the use of a harvest weed seed destructor at wheat harvest to destroy *Lolium multiflorum* seed that is in the fine chaff portion of the harvest chaff. The *Lolium multiflorum* seed would have to be retained on the plant until wheat harvest for a harvest weed seed destructor to be effective. The seed retention and distribution of Italian ryegrass prior to wheat harvest and at the time of harvest were studied in Kentucky during the summer of 2020. Prior to harvest wheat heads, *Lolium multiflorum* seed heads, and the top layer of the soil debris was collected from within a m² area for each half acre *Lolium multiflorum* infestation in two Kentucky wheat fields. The wheat seed heads were collected for grain moisture analysis of the field. *Lolium multiflorum* seed heads and ground debris samples were cleaned and analyzed for total *Lolium multiflorum* seed each. At wheat harvest four one-acre plots were established in a *Lolium multiflorum* infested wheat field in Princeton, KY. Combine head shatter losses and chaff were collected in four 1m² areas within each 0.2 ha plot. A grain tank sample was also collected at the end of each plot. Samples were cleaned and analyzed for *Lolium multiflorum* seed counts per 1m². The results from the pre harvest collections showed that a majority of the seed was retained on the seed head with approximately 11,000 *Lolium multiflorum* seeds/m² retained on the seed heads at both the Young Road and UKREC fields. In comparison, approximately 2500 and 4000 *Lolium multiflorum* seed/m² were found to within the ground samples for the Young Road and UKREC fields, respectively. The at harvest study revealed that 7000 *Lolium multiflorum* seeds/m² were contained in the combine chaff and was significantly greater than the proportion of seeds shattered at the combine head at 4500 *Lolium multiflorum* seeds/m². Grain tank sample analysis revealed that 5000 *Lolium multiflorum* seeds/m² were contained in the grain tank and was equivalent to both the chaff and head shatter proportions. Overall results of this study show that *Lolium multiflorum* seed is primarily retained on the seed head up to wheat harvest and that the majority of *Lolium multiflorum* seeds are contained in the combine chaff at harvest. These results indicate that the harvest weed seed control is possibly a viable *Lolium multiflorum* control option in Kentucky wheat.

Presentation Type: Research Results

Title: Corn Response to In-Furrow Fertilizer and Fungicide across Rye Cover Crop Termination Timings

Presenter: Dan Quinn, Ph.D. candidate

Advisor(s): Dr. Chad Lee

Abstract

Farmers looking to maximize both soil conservation and ecosystem benefits of a rye cover crop (RCC) may choose to delay termination closer to corn planting. However, delaying RCC termination may reduce corn yield due to increased N immobilization and seedling disease potential. The objective of this trial was to evaluate corn growth and yield in response to in-furrow (IF) fertilizer and fungicide across different RCC termination timings. A six site-year trial was established at three locations in Kentucky in 2019 and 2020 to evaluate corn response to two RCC termination timings (21d before corn planting and 1d after corn planting) and three IF starter treatments (fertilizer, fungicide, and fertilizer + fungicide). A late-terminated RCC resulted in statistically greater ($P \leq 0.1$) shoot biomass, early-season (Apr – May) soil moisture, and preplant inorganic soil N compared to an early-terminated RCC. However, a late-terminated RCC reduced corn plant stand by an average of 31% at two of three locations and reduced corn grain yield by an average of 15.7% across all three locations. In addition, the inclusion of IF fertilizer, fungicide, or fertilizer + fungicide did not improve corn grain yield in any site-year and no interaction between RCC termination timing and IF starter application was observed. Overall, our results suggest IF fertilizer and/or fungicide application does not ameliorate corn stand loss and yield reductions following a late-terminated RCC. In addition, farmers should look to terminate a RCC earlier (14 – 21d before planting) to reduce potential corn stand and yield loss.

Presentation Type: Research Results

Title: 2020 Angular Leaf Spot Observational and Field Studies

Presenter: Andrea Keeney, Ph.D. student

Advisor(s): Dr. Andy Bailey

Abstract

Pseudomonas syringae pv. *tabaci* is the causal agent of Angular Leaf Spot (ALS) in dark tobacco. ALS is the most prevalent foliar disease in dark tobacco production to date. Streptomycin is an antibiotic bactericide and the standard control used by dark tobacco producers to combat this bacterial disease. This research project evaluates direct and plant-mediated inhibitory effects of fifteen different antibiotic, biocontrol and/or synthetic bactericide products. Products tested are either labeled or have the potential to be labeled for dark tobacco. Field trials have been ongoing since 2015 at the University of Kentucky Research and Education Center in Princeton, KY and at Murray State University in Murray, KY. Since 2016, there has been multiple cases of resistance to Streptomycin documented.

A monitoring project was established in 2020 that includes 30 grower fields to observe different growing and management practices being applied by dark tobacco growers that may influence angular leafspot incidence and severity. Seventeen variables are being investigated in this monitoring study from greenhouse management to harvest. Out of 30 fields monitored, there were four fields that presented with ALS symptoms. Tissues samples were taken from these four fields and screened to be sure *P. syringae* pv. *tabaci* was present and then were screened for resistance to Streptomycin and copper. One of the four samples screened had resistance to Streptomycin.

Presentation Type: Research Proposal

Session II

Title: Biochemical and Physical Root Phenotyping as a Predictor of Phosphorus Extraction Potential

Presenter: Rebecca McGrail, Ph.D. candidate

Advisor(s): Dr. Dave McNear

Abstract

The Green Revolution directly improved crop yields through inorganic fertilizer availability, pesticide and herbicide applications, irrigation, improved plant varieties for disease/pest pressures, and adoption of semi-dwarf grains. Global wheat yields increased 209% following the adoption of semi-dwarf cultivars with inorganic fertilizer applications. However, the impact of the Green Revolution on both the physical and biochemical phenotypes of roots has not been evaluated. This study characterized organic acid profiles and root system architecture of a diverse panel of winter wheat cultivars. Cultivars evaluated included six wild-types and four semi-dwarf cultivars ranging from 1808 to 2002. Root tip citric, malic, and oxalic acid concentrations were determined by HPLC following 24 days of growth in P-sufficient or P-deficient media. Cultivars were also grown in P-deficient agar and imaged across 20 days of growth via light tomography to evaluate root system architecture traits including maximum number of roots and network length, width, volume, and surface area. Under P-sufficient conditions both wild type and semi-dwarf cultivars primarily produced citric acid, but under P-deficient conditions oxalic acid was the primary organic acid produced. Further, semi-dwarf cultivar root tips contained half the concentration of acids as wild-type plants suggesting an impact of semi-dwarfism on P-acquisition. Differences in root system architecture parameters were best explained by breeding era rather than dwarfing status. These results suggest modern fertility practices and breeding have resulted in both physical and biochemical changes to roots. A pot study was additionally conducted to verify the P extraction potentials predicted by these results.

