

2024

# SUMMER SCIENCE & ENGINEERING SYMPOSIUM | 2024



6TH ANNUAL

July 30th, 2024



# SUMMER SCIENCE & ENGINEERING SYMPOSIUM | 2024

**Organized By:** Mississippi Academy of Sciences and Mississippi State University  
**Venue:** Mississippi State University, Bost Conference Center Mississippi State, (Starkville Campus), MS 39759

## Symposium Chairs

Dr. K. Raja Reddy, Chair  
 Dr. Jason Keith, Co-Chair  
 Dr. Scott T. Willard, Co-Chair  
 Dr. Ham Benghuzzi, MAS Divisional Advisor

### *Scientific Committee Coordinators*

Dr. Jamie Larson, Chair  
 Dr. Raju Bheemanahalli, Co-chair  
 Dr. Shrinidhi Ambinakudige, Co-chair  
 Mississippi State University  
 Mississippi State, MS

### *Awards Committee*

Dr. Michelle Tucci, Chair  
 The University of Mississippi Med. Center,  
 Jackson, MS

### *Exhibit Coordinator*

Ty Tipton  
 Thomas Scientific

## Major Events

Time	Event
8:30-9:30 AM	Registration, poster set up and breakfast
9:30-10:30 AM	Opening of the event/welcome speeches
10:30-11:30 AM	3-minute oral presentations
11:30-12:00 PM	Networking
12:00-1:00 PM	Lunch break
1:00-3:30 PM	Poster presentations and judging
3:30-3:45 PM	Coffee break
3:45-4:45 PM	Round table discussion
4:45-5:15 PM	Awards and recognitions
5:15 PM	Closing remarks

## Symposium Sponsors

Mississippi State University, MS  
 Bagley College of Engineering  
 DAFVM (Division of Agriculture, Forestry, & Veterinary Medicine)  
 Graduate School  
 MAFES (Mississippi Agricultural and Forestry Experiment Station)  
 Office of Research and Economic Development  
 Department of Food Science, Nutrition & Health Promotion  
 Department of Plant and Soil Sciences  
 College of Forest Resources  
 College of Veterinary Medicine  
 Mississippi Research Consortium, MS  
 USDA-ARS, Southeast Area, Stoneville, MS

[msacad.org](https://msacad.org)

## TABLE OF CONTENTS

<b>PROGRAM.....</b>	<b>3</b>
<b>COMMITTEES AND JUDGES .....</b>	<b>4</b>
<b>PRESIDENTIAL AWARD.....</b>	<b>5</b>
<b>PRESENTER INDEX .....</b>	<b>5</b>
✓ <b>3-MINUTE ORAL PRESENTATION (3-M).....</b>	<b>9</b>
<b>POSTER (P).....</b>	<b>12</b>
✓ <b>HIGH SCHOOL POSTER (HS-P).....</b>	<b>12</b>
✓ <b>UNDERGRADUATE POSTER (U-P) .....</b>	<b>13</b>
✓ <b>GRADUATE STUDENT POSTER (G-P).....</b>	<b>20</b>
✓ <b>INVESTIGATOR POSTER (I-P) .....</b>	<b>30</b>