Presentation Type: Research Results

Title: Long-term Selection has Altered Maize Root Traits Relevant to Soil Carbon Storage

Presenter: Brian Rinehart, M.S. student

Advisor(s): Dr. Hanna Poffenbarger and Dr. Dave McNear

Abstract

Maize breeding has historically focused on selection for aboveground traits, with little attention to any resultant changes in belowground traits. Recent work has shown that belowground carbon inputs contribute more to the formation of soil organic carbon than aboveground inputs. In particular, deep root systems with high root length density and branching intensity promote efficient carbon stabilization through aggregation and mineral association. The aim of this research was to assess breeding-driven changes in root traits that are relevant to soil carbon storage. We grew twelve hybrids, three from each of four breeding eras spanning 1936 – 2014, in a replicated greenhouse study. The plants were terminated after 28 days of growth and roots were separated from aboveground biomass and washed. Roots were imaged at high resolution and analyzed for architectural and morphological traits by depth. Preliminary results show that the earlier hybrids had greater below-ground mass, greater total root length, and a potentially deeper and more even distribution of mass and length at depth. These findings suggest a difference in both total carbon deposition via the roots and the distribution of that carbon in the soil profile.

Presentation Type: Research Results

Title: Feed supplementation with natural red clover product decreases ammonia emissions from soil-applied livestock waste

Presenter: Alayna Jacobs, Ph.D. candidate

Advisor(s): Dr. Rebecca McCulley

Abstract

Worldwide meat consumption is projected to increase dramatically, posing challenges to increase livestock production efficiency and limit adverse environmental effects from animal waste. Ruminant livestock production is the largest contributor of greenhouse gases within the food production sector. Agriculture is responsible for large amounts of atmospheric ammonia emissions, which form fine particles detrimental to air quality. Recent work shows that livestock feed supplementation with biochanin A (BCA), a naturally produced isoflavone compound present in red clover (*Trifolium pratense* [L.]) leaves, increases animal weight gains by improving protein digestibility via alteration of the rumen microbial community. Despite production benefits, the overall environmental implications of BCA supplementation have not been evaluated, including how animal waste affects soil trace gas emissions. This study compared trace gas emissions from soils amended with urine from lambs fed no BCA and lambs fed BCA at two dosages (0.45 and 0.90 g day⁻¹). In laboratory mesocosms, ammonia emissions from soil amended with urine from lambs fed 0.90 g BCA per day were significantly lower than soils amended with urine from lambs fed no BCA for the first seven days of incubation (0.469 vs 0.324 mg ammonia m⁻³ day⁻¹, respectively). Carbon dioxide, methane, and nitrous oxide emissions were not affected by BCA feed supplementation. This study demonstrated that BCA supplementation decreased short-term ammonia losses from livestock urine deposition on soils, suggesting that natural plant products may be helpful in minimizing negative environmental consequences and maximizing production efficiency in the more intensive livestock production systems of the future.

Presentation Type: Research Results

Title: Effects of topographic heterogeneity on cover crop decomposition rates and soil microclimate

Presenter: Sam Leuthold, M.S. student

Advisor(s): Dr. Hanna Poffenbarger

Abstract

Rolling hill style terrain is common in agricultural land throughout the Southeastern United States. In such landscapes, downslope movement of soil, nutrients, and water can lead to nutrient use inefficiencies, soil degradation, and inconsistent yields from year to year. Integrating a cover crop into these systems can reduce erosion and mitigate nutrient losses, while potentially providing a source of nitrogen to the cash crop as the cover crop residue decomposes. However, it is unknown how topographic heterogeneity affects the rate of cover crop biomass decomposition and nitrogen release across a given field. Here we present the results of a two-year litterbag study in Central Kentucky where we evaluated the effect of landscape position (summit, backslope, and toeslope) on soil microclimatic variables (i.e., soil moisture and soil temperature), as well as the decomposition rate of two cover crop treatments: a cereal rye (*Secale cereale* L.) monoculture, and a cereal rye/crimson clover (*Trifolium incarnatum*) mixture. In the cereal rye treatment, soils were wetter and cooler on the toeslope and decomposition proceeded more quickly than on the backslope or summit. In the mixture treatment, the effect of landscape position on microclimatic variables was smaller than in the rye, and the decomposition rate was more consistent across landscape positions. These results show that cover crop benefits vary in magnitude across areas of complex terrain and that decay of cover crop mixtures may be less sensitive to topography than that of monocultures.

Presentation Type: Research Results

Title: Lateral Spacing of Subsurface Poultry Litter Bands - Impact on Gaseous Nitrogen Emissions

Presenter: Jason Simmons, Ph.D. candidate

Advisor(s): Dr. Edwin Ritchey

Abstract

A new application method was developed for banding poultry litter (PL) below the soil surface with minimal soil disturbance to reduce ammonia (NH₃) volatilization. There is limited knowledge on how this application method will impact nitrous oxide (N₂O) emissions. The objective of this study was to determine if adjusting PL lateral subsurface band placement in relation to corn rows can affect N₂O and NH₃ emissions. A two-year field experiment was initiated May 2014 with six treatments that consisted of an untreated control (UTC), 32% urea ammonium nitrate surface banded (Fert), PL surface broadcast (PLBr), and 3 subsurface banded PL treatments. The subsurface PL treatments were 1 (PLSub1), 2 (PLSub2), or 3 (PLSub3) lateral bands in the inter-corn row area. Treatments receiving N amendments were applied at the rate of 180 kg total N ha⁻¹ each spring prior to corn planting. Nitrous oxide emission results varied for each growing season and pulses of N₂O coincided with rainfall events larger than 1-cm. Subsurface banding of PL resulted in significantly lower ($P < 0.1$) N₂O emissions compared to PLBr in 2014. That same trend continued in 2015 with the PLSub2 treatment. Placing PL under the soil surface significantly reduced NH₃ volatilization compared to PLBr and Fert in 2014 and 2015. The lateral spacing of PL did not influence NH₃ volatilization among PLSub treatments. These results suggest that subsurface banding PL conserves N by reducing N₂O and NH₃ losses compared to traditional surface broadcast PL in no-till corn.

Presentation Type: Research Results

Session III

Title: Management Practices and Environmental Factors Affect Soil Retention of Corn-Derived Carbon

Presenter: Travis Banet, Ph.D. student

Advisor(s): Dr. Hanna Poffenbarger

Abstract

Understanding the efficiency with which crop carbon inputs are retained in soil can help make decisions to optimize cropland sustainability. However, the proportion of soil carbon inputs that are recovered as soil organic carbon is dependent upon numerous factors such as climate, soil texture, and management strategies. The complexity of residue C retention is reflected in research conducted over the last 30 years which shows that a wide range of corn-derived carbon inputs are retained in soil (0% – 58%) and that the percentage of total soil organic carbon derived from crop inputs can vary drastically (0% – 74%). Data was extracted from literature that used the natural ^{13}C abundance method to quantify the inputs of corn root and residue carbon into soil while managed in continuous corn monoculture. Extracted data was analyzed using a combination of linear and nonlinear regressions as well meta-analysis techniques. Converting native systems to a continuous corn crop resulted in a rapid loss of ~24% total SOC. Furthermore, corn-derived carbon accumulated in the total SOC pool at a rate of approximately 2% annually as indicated by non-linear regression. Applying meta-analysis techniques showed that the different strategies implemented for tillage, nitrogen fertilization, and crop residue management do not significantly influence the retention efficiency of corn-derived carbon, nor the proportion of the total SOC pool that is corn-derived. Finally, a trend was observed in which greater quantities of SOC were retained in fine textured soils and in pedogenically immature soils.

Presentation Type: Research Results

Title: Selenium removal and pollution swapping potential of passive anaerobic bioreactors receiving coal slurry impoundment wastes

Presenter: MD Anik Mahmud, M.S. student

Advisor(s): Dr. Elisa D'Angelo

Abstract

Worldwide, selenium is a major contaminant of concern for coal and metal ore mining industries. In the eastern USA, for example, billions of liters of wastewaters with elevated Se oxyanion concentrations are generated during coal washing, which is often stored in >700 man-made impoundments built into remote mountain valleys. Unlined impoundments tend to leak contents into nearby streams, which has detrimental effects on sensitive biota like fish. The goals of this project were to evaluate the capacity of passive anaerobic bioreactors (PAB) (i) to remove Se from coal slurry leachate and (ii) not to contribute other pollutants (e.g., nutrients, trace elements, greenhouse gases) to the surrounding environment ("pollution swapping"). Selenate removal and pollution swapping were evaluated in PAB filled with biofuel plant substrates (hardwood chips, switchgrass, miscanthus, and timothy hay) in triplicate laboratory batch reactors fed synthetic coal slurry over 7 months. PAB water and headspace gases were sampled with time and analyzed for pH, Eh, Se and trace elements, nutrients, and dissolved organic C, CO₂, CH₄, and N₂O. Pollutant concentrations were compared with pristine streams to calculate Canadian Water Quality Indices (CWQI). In all but wood chip PAB, rapid DOC increase prompted bacterial activity, rapid Eh decrease, rapid denitrification and selenate reduction. In wood chip PAB, extremely low pH (<4.5) strongly inhibited selenate reduction and final denitrification step, which resulted in high concentrations of dissolved selenate and N₂O in effluents. Miscanthus is preferred over other substrates due to significantly higher Se removal rates and CWQI values in PAB systems.

Presentation Type: Research Results

Title: Application of iron oxide nanoparticles against infections induced by drug-resistant pathogens

Presenter: Jarad Cochran, Ph.D. student

Advisor(s): Dr. Olga Tsyusko

Abstract

The occurrence of pharmaceutical antimicrobials in ecosystems is one of the largest issues in environmental pollution. These pharmaceuticals are released into the environment through several routes, including sewage waste, agriculture runoff, and the application of biosolids as fertilizer. Once released, antimicrobials and their residuals may lead to adverse effects in the environment, such as promoting the growth of antimicrobial resistant (AMR) pathogens and degrading soil health. To decrease pharmaceutical antimicrobials in the environment and to reduce AMR pathogens in agricultural settings, new sources of effective and environmentally safe antimicrobials are needed. The purpose of this project is to test the application of alternative treatments such as iron oxide nanoparticles (IONP), which can be naturally found in soils, against AMR *Klebsiella pneumoniae* and *Staphylococcus aureus*, the causative agents of mastitis in dairy cattle. To assess efficacy of IONP and their potential unintended toxic effects, this project will utilize a soil nematode *Caenorhabditis elegans*. This model organism is frequently used to screen for anti-infective compounds against AMR pathogens and toxicity of nanoparticles. Results so far show that IONP have a low toxicity to *C. elegans*, indicating their low environmental impact compared with other more toxic antimicrobials. To assess anti-infective properties of IONP, *C. elegans* infected with *K. pneumoniae* or *S. aureus* will be exposed to IONP in future work.

Presentation Type: Research Proposal

Title: In Search of Dopamine's Significance in Higher Plants

Presenter: Tim Shull, Ph.D. candidate

Advisor(s): Dr. Jan Smalle

Abstract

The widespread presence and physiological activity of the neurotransmitter dopamine in higher plants has intrigued plant biologists for years, with several studies describing the impact of dopamine on plant growth and development. Nonetheless, the underlying molecular mechanisms of dopamine-induced growth responses remain poorly defined. In order to uncover these mechanisms, I am employing a forward genetic screen in the model plant *Arabidopsis thaliana* to identify single nucleotide polymorphisms which impart resistance to the growth-inhibiting effects of dopamine. Traditionally, identifying a polymorphism that confers dopamine resistance would require extensive experimentation using markers to identify genomic regions linked to dopamine resistance. However, the rapid advancement of genomic sequencing technology has given rise to techniques that allow the identification of causal mutations through the sequencing of pooled segregating populations, in which the ratios of polymorphisms are used as markers to identify genomic regions linked to the mutation and as well as the mutation itself. I will attempt to use this technology to expedite the identification of polymorphisms which confer dopamine resistance, which will provide valuable information about the physiological significance of dopamine in higher plants. My presentation will briefly cover the impact of dopamine on plant growth and development in *Arabidopsis*, an introduction to bulked segregant sequencing and my progress in gathering *Arabidopsis* plant lines resistant to dopamine.