**PROGRAM s**

PROGRAM	
TIME	EVENT
8:30-9:30 AM	<b>REGISTRATION, POSTER SET UP AND BREAKFAST</b> Location: Bost Conference Center, Mississippi State University, Mississippi State, MS
9:30-10:00 AM	<b>OPENING OF THE EVENT/ WELCOME SPEECHES</b> <i>Dr. K. Raja Reddy</i> Symposium Chair, Mississippi State University <i>Dr. Ham Benghuzzi</i> Executive Director, Mississippi Academy of Sciences <i>Dr. Scott Willard</i> Dean CALS, and Director, MAFES, Mississippi State University <i>Dr. Babu Patlolla</i> , Dean, Alcorn State Uni. and MAS President <i>Mr. Archie Tucker</i> , Director, Southern Region, USDA-ARS, the MAS Presidential Award Recipient
10:00-11:30 AM	<b>3-MINUTE ORAL PRESENTATIONS</b> <i>Moderators: Dr. Shrinidhi Ambinakudege and Dr. Jagman Dhillon</i> Mississippi State University
11:30- 12:00 PM	<b>NETWORKING</b>
12:00 -1:00 PM	<b>LUNCH BREAK</b>
1:00 -3:30 PM	<b>POSTER PRESENTATIONS AND JUDGING</b> <i>Coordinator: Dr. Raju Bheemanahalli and Dr. Shrinidhi Ambinakudege</i> Mississippi State University
3:30-3:45 PM	<b>COFFEE BREAK</b>
3:45-4:45 PM	<b>ROUND TABLE DISCUSSION</b> <i>Moderator: Dr. Michelle Tucci</i> JMAS, Editor, University of Mississippi Medical Center, Jackson <b>Topic: Interdisciplinary Studies,</b> <i>Dr. Jamie Dyer</i> , Interim Dean, Interdisciplinary Studies, Mississippi State University <i>Dr. Wes Schilling</i> , Professor, Department of Food Science, Nutrition, & Health Promotion, Mississippi State University <i>Dr. Mark Lawrence</i> , Professor and Director Feed the Future Innovation Lab for Fish, CVM, Mississippi State University
4:45-5:15 PM	<b>AWARDS AND RECOGNITIONS</b> <i>Dr. Michelle Tucci</i> , JMAS, Editor University of Mississippi Medical Center <i>Dr. K. Raja Reddy</i> , Symposium Chair Mississippi Academy of Sciences
5:15 PM	<b>CLOSING REMARKS</b> <i>Dr. K. Raja Reddy</i> , Symposium Chair



**COMMITTEES AND JUDGES****Scientific Committee***Jamie Larson, Chair**Raju Bheemanahalli, Co-chair**Shrinidhi Ambinakudige, Co-chair*

Aboughanem, Nina	Krishnan, Krish
Adhikari, Bikash	Kumar, Neeraj
Ahn, Seung-Joon	Larry McDaniel
Amiri, Esmaeil	Li, Jiaxu
Anapalli, Saseendran	Li, Xiaofei
Avila, Luis	Matthews, Allison
Ayankojo, Ibukun Timothy	McCarty, Jack
Ballamoole, Snehalatha	McGee, Marcus
Ballard, Iva	Mendu, Lavanya
Beeson, Vanessa	Nanduri, Bindu
Bellaloui, Nacer	Nannapaneni, Rama
Bi, Guihong	McDaniel, Olga
Brasher, Karen	Orlinski, Pawel
Bumguardner, Ameer	Patlolla, Babu
Byrd, John	Phillips, Westin
Cameron, Joe	Pradhan, Prabhakar
Clary, Renee	Rai, Aswathy
Crow, Whitney	Reddy, Krishna
Czarnecki, Joby	Reed, Vaughn
Dash, Padmanava	Rutland, Will
Dharan, Vandana	Sabanadzovic, Sead
Dhillon, Jagman	Samiappan, Sathish
Dutta, Dipangkar	Shan, Xueyan
Esmaeil Amiri	Shankle, Mark
Eziashi, Christiana	Shrestha, Amrit
Feng, Chunda	Sivaraman, Vaidyanathan
Florencia Meyer	Tewelde, Haile
Kaur, Navneet	Thenveettil, Naflath
Fosu, Boniface	Valizadeh Gever, Bit
Ganapathi Shanmugam, Shankar	Valsala Sankara Pillai, Lekshmy
Gangishetty, Mahesh	Willis, Emma
Gibson, Tina	Wilson, Jeff
Henn, Alan	Woolfolk, Sandra
Howell, David	Zhang, Ping
Iqbal, Umar	
Kodadinne Narayana, Nisarga	

**Local Arrangement Members**

Allam, Manoj Kumar Reddy	Lopez, Evita
Bista, Mohan Kumar	Maddirala, Suryateja Reddy
Brand, David	Mukesh, Rudhan
Chandavarapu, Raveendra	Nekkalapudi, Lahari
Chinthalapudi, Durga Purushotham Mahesh	Poudel, Sujan
Earp, Mary-Margaret	Rodgers, Kathleen
Hosahalli, Vijaykumar	Sahota, Jasmine
Kovvuri, Yashwanth Reddy	Sivarathri, Bala Subramanyam