Presentation Type: Research Results

Title: Differentially Expressed Genes in Grapevine Associated with Epigenetic Changes Identified after Combined Drought and Heat Stress Removal

Presenter: Jia Tan, Ph.D. candidate

Advisor(s): Dr. Robert Geneve and Dr. Carlos Rodriguez Lopez

Abstract

Grapevine cultivar *V. vinifera*. L. cv. Cabernet Sauvignon is widely used for winemaking all over the world. Drought and heat stresses are two of the major abiotic stresses that reduce grape quality and yield. Drought and heat tolerance are poorly characterized in perennial crops such as grapevine. In this study, RNA-sequencing analysis of leaf tissues of Cabernet Sauvignon plants under drought, heat, and combined stress was carried out. Physiological responses such as the stomatal conductance, stem water potential and leaf temperature were also measured. Physiological data suggested a significant difference in stomatal conductance, leaf temperature and stem water potential during stress, where no significant difference was observed during recovery. Data analysis with the criteria of a fold change ≥ 2 and a Padj value < 0.05 resulted in the identification of a total of 533, 112, and 1117 differentially expressed genes (DEGs) for drought, heat, and combined stress, respectively. The combined stress resulted in significantly more differentially expressed genes than individual stress. Gene Ontology (GO) analysis revealed DEGs that are associated with epigenetic changes after stress removal, such as histone modification, protein methylation, and protein alkylation. Alteration of the expression of those epigenetic changes-related genes suggests the potential establishment of epigenetic memory after stress removal.

Presentation Type: Research Results

Session IV

Title: The Role of the Transcription Factor LBD40 in Arabidopsis Embryogenesis

Presenter: Sanjay Joshi, Ph.D. candidate

Advisor(s): Dr. Sharyn Perry

Abstract

Somatic Embryogenesis (SE) is a process by which an embryo is derived from a single somatic cell or group of somatic cells that is regulated by key transcription factors (TF), including AGAMOUS-like 15 (AGL15). SE is a valuable means to generate transgenic plants to meet food demands or test gene function but is poorly understood. One of the intriguing proteins with which AGL15 interacts in yeast 2-hybrid assays is LBD40. LBD40 encodes a LATERAL ORGAN BOUNDARIES (LOB)-domain TF that is unique to plants, is specifically expressed during seed development, and has a role in supporting SE. In planta protein interaction of AGL15 and LBD40 has now been documented using co-immunoprecipitation. Siliques and SE tissue with epitope-tagged transgenes were used for Chromatin-Immunoprecipitation (ChIP) that allows one to determine where TFs bind to DNA in vivo, a step necessary to understanding genes directly controlled by a TF. More than four hundred binding regions for LBD40 were found genome-wide in three biological replications of ChIP-sequencing. RNA-seq results of 7-8 days old seeds from a *lbd40/41* mutant line compared to wild type seeds showed genes as significantly expressed and repressed targets. More than seven hundred genes had increased RNA (785 genes) in the mutant, while 2086 genes were downregulated (decreased RNA accumulation) in the mutant line compared to wild type. The Gene Ontology (GO) enrichment analysis of these regulated genes showed overrepresentation of biological processes that are associated with SE, further indicating the importance of LBD40 in SE.

Presentation Type: Research Results

Title: Seed size matters: Understanding the cellular and molecular mechanisms of coenocyte endosperm that control the seed size in *Arabidopsis thaliana*.

Presenter: Mohammad Foteh Ali, Ph.D. candidate

Advisor(s): Dr. Tomo Kawashima

Abstract

In flowering plants including *Arabidopsis thaliana*, the seed is generated by double fertilization, where the pollen tube contains two sperm cells, one fertilizes the egg cell in the ovule to generate the diploid embryo and the other one fertilizes the homodiploid central cell to generate the triploid endosperm. The endosperm serves as a nourishing tissue for the embryo development. Endosperm development mainly consists of four phases: coenocyte, differentiation, cellularization, and cell death. During the coenocytic phase, the endosperm enlarges rapidly, and endosperm nuclei keep dividing without cytokinesis. After 10th nuclear division, this one large coenocytic endosperm cell then undergoes cellularization. The duration of the coenocytic phase is linked with the final seed size; however, the detailed molecular and cellular mechanisms of the coenocytic phase of endosperm development are largely unknown. Using confocal microscopy live-cell imaging with a combination of genetic approaches, we identified the dynamics of the coenocytic phase of endosperm development in *Arabidopsis thaliana*. We identified that the filamentous actin (F-actin) in the coenocytic endosperm is uniquely structured, and controls nuclear movement. Our preliminary results indicate that when the F-actin structure is disrupted in the coenocytic endosperm, the size of coenocytic endosperm and final seed size decreases. By contrast, stabilization of F-actin increases the size of coenocytic endosperm and final seed size. Further investigation of cellular changes in these F-actin manipulated coenocytic endosperms is underway. Our results provide a new insight into understanding the role of the F-actin cytoskeleton during coenocytic endosperm development, which determines the final seed size.

Presentation Type: Research Results

Title: chromoMap: An R tool for interactive genomic visualization of multi-omics data

Presenter: Lakshay Anand, Ph.D. student

Advisor(s): Dr. Carlos Rodriguez Lopez

Abstract

chromoMap is an R package for constructing interactive visualizations of chromosomes/chromosomal regions, and mapping of any chromosomal feature with known coordinates (i.e. protein coding genes, transposable elements, non-coding RNAs, microsatellites, etc.) and regional characteristics (i.e. genomic feature density, gene expression, DNA methylation, Chromatin modifications, etc.) of organism with an genome assembly. ChromoMap can also integrate multi-omic data (genomics, transcriptomics and epigenomics) in relation to their occurrence across chromosomes. ChromoMap's flexibility allows for concurrent visualization of genomic data in each strand of a given chromosome, or of more than one homologous chromosome; allowing the comparison of multi-omic data between genotypes (e.g. species, varieties, etc.) or between homologous chromosomes of phased diploid/polyploid genomes. ChromoMap takes tab-delimited files (BED like) to specify the genomic co-ordinates of the chromosomes and elements to annotate. Rendered chromosomes are composed of continuous loci of specific ranges, which, on hover, display detailed information about the elements annotated within that locus range. By adjusting parameters on a single function, users can generate a variety of plots that can either be saved as static image or as HTML documents. ChromoMap's can be used to visualize polyploidy, create chromosome heatmaps, map groups of elements, add hyperlinks to elements, multi-species chromosome visualization. Here I will showcase chromoMap functionalities using examples from recent literature that have used this package.

Presentation Type: Research Results

Title: Transcription Factor bHLH92 Affects Monoterpenoid Indole Alkaloid Biosynthesis Possibly via Protein-protein Interaction in *Catharanthus Roseus*

Presenter: Joshua James Singleton, Ph.D. student

Advisor(s): Dr. Ling Yuan

Abstract

The medicinal plant, *Catharanthus roseus* produces pharmaceutically valuable monoterpenoid indole alkaloids (MIAs), such as the anticancer drugs Vinblastine and Vincristine. The low yield of these complex molecules in *C. roseus* results in high production costs. Metabolic engineering strategies have been hindered by our limited understanding of the regulation of MIA biosynthetic pathway. MIA biosynthetic pathway is known to be regulated by two classes of jasomonte (JA)-responsive bHLH transcription factor (TF), CrMYC2 (subgroup IIIe) and BIS1/BIS2/BIS3 (subgroup IVa). However, overexpression of these TFs does not lead to substantial increased MIA accumulation. In silico analysis revealed that the bHLH TF binding sites (G/E-box) are prevalently present in the promoters of MIA pathway genes. We thus speculated the involvement of novel bHLH activators in regulating the MIA genes. Through co-expression analysis we identified a previously uncharacterized bHLH TF, bHLH92 (subgroup II) which co-expresses with CrMYC2 and MIA pathway genes. Transient overexpression of bHLH92 in *C. roseus* upregulated MIA pathway genes. In Arabidopsis, subgroup II bHLH TFs commonly interact with subgroup III bHLH TFs to promote nuclear localization and subsequently activate target genes. We thus hypothesized that a subgroup III bHLH TF acts in combination with bHLH92. We subsequently identified a *C. roseus* subgroup III bHLH TF, a homolog of the Arabidopsis DYSFUNCTIONAL TAPETUM 1 (AtDYT1), which co-expresses with the MIA genes. My ongoing efforts focus on the characterization of bHLH92 and its possible combinatorial regulation with DYT1 to regulate MIA pathway genes. In Arabidopsis, AtDYT1 is not known for the involvement in specialized metabolism. Our work suggests that *C. roseus* has evolved the co-regulatory mechanism of subgroup II-III bHLH TFs for the biosynthesis of specialized metabolites.

Presentation Type: Research Proposal

Title: Heritable DNA demethylation increases phenotypic variability in soybean.

Presenter: Tajbir Raihan, Ph.D. student

Advisor(s): Dr. Carlos Rodriguez Lopez

Abstract

Organism epigenetic variability (epiallelic variation) incorporates an array of mechanisms capable of altering the phenotype without changing the underlying DNA sequence. Plants naturally exhibit variation in gene methylation which affects their expression level. It has been proposed that this natural variability can be enhanced, in an analogous form to genetic mutation breeding, by chemically treating plants to induce global methylation changes, in order to generate new phenotypes that can be used for crop improvement. We created a hypomethylated soybean population by chemically treating germinating soybean seeds with five different concentrations (Control, 0.01mM, 0.1mM, 0.5mM, 1.0 mM, 1.5mM) of the DNA demethylating agent, 5-azacytidine. DNA demethylation followed a sigmoidal response to 5-azacytidine dosage. Analysis of phenotypic variability of important agronomic traits (e.g. germination time, emergence, plant height, mass, canopy area, flowering time, seed number, seed nutrient) indicate that the epialleles are generated in a stochastic manner, analogous to that observed in genetically mutagenized populations. 300 seeds collected from this epimutant population were then planted to determine if 5-azacytidine induced epigenetic and phenotypic variability is maintained in subsequent generations. Similar stochastic demethylation and random phenotypic diversity in second generation too but in comparatively smaller proportion. This stochastically hypomethylated population will be a powerful tool for plant improvement via the generation of transgenerationally stable variability and for the identification of loci controlling traits of interest.

Presentation Type: Research Results

Poster Session

Title: Compete Nitrogen Mass Balance Dynamics for Poultry Litter in a Continuous Corn Rotation

Presenter: Stacy Antle, Ph.D. student

Advisor(s): Dr. Edwin Ritchey

Abstract

Cost effective and agronomically optimum nitrogen (N) rates can be established by knowing the N use efficiency (NUE), defined as the portion of applied N that is utilized by the plant. Knowing NUE for organic and/or inorganic N will help a producer apply the proper amount of N. Mass balance of N can be determined by investigating source uptake and loss to establish a more efficient NUE. Nitrogen can rapidly increase as organic forms mineralize to ammonium and then nitrify to nitrate, which are available to the plant. It is assumed a portion of organic N becomes available for plant uptake during the first growing season can be as much as 50%. Nitrogen availability with organic fertilizer sources, such as poultry litter (PL), can vary due to manure type, application method, environmental conditions, and application rate. Previous studies have shown that N availability from PL is limited due to mineralization in the soil where it is converted to ammonium and nitrate (plant available forms), or immobilized where plants can't utilize and will become unavailable. Nitrate-N can be leached into groundwater or denitrify and enter the atmosphere as a greenhouse gas. A field study will investigate plant uptake and the overall mass balance of nitrogen to determine the fate of the applied N. Knowing the fate and factors that contribute to N transformations of PL may provide insight to management practices that improve the NUE and lead to more cost-effective use of PL

Presentation Type: Research Proposal

Title: The Use of Digital Camera Imagery to Assess Cool- and Warm-Season Grass Ratios in Pastures

Presenter: Jordyn Bush, M.S. student

Advisor(s): Dr. Chris Teutsch

Abstract

Remote sensing has been used in agriculture to assess agronomic attributes in row crops, and may be useful for making management decisions in forage production. As climate change pushes temperatures upward, potential exists for warm season (C4) grasses that thrive in warmer conditions to encroach into pastures that have been planted into perennial cool season (C3) grasses. Remote sensing technology may be able to detect the ratio of warm and cool season grasses, which display a color dynamic at different times of the year due to alternate periods of seasonal dormancy and the concomitant loss of green color. The objective of this study was to analyze digital camera imagery of test plots with known percentages of dead (brown) and alive (green) forage to simulate a pasture with cool and warm season grasses. Strips were sprayed in paddocks with non-selective herbicide at 25, 50, and 75% of the total area. Thirty digital images were captured over each paddock in a random pattern and then analyzed using the Canopeo application (OSU, Stillwater, OK) to determine total green canopy cover percentage of each image, which was then averaged to calculate the green canopy cover percentage in each paddock. Equations for correlations on two separate test dates were $y=0.0488+0.7497x$ and $y=0.1749+0.6165x$, both having $p<0.001$. $R^2=0.9877$ and 0.9559 respectively. Future applications of this method includes detecting and monitoring warm season grass encroachment in temperate pastures in the transition zone and modifying management recommendations for producers experiencing changes in botanical composition.