**PRESIDENTIAL AWARD**

Mr. Archie Tucker

Area Director, United States Department of Agriculture, Agriculture Research Service (USDA, ARS), Southeast Area, Stoneville, Mississippi



Archie Tucker serves in a SES position as the Area Director for the United States Department of Agriculture, Agriculture Research Service (USDA, ARS), Southeast Area in Stoneville, Mississippi. He is responsible for providing leadership and operational accountability for the ARS research programs in the states of Mississippi, Alabama, Louisiana, Tennessee, Arkansas, Georgia, Florida, North Carolina, South Carolina, Puerto Rico, and the Virgin Islands. This includes approximately 1,550 employees, of which 485 are Ph.D. scientists, and oversees an annual budget of 354 million dollars. Archie held prior positions in ARS as Associate Area Director, Assistant Area Director, Deputy Area Director, Area Administrative Officer, Area Property Management Officer, and Biological Science Technician. Archie has been in ARS for 48 years, starting as a 16-year-old high school student. He received the 2022 Meritorious Executive Presidential Rank Award and a Secretary Honor Award in recognition and appreciation of exceptional performance and outstanding contributions to the success of the USDA.

**PRESENTER INDEX**

TIME	ABBREVIATION
10:15 – 11:00 AM	3M: 3-Minute Oral Presentation
1:00 – 3:30 PM	HS-P: High School Poster
	U-P: Undergraduate Poster
	G-P: Graduate Poster
	I-P: Investigator Poster

**3-MINUTE ORAL PRESENTATION (3M)**

NAME	ID	TITLE
Aniruddha Acharya	I-3M1	Symplastic Barrier- A paradigm shift in ion regulation
Hafez Ahmad	G-3M2	Predicting Hypoxia in the Northern and Eastern Gulf of Mexico: A Machine Learning Approach Combining Remote Sensing and Field Data
Mariam Ageli	G-3M3	Evidence of deterministic community assembly from fossil diatoms in ancient Lake Towuti, Indonesia
Md Salman Bashit	G-3M4	Creating Practicability Envelopes for UAS Bathymetric Sonar Data Collections Across Inland Waterbodies in Mississippi
Mohammad Shakiul Islam	U-3M5	Dynamic monitoring of phycocyanin concentration in Western Mississippi Sound: Integrating Machine Learning Algorithms and Feature Selection Techniques with Uncrewed Aircraft Systems Imagery and Autonomous Surface Vessel Data
Pelumi Abimbola	G-3M6	Serotype classification using fine-tuned large language model
Ping Zhang	G-3M7	Deep Learning System for Bruised Fruit Classification
Sujan Poudel	G-3M8	Quinoa Drought Tolerance: Morpho-physiological Responses During Flowering
Udit Bhatta	G-3M9	Towards Resilience: Flood Risk and Social Vulnerability in Mississippi
Rajanna Adireddy	I-3M10	Peanut Responses to Elevated Temperatures, Water Stress, and Biochar

**POSTER PRESENTATION**

NAME	ID	TITLE
<b>HIGH SCHOOL POSTER</b>		
Joe Yang	H-P1	Divergent Survival Patterns in Boar Spermatozoa Linked to Oxidative Stress during Prolonged Chilled Storage
Pranav Reddy	H-P2	Applying Geospatial Analysis to Model Future Climate-Driven Bacterial Growth and Antimicrobial Resistance on a Global Scale
Rohan Alamgir	H-P3	Design And Synthesis of Plasmonic-Magnetic Nanoparticles for Chemotherapeutic Drug
Roman Luckett	H-P4	Simulating Lithium Breeding Materials for Nuclear Fusion
<b>UNDERGRADUATE POSTER</b>		
Abhinav Dhakal	U-P5	Deep Neural Networks for Predicting Soil Properties from Spectral Data
Aiden Leise	U-P6	POSS: Not Your Ordinary Bandage!!
Almia Valentine	U-P7	Innovation Hydrogel Composites for The Treatment of Craniofacial Defects in Adolescents
April Guo-Yue	U-P8	Exploring a Novel Immune Modulation Approach for Monomeric Interferon Gamma (IFN $\gamma$ ) Design