Presentation Type: Research Results

Title: Optical Sorter-Based Line Selection Lowers Deoxynivalenol in Soft Red Winter Wheat

Presenter: W. Jesse Carmack, Ph.D. candidate

Advisor(s): Dr. Dave Van Sanford

Abstract

Fusarium head blight (FHB) of wheat (*Triticum aestivum* L.) results in discolored fusarium damaged kernels (FDK) contaminated with deoxynivalenol (DON). DON accumulation, a primary measure of FHB resistance, can be used as a basis for selection, but testing each genotype in several genetically variable populations is expensive and time consuming. Therefore, FHB resistance breeding decisions are routinely based on in-field phenotypic evaluation. However, using an optical sorter as an alternative to in-field evaluation, selection for FHB resistance can be quickly performed post-harvest. The objective of this study was to utilize an optical seed sorter to select breeding lines with enhanced FHB resistance (lower DON accumulation in harvested grain). Applying the basic understanding that FHB often results in discolored grain, we developed an optical sorter-based direct selection strategy that effectively lowered DON accumulation in soft red winter wheat. F4 derived breeding lines were grown in an inoculated disease nursery over several years in Lexington, KY. Grain from each breeding line was sorted using an optical seed sorter calibrated to reject scabby (discolored) seed. The accepted (non-scabby) seed was used to plant subsequent generations. DON accumulation was lowered each cycle of among line selection with the optical sorter. Our findings suggest that optically sorting grain may be an effective breeding strategy for lowering DON accumulation associated with FHB.

Presentation Type: Research Results

Title: Kentucky Wheat Breeding Lines: Identifying Their Aroma, Flavor and Dough Functionality to Source Local Artisan Bakeries

Presenter: Maria Paula Castellari, M.S. student

Advisor(s): Dr. Dave Van Sanford

Abstract

Soft Red Winter (SRW) wheat is grown on almost 400,000 acres in Kentucky and sold to millers as an agricultural commodity. An interest in identifying value added markets for Kentucky wheat, such as artisan-baked goods is growing rapidly. To know if we can breed wheat that produces good flour for these markets, two things that must be done: 1) assess variation in wheat varietal flavor and aroma profiles and gluten strength; 2) determine the heritability of these traits or characteristics. These are the objectives of this research. For this purpose, approximately 220 adapted SRW wheat breeding lines and cultivars from the University of Kentucky breeding program will be evaluated for flavor, aroma, and dough functionality using a sensory panel method. First, the aroma of a porridge-like preparation will be evaluated; those entries with favorable ratings will move to the baking and dough functionality screen. A sensory evaluation of the baked bread will be performed to assess the flavor and aroma characteristics. Protein content and kernel hardness will be measured with a Near Infrared (NIR) Spectroscopy and gluten strength will be estimated through the Wheat Meal SDS Sedimentation Volume Test and loaf volume. The ultimate measure of success will be identifying breeding lines that have desirable flavor, aroma, and dough properties in combination with superior agronomic traits and the capacity to be grown in Kentucky and sold to local artisan millers and bakers.

Presentation Type: Research Proposal

Title: Novel Function of Myosin XI_G in Gamete Nuclear Migration during Fertilization in Arabidopsis

Presenter: Umma Fatema, Ph.D. candidate

Advisor(s): Dr. Tomo Kawashima

Abstract

Abstract Fertilization is the process of fusion of male and female gametes to develop a new individual. In most animals, microtubules drive the migration of the female pronucleus toward the male pronucleus for fertilization. By contrast, the fertilization process in flowering plants is dependent on actin filament (F-actin) dynamics; F-actin, not microtubules, is responsible for sperm nuclear migration (Kawashima et al., 2014). The molecular and cellular mechanisms by which flowering plants utilize F-actin for fertilization are largely unknown. Using the pharmacological and genetic approaches with the combination of live-cell confocal imaging, we have identified the involvement of the class XI myosin, XI-G, in the active movement of F-actin essential for sperm nuclear migration (Ali et al., 2020). The primary function of plant class XI myosins is a cargo transporter along F-actin, and we discover a non-canonical function of XI-G that can generate forces for the dynamic whole cell-level movement of F-actin for fertilization. I am further investigating the mechanism of how XI-G plays its role in the unique F-actin dynamics in the female gamete cell. Knowledge from this project will shed light on our profound understanding of fertilization and cytoskeleton usage in flowering plants. References: Ali, M.F., Fatema, U., Peng, X., Hacker, S.W., Maruyama, D., Sun, M.-X., Kawashima, T., 2020. ARP2/3-independent WAVE/SCAR pathway and class XI myosin control sperm nuclear migration in flowering plants. Proc. Natl. Acad. Sci. <https://doi.org/10.1073/pnas.2015550117> Kawashima, T., Maruyama, D., Shagirov, M., Li, J., Hamamura, Y., Yelagandula, R., Toyama, Y., Berger, F., 2014. Dynamic F-actin movement is essential for fertilization in Arabidopsis thaliana. eLife 3, e04501. <https://doi.org/10.7554/eLife.04501>

Presentation Type: Research Results

Title: Evaluating Growing Degree-Days as a Predictor for Cool-Season Crop Growth

Presenter: Chelsea Maupin, M.S. student

Advisor(s): Dr. Krista Jacobsen

Abstract

Crop planning tools based on growing degree-day (GDD) modeling can aid winter greens producers in central Kentucky to optimize their production systems through crop planning which is based on daily temperature rather than calendar days. However, existing temperature-based crop planning tools need improvement because the models do not consider how wintertime low-light conditions may affect model performance. The purpose of this research is to elucidate how well GDD modeling approaches can predict crop growth during winter and identify areas of poor model fit where additional environmental factors may need to be considered. The results of this research will inform the future development of decision tools to aid producers in crop scheduling to achieve marketing goals. Three model crops utilized in the UK Salad Bar program, a local food procurement effort by UK Dining, have been selected for this project. These include lettuce ('Salanova Red Sweet Crisp,' 'Salanova Green Sweet Crisp,' 'Salanova Red Incised,' and 'Salanova Green Incised'), spinach ('Corvair') and carrot ('Yaya'). GDD models are based on crop growth stage collected via non-destructive sampling methods which document vegetative and root growth appropriate to the crop and market stage (e.g. leaf count and root diameter). Preliminary data collection to inform model development are from three planting successions on the University of Kentucky Horticulture Research Farm and three participating cooperator farms in central Kentucky (Fayette Co., Woodford Co., and Scott Co.). Preliminary GDD regression data indicate reasonable model fit ($R^2 > 0.67$) during months when light is not limiting, with poorer model fit at later planting dates. A minimum of two additional seasons of data, as well as exploring higher-resolution methods of calculating GDD, will improve model fit and guide additional research efforts.