**POSTER PRESENTATION**

NAME	ID	TITLE
Ashya Richardson	U-P9	Neuropeptide Y Y1 Receptor Antagonist Attenuates Fetal Inflammation, Lipid Peroxidation, and Fetal Growth Restriction Following Maternal Inflammation and Reduced Uterine Perfusion Pressure in Rats
Avery Holt	U-P10	Blood Sodium Concentration Levels in Turtles Across Water Bodies in Oktibbeha
Brandon Bernard	U-P11	High-Resolution Characterization of Champion Sheep and Goat Gastrointestinal Microbiota Using Full-Length 16S Sequencing
Cory Toyota	U-P12	SARS-CoV-2 RNA Detection by RT-qPCR in Millsaps College Wastewater
Daxton Murphy	U-P13	Adrenal Cortex Changes in Female Ovariectomized Rats
Heidi Askeland	U-P14	Enhancing Tree Genetic Diversity Assessment Using Linkage Disequilibrium
Jack Nelson	U-P15	Intra-Species Differences Impact Sperm Cryosurvival
Jessica Bryant	U-P16	Optimization of a Two-Step Synthesis of Azomethine Imines for Use in Organocatalyzed Addition Reactions
Ke'Daja Freelon	U-P17	Using a Genetic Approach for the Identification and Phylogenetic Study of Larval Fish Species in the Seasonally Flooded Forests Alongside the Pascagoula River
Kelsey Harmon	U-P18	TRAPS - A Visual Analytic Tool for Public Health Surveillance
Lehmann Matheny	U-P19	Perinatal Inflammation Involvement in Homeostatic Responses to Sleep Disturbances and Attention-Deficit/Hyperactivity Disorder (ADHD)-like Behaviors in Adolescent Rats Using Machine Learning-Based Pattern Analysis
Mabry Temple	U-P20	Agomelatine Reduces Systemic Lipopolysaccharide-Induced Attention-Deficit/Hyperactivity Disorder (ADHD)-like Behaviors in Juvenile Rats.
Madeline Harris	U-P21	Enhanced Susceptibility to Ischemic Stroke-Induced Brain Damage, Sensory, and Motor Dysfunction in Adult Rats Following Intrauterine Growth Restriction
Madisyn Avery	U-P22	Maternal Inflammation Exacerbates Intrauterine Growth Restriction-Induced Neonatal Oxidative Stress and Neurobehavioral Deficits in Juvenile Rats
Prasanna Guduru	U-P23	Use of Y1 Receptor Antagonist Can Improve Bone Quality in Female Adult Sle Mice
Sadhan Ghimire	U-P24	AI-assisted chatbot for community Resources Referrals
Sasha Goodnow	U-P25	Studying The Impacts of Southern Pine Beetle on Loblolly Pine in the Homochitto National Forest Using Remote Sensing
Soyab Karki	U-P26	Modeling Weather and Mycotoxin Contamination in Multi-State Field Trials
Wolfgang Kramer	U-P27	Synthesis of Isoindolone Piperidines as Kinase Inhibitors: Preparation of Photochemical Starting Materials
Wolfgang Kramer	U-P28	Photochemical Key Steps in the Synthesis of Isoindolone Piperidines as Kinase Inhibitors: Asymmetric Photochemical Cyclization
Wolfgang Kramer	U-P29	Pyridine-based HIV Integrase Inhibitors: Side-Chain Development
<b>GRADUATE POSTER (G-P)</b>		
Abduselam Mohammed Nur	G-P30	Integrating Autonomous Surface Vessel Data and UAS Imagery for Accurate Turbidity Estimation over the Oyster Reef in the Western Mississippi Sound: A Machine Learning Approach
Afra Anan Bhuiyan	G-P31	Investigating the Biocontrol Activity of Root Endophytes against Fungal Pathogen Xylaria necrophora in Soybean
Aldon Helmert	G-P32	Optimizing Baseline Distance in Stereo Vision
Anitha Madapakula	G-P33	Impact of Climate Change in the Productivity of Major Field Crops in Senegal Using the DSSAT Simulation Model
Ayman Almashwali	G-P34	Weed Detection and Classification Using YOLOv8: Enhancing Agricultural Efficiency with Machine Learning.
Bala S Sivarathri	G-P35	Can seed priming with biostimulants boost soybean germination and seedling vigor?
Bipin Bastakoti	G-P36	Assessing Soil Health and Land-Use Sustainability in Vermilion-Teche Basin, Louisiana
Carlos Rivera	G-P37	Integrative genomic annotation of Populus deltoides
Chinwendu Umeojiakor	G-P38	Nonthermal Plasma Assisted Desorption and In-situ Conversion of Captured CO <sub>2</sub> from Atmospheric Air
Daniel Egerson	G-P39	Developing Decision Support Tools (DSTs) for enhancing participation in USDA's Conservation Reserve Program: What do stakeholders expect to see?
Durga P M Chinthalapudi	G-P40	Dissecting the Role of Cover Crops and Nitrogen Fertilization in microbially-mediated Nutrient Cycling in Corn Systems
Emmanuel Oladejo	G-P41	Effects of DL-Methionine on the Growth Performance and Blood and Liver Antioxidant Status in Growing Pigs



**POSTER PRESENTATION**

NAME	ID	TITLE
Farzana Nazneen	G-P42	An Effective Live-Attenuated Zika Vaccine Candidate with Modified 5' Untranslated Region
Farzana Nazneen	G-P43	Elucidating the Mechanism of Interleukin-17A Signaling in the Pathogenesis of West Nile Virus
Froilan Aquino	G-P44	Method for In-Situ Biomethanation of Biogas from the Anaerobic Digestion of Liquid Food Waste.
Haley Williams	G-P45	Assessing Heat Responses of South Mississippi Grown Interspecific Hybrid Bunch Grapes
Himani Joshi	G-P46	Rumen Microbiome Signature-Based Machine Learning Model for Heat Stress Prediction
Jasmine Sahota	G-P47	Characterizing Frass Associated Microbiome for Enhancing Plant Growth
Jenny Ryals	G-P48	Improving Stem Cutting Propagation of Grapevine Species
Lahari Nekkallapudi	G-P49	Evaluating the Impact of Cover crop and Nitrogen treatments on Soil Microbial dynamics in Sweet Potato production system
Landry Smith	G-P50	Identifying Trends in Racial and Ethnic Disparities in Labor Neuraxial Use
Vijaykumar Hosahalli	G-P51	Chilling Tolerance of Diverse Soybean Genotypes during Seedling Emergence
Manikanta Thati	G-P52	Numerical Evaluation of Engineered Wood Beams with Honeycomb Core
Mohan Kumar Bista	G-P53	Do Multiple Abiotic Stresses Affect the Early Growth and Development of Cotton Differently in Current and Future CO <sub>2</sub> Levels?
Namita Sinha	G-P54	Effect of Corn Hybrid, Plant Population, and Nitrogen Rate on Grain Yield and Quality
Nishat Shermin	G-P55	Persistent Extreme Heat Exposure Among Socially Vulnerable Communities in the Contiguous United States: A Two-Decade Analysis
Notsile Dlamini	G-P56	MicroRNA Profiles of Seminal Plasma Extracellular Vesicles Reflect Boar Sperm Quality
Oluwafemi Oyedele	G-P57	Macrofauna Accelerates Nutrient Cycling Through Litterfall in Cocoa
Prasanna Bayalusime	G-P58	Climate Change Impact Assessment and Adaptation and Mitigation Measures for Major Field Crops in Guatemala and Honduras: Feed the Future Countries
Raveendra Chandavarapu	G-P59	GWAS Reveals Genetic Regions Associated with Chilling Tolerance in Rice
Ruchita Bhattarai	G-P60	Agricultural Yield Prediction Under Changing Climate in USAID - Feed the Future Countries: A Case Study of Cambodia
Rui Peng	G-P61	Determine Optimum Planting Window and Increase Soybean Production in Eastern MS
Rui Peng	G-P62	Design Subsurface Drainage Systems for Spring Field Operations in Mississippi State
Sharon Samuel	G-P63	Association Between Food Security, Dietary Quality, And Diagnosed Periodontitis: Analysis of NHANES 2015-2018
Shazeed-UI Karim	G-P64	Develop An Animal Model for Chikungunya Virus (CHIKV) Infection in Heart
Sitha Som	G-P65	The Sre Ambel floodplain of Southwest Cambodia: Analysis of Forest Cover, Plant Species Composition, and Ecosystem Services for Sustainable Forest Management
Sujan Poudel	G-P66	Effects of Water Deficit on Cowpea: Physiology, Yield, and Quality
<b>INVESTIGATOR POSTER (I-P)</b>		
Bikash Adhikari	I-67	Row Crops Response to Waterlogging During Vegetative and Reproductive Stages
Jiaxu Li	I-P68	Role of Peptides in Regulating Rice Responses to Drought
Lekshmy VS Pillai	I-P69	Warmer Nighttime Disrupts the Day-Night Assimilate Utilization and Yield Potential in Soybean
Naflath Thenveettil	I-P70	Elevated Air Temperatures Damage the Reproductive Behavior of Cotton under Current and Future CO <sub>2</sub>
Navneet Kaur	I-P71	Quantifying Temperature Effects on Sorghum Grain Yield and Quality
Nisarga K Narayana	I-P72	Deciphering Crop Responses to Water Deficit Stress During the Vegetative Stage
Ramandeep Kumar Sharma	I-P73	Reviewing The Literature on Machine Learning Techniques in Maize and Soybean Yield Prediction
Sahila Beegum	I-P74	County-level Estimation of Optimal Planting Dates to Maximize Cotton Fiber Quality in the U.S.
Serge Leugoue Kameni	I-P75	Semen Quality Decline During 7-Day Storage: Mechanistic Determinants in Boar Sperm
Wei Dai	I-P76	Aggregation Variations in a No-Till Corn System with Combined Soil Amendments and Cover Cropping Practices