Presentation Type: Research Proposal

Title: Characterizing Karst Toposequences in Kentucky's Inner Bluegrass

Presenter: Annie McGraw, M.S. student

Advisor(s): Dr. Chris Shepard

Abstract

The Bluegrass physiographic region of Kentucky is underlain by the late Ordovician Lexington Limestone formation. This area has many identifiable karst features, including sinkholes. Karst sinkholes and associated soils coevolve, which may influence the storage of carbon across karst landscapes. Two sinkholes on the University of Kentucky's C. Oran Little Animal Research Center in Woodford County, central Kentucky, were selected for analysis. A total of nine pedons between the two sites were described, sampled, and analyzed for various physical, chemical, and mineralogical properties. As a general trend, measured total carbon levels decrease with sampling depth, and at most sampling depths, the toeslope and footslope positions have higher carbon stocks as compared to other positions. Differences in parameters measures like total carbon and metal concentrations could be linked to the physical properties that can then be compared across sites and hillslope positions. Discrepancies in carbon trends between sinkholes could be a result of differences in amounts of mineral associated- versus particulate organic matter. Pairing carbon data with soil physical, chemical, and mineralogical data will give us a better understanding of how these variables interact in karst systems as they evolve. Globally, soils hold about 80% of terrestrial C which means understanding the properties that control C sequestration in karst soils vital for quantifying the global carbon cycle. An estimated 20% of the world's land surface is underlain by lithologies favorable for karst terrain formation making the characterization of the soils in these landscapes applicable outside of the Bluegrass.

Presentation Type: Research Results

Title: Nitrogen Application to Summer Annual Forages May be Uneconomical

Presenter: Kelly Mercier, Ph.D. candidate

Advisor(s): Dr. Chris Teutsch

Abstract

As annual forage systems incur establishment costs every year, they are often considered a "breakeven proposition at best" (Ball et al., 2007). Including legumes may improve profitability by increasing yield or by reducing N costs. This study was designed to evaluate the economic effects of increasing both species diversity and N on summer annual forage mixtures. This study was conducted in Princeton and Lexington, Kentucky in 2018 and 2019. A randomized complete block with 4 replications was used. Forage treatments were a sudangrass monoculture, a simple mixture of two grasses and one legume, and a complex mixture of four grasses, four legumes, and three forbs. Nitrogen treatments were 0, 56, 112, 168, or 224 kg N/ha. Forages were harvested 3x each year at a target of 90 cm. In three out of four environments there was no yield increase when planting a mixture as compared to a monoculture. Swards were dominated by grasses, most likely due to their competitive dominance and high seeding rates in this experiment. If choosing to plant a mixture, it is important to select species that are morphologically and developmentally compatible. Economic analyses showed that N application was most often not economically feasible, however, in situations where planting summer annuals is a necessity, such as in a pasture renovation sequence, grazing can be more economical than haying.

Presentation Type: Research Results

Title: Breaking down biofilms: Understanding the mechanisms and impacts of *Pediococcus* resilience on ethanol fermentation

Presenter: Kent Pham, Ph.D. student

Advisor(s): Dr. Luke Moe

Abstract

The genus *Pediococcus* falls under the category of lactic acid bacteria that can be found as contaminants in ethanol fermentors. The presence of *Pediococcus* in fermentors can reduce the final yield of ethanol as *Pediococcus* competes with brewer's yeast for available hexoses. The lactic acid produced as an end product of *Pediococcus* catabolism also reduces the pH to a point intolerable by most yeast. Members of the genus have also been detected as part of biofilms in fermentors, granting them increased persistence into the following fermentation cycle. So far, not much has been published regarding *Pediococcus*' survivability in ethanol fermentors. Therefore, this study serves as the foundation to better understand how *Pediococcus* species can survive in an industrial fermenting setting. To do this, we have developed methods to induce the production of a biofilm in vitro. We have also curated a library of *Pediococcus* strains to search for any genetic differences that may result in different responses in a fermentor. The data collected here will create a baseline from which we can better study and understand the behavior of *Pediococcus*.

Presentation Type: Research Proposal

Title: Can Robotic Mowers Maintain high NDVI Values on Tall Fescue Turf under Reduced Irrigation?

Presenter: Sara Qian, Ph.D. student

Advisor(s): Dr. Jason Unrine and Dr. Travis Shaddox

Abstract

A completely randomized study was conducted from October 2019 to September 2020 at turf center at University of Kentucky, Lexington, KY on tall fescue (*Festuca arundinacea*). The study was designed to compare the turf quality under reduced irrigation with robotic or rotary mowers. The required irrigation was calculated based on reference evapotranspiration (ET_{ref}) with the location weather, using the Penman–Monteith Equation. Treatments consisted of two types of mowers with different percentage of ET_{ref}, which are 1) rotary mowers with 80% ET_{ref} replacement (ROT80), 2) robotic mower with 70% ET_{ref} replacement (ROB70), and 3) robotic mower with 60% ET_{ref} replacement (ROB60). The normalized difference vegetation index (NDVI) was used to determine the density of greenness of turfgrasses, which is strongly associated with turf quality. During the whole growing season, robotic mower plots (ROB60 and ROB70) show no differences (except in April 2020) on NDVI values. Higher values of NDVI were found in robotic plots (0.77) than rotary plots (0.71) during the growing season. Overall, robotic mowers resulted in greater NDVI than rotary plots with reduced irrigation, which was likely caused by a sharper leaf cut from the robotic mowers.

Presentation Type: Research Results

Title: Characterizing Western Kentucky's Fragipans

Presenter: Hannah Somerville, M.S. student

Advisor(s): Dr. Chris Shepard

Abstract

Fragipans are a lesser studied soil feature found in the aeolian soils of the southeastern US. First described around the turn of the century, these impermeable soil units prevent the downward movement of water and roots into the soil. The stunting of roots by fragipans has been found to heavily decrease crop yields. Perched water above the fragic feature causes unique engineering problems, largely preventing development on soils containing fragipans. This study focuses on describing in situ fragipans in the Western Coal Fields of Kentucky to better understand their genesis, evolution, and pedogenic features. Fragipans are more developed when they have larger structural units (prisms). Fragipans with larger prisms also exhibited higher concentrations of oxalate extractable silica, suggesting a relationship between fragipan development and silica content. Larger fragipans also tended to have higher bulk density measurements. There is a significant, positive relationship ($R^2=0.85$) between the bulk density of the fragipan and the concentration ratio of silica to aluminum, further indicating a relationship between fragipan development and silica content. Spatial trends were also observed throughout the dataset with the most developed fragipans being found to the north of the study area, closer to the aeolian loess source. Moving forward, further mineralogical analysis will help us understand how the fragipan develops and why fragipan prisms have higher silica contents. This project also aims to produce the first quantitative age data for fragic horizons using both optically stimulated luminescence and cosmogenic radionuclide dating methods.