## ABSTRACTS

## 3-MINUTE ORAL PRESENTATION (3-M)

**I-3M01 Symplastic Barrier- A paradigm shift in ion regulation***Aniruddha Acharya<sup>1</sup>*<sup>1</sup>*Delta State University, MS, USA*

Due to the highly variable and heterogeneous nature of soil, vascular plants have evolved to selectively uptake water and minerals through roots while countering several abiotic and biotic stressors. Several checkpoints regulate ions' transport through plants' cells and tissues. The regulatory mechanisms consist of several molecular, cellular, physiological and anatomical components that work in tandem with the internal physiological requirements of a plant and their external environment. Several molecular components such as aquaporins, channels, transporters and pumps have been characterized along with cellular signaling pathways that regulate transport. Anatomically, apoplastic barriers such as the Casparian strip and intercellular connections such as plasmodesmata have been well characterized, however the existence of a symplastic barrier is not confirmed. Recent investigations involving endogenous ion distribution in seedling roots of *Pinus pinea*, *Zea mays* and *Arachis hypogaea* indicates the existence of radially arranged phosphorous-rich cells that may function as symplastic barrier and complement the role of apoplastic barrier in absence of the Casparian strip. These radially arranged phosphorous-rich cells form a ring like structure termed as "P-ring" that encircles the vascular tissues. Anatomical observations indicate that they are unlikely to be apoplastic in nature. At the same time, preliminary data through physiological investigations imply that the structure is relatively inert to external temperature and ion fluctuations. These cells were localized in strikingly similar positions surrounding the vascular tissues in seedling roots of plants that are evolutionarily distinct signifying their fundamental importance that may include ion regulation.

**G-3M02 Predicting Hypoxia in the Northern and Eastern Gulf of Mexico: A Machine Learning Approach Combining Remote Sensing and Field Data***Hafez Ahmad<sup>1</sup>, Felix Jose<sup>2</sup>, Padmanava Dash<sup>1</sup>, Shakila Islam Jhara<sup>3</sup>*<sup>1</sup>*Department of Geosciences, Mississippi State University, Mississippi, USA, <sup>2</sup>Department of Marine & Earth Sciences, Florida Gulf Coast University, USA, <sup>3</sup>Department of Oceanography, University of Chittagong, Bangladesh*