Presentation Type: Research Results

Title: Effect of vine spacing and cane pruning length on Vignoles and Noiret grapevines

Presenter: Patsy Wilson, Ph.D. candidate

Advisor(s): Dr. Seth DeBolt

Abstract

Vine balance is influenced by a variety of factors including climate and canopy management. The variable climate in Kentucky can pose challenges to maintaining vine balance; however controlling canopy management methods such as pruning can help offset climatic challenges. The predominant vine pruning method used in Kentucky is spur pruning. This method of pruning is successful, however, achieving long-term vine balance can be difficult. Vine decline and frequent cordon replacement is necessary on lower vigor vines and vines that are spaced 8 feet apart when spur pruned. The effects of in-row vine spacing on vine growth metrics (vine-size, internode length, cane diameter, yield and fruit chemistry) were evaluated on Vignoles and Noiret. Vines were planted at 3.5, 4.0, 4.5, or 5.0 feet between vines and 10 feet between rows and cane pruned. Rootstock for each cultivar included Vignoles/1103P and Noiret/Riparia Gloire. The number of buds per cane was adjusted to provide shoot density of 4 shoots per foot of row on all vines. Preliminary data suggest that vine size (measured as dormant pruning weight per foot of row) increased as vine spacing was reduced. Internode length and cane diameter also increased as vine spacing was reduced. This data suggests that vine size begins to decline when vines are spaced at >5.0 feet. Vines planted to 4.0 and 4.5 feet maintain consistent vigor and vines spaced at 3.5 feet are increase in overall vine size.

Presentation Type: Research Results

Title: Predicting future US crop phenology dynamics under climate change using an integrated remote sensing and machine learning method: A case study in Kentucky cropping systems

Presenter: Yanjun Yang, Ph.D. candidate

Advisor(s): Dr. Wei Ren

Abstract

Crop phenology provides essential information for monitoring and modeling crop growth dynamics and productivity. A warming trend has been well documented in most regions around the world over the past decades, and this trend is projected to accelerate in the future. The impact of historical climate change on crop phenology has been widely reported using multiple methods, such as crop/ecosystem models, climate observations, and remote sensing, from site to global scales over the past several decades. However, little concerns were investigated about crop phenology shifts to future climate change under different climate scenarios. Predicting future crop phenology dynamics is critical for enabling agricultural activities to adapt to climate change. In recent years, the machine learning (ML) approach has shown great success in simulating and modeling crop parameters in agriculture. This study proposes an innovative approach to investigate future crop phenology dynamics by combining climate model outputs and remote sensing-based crop phenology via XGBoost (eXtreme Gradient Boosting). The objectives of this study are to (1) analyze future climate temperature and precipitation changes using GFDL-ESM2M climate model under RCP 4.5 and 8.5 downscaling scenarios in the contiguous United States during 2008-2099; (2) predict four future corn phenological stages (planting, heading, mature, and harvesting dates) using machine learning approach in combination with climate models and provide the datasets across the US during 2008-2099; (3) evaluate the potential impacts of climate variability and change on crop phenology under different scenarios; and (4) analyze the potential vulnerability of future Kentucky crops with phenology dynamic changes.

Presentation Type: Research Proposal

Title: Host genetic control of nodulation specificity in *Medicago truncatula*

Presenter: Xiaocheng Yu, Ph.D. candidate

Advisor(s): Dr. Hongyan Zhu

Abstract

Legumes are able to form root nodule symbioses with soil bacteria called rhizobia. Rhizobia in nodules can convert atmospheric nitrogen into ammonium that can be used by plants. On a global scale, the legume-rhizobia symbiosis provides more than half of the amount of nitrogen produced by the chemical fertilizer industry. However, not all legumes can form symbioses with all rhizobia and there exists a high level of specificity within and between legume species. Such specificity is determined by complex signal communications between the interacting partners. Getting knowledge of genetic mechanisms controlling symbiotic specificity will help to improve nitrogen fixation efficiency. The objective of this study was to investigate the genetic control of nodulation specificity in *Medicago truncatula* concerning the rhizobial strain *Sinorhizobium medicae* ABS7 using an F2 population derived from the cross of DZA220H (Nod-) and DZA045 (Nod+). DZA045 forms nitrogen fixation nodules with ABS7 but DZA220H is resistant to infection and nodulation by this strain. Genetic analysis revealed a single dominant gene that confers resistance to nodulation in DZA220H. Genetic mapping located the gene locus within a 300-kb genomic region on chromosome 8. Work is in progress to clone the underlying gene and to characterize the molecular mechanisms regulating this specificity.

Presentation Type: Research Results

Title: Bioinformatics Study of the Plant Polyadenylation Complex

Presenter: Lichun Zhou, Ph.D. student

Advisor(s): Dr. Art Hunt

Abstract

Message RNA polyadenylation is an essential step for most of eukaryotic mRNA transport, translation and turnover. In Arabidopsis, FY is one of the RNA end-processing factors that recognizes the RNA substrate. FY is the plant ortholog of WDR33, a mammalian protein that recognizes the AAUAAA polyadenylation signal as part of a complex with two other proteins, CPSF160 and CPSF30. Plant FY orthologs are consist of a conserved N-terminal domain with seven WD motifs and a plant-specific C-terminal region. This novel C-terminal domain two PPLPP motifs that interact with a WW domain in another protein, FCA. The FY-FCA interaction is important for flowering time but not for overall mRNA polyadenylation. In our study, we hypothesize that the C-terminal domain of FY has regulatory functions, and that the evolution of this region may contribute to differences in FY functioning in different plants. To test this hypothesis, we compared FY sequences in 17 plant species, focusing on the frequencies of synonymous and non-synonymous changes. We found that the WD-containing domain is highly conserved and subject to purifying selection. In contrast, the C-termini are much more divergent and seem to be under positive selection. This result supports the hypothesis that the FY C-terminus might acquire new roles or functions in different plant species. In future work, we will expand this project to include all polyadenylation factors in plants.

Presentation Type: Research Results