The increasing areal extent and frequency of hypoxia, characterized by lower dissolved oxygen levels in the inner continental shelf of the Gulf of Mexico (GoM), pose a growing threat to the marine ecosystem and the food chain. Reliable estimation and prediction of hypoxic events and their ever-expanding spatial extent along the Louisiana-Texas shelf is essential for the effective management of marine resources in the region. This study leverages field data and remote sensing techniques to train machine learning models for classifying hypoxic patches in the northern and eastern regions of the GoM. The field data revealed a general increase in hypoxic events from 1970 to 2014. Additionally, the top-performing models, such as Random Forest and XGBoost, exhibited exceptional results, with accuracy, precision, recall, and F1-score all exceeding 92%. In both the Random Forest and XGBoost models, the key influential features were chlorophyll-a and remote sensing reflectance at various wavelengths, including 531, 547, 555, 667, 678, 412, and 645nm. Analysis reveals significant variations in the extent of hypoxic areas across seasons,

with peak occurrences during the summer months. The mean hypoxic area during summer spans approximately 69,363.072 km<sup>2</sup>, reaching a maximum of 169,890.100 km<sup>2</sup>. Hypoxic regions are predominantly detected near the coast, particularly within river mouths, with notable concentrations observed for the Mississippi and Atchafalaya rivers. Additionally, smaller rivers, such as the Apalachicola River, Pearl River, and Suwannee River, exhibit increased areas of hypoxic zones. This study provides crucial information for decision-making and sustainable resource management in the region, emphasizing the importance of collaborative efforts to preserve environmental health and economic resilience along the Gulf Coast.

**G-3M03 Evidence of Deterministic Community Assembly from Fossil Diatoms in Ancient Lake Towuti, Indonesia***Mariam Ageli<sup>1</sup>, Paul B. Hamilton<sup>2</sup>, Andrew J. Bramburger<sup>3</sup>, R. Paul Weidman<sup>4</sup>, Zhuoyan Song<sup>1</sup>, James Russell<sup>5</sup>, Hendrik Vogel<sup>6</sup>, Doug Haffner<sup>1</sup>*<sup>1</sup>*Great Lakes Institute for Environmental Research, University of Windsor, <sup>2</sup>Canadian Museum of Nature, <sup>3</sup>Environment and Climate Change Canada, <sup>4</sup>BC Public Service, <sup>5</sup>Brown University, <sup>6</sup>University of Bern*

Ecologists have tried to ascertain whether there are rules of assembly which determine community composition and relative abundance. Despite the fact that many classical studies viewed diatoms as being opportunistic and stochastically-distributed, more recent studies have demonstrated that diatoms are in fact tracking changes in their environment, and are therefore deterministic in their distribution. To resolve whether the drivers in diatom community composition and abundance over extensive periods of time were stochastic or deterministic, we analyzed the diatom fossil records from deep drilling cores from ancient Lake Towuti (>1 My old). The fossil record of Lake Towuti contains two separate growths of a planktonic diatom community which persisted for ~50 kyr each. These growths were separated by ~100 kyr-period of being mostly absent. Each growth was dominated by the same five provisional taxa of *Aulacoseira*. The aim of this study was to investigate whether the taxa of *Aulacoseira* were deterministically or stochastically distributed within these two historic growth periods. We used stratigraphically constrained hierarchical clustering analysis (CONISS) to identify stratigraphic zones with similar diatom assemblages and nonmetric multidimensional scaling (NMDS) to determine changes in *Aulacoseira* species composition through time. Our results show that the upper sections of both layers were dominated by *A. towutiensis* (67.9%±16.9). The lower sections of both layers were dominated by either *A. sumatrensis* var. *rectangularis* (64.5%±26.7%) or *A. sumatrensis* var. *elongata* (56.0%±14.7). The CONISS and NMDS analyses demonstrate similar successional patterns in species composition in both upper and lower planktonic layers. The repeated pattern in community composition after extensive periods of time (~100 kyr) provides evidence that the diatom communities in the planktonic layers were regulated primarily by deterministic processes, likely related to lake mixing patterns.

**G-3M04 Creating Practicability Envelopes for UAS Bathymetric Sonar Data Collections across Inland Waterbodies in Mississippi***Md Salman Bashit<sup>1</sup>, Narcisa Pricope<sup>1</sup>*<sup>1</sup>*Mississippi State University, Mississippi State, MS, USA*

Rapid developments in bathymetric data collection technology and capabilities, especially miniaturization and mounting on unoccupied aerial systems (UAS)/drone platforms, have revolutionized the collection of 3-D data using active remote sensing sensors. Depth measurements of resources below water surfaces involve significant time, cost, labor, and technology-intensive tasks over various spatial scales that have variable success across the remote, dangerous, turbid, and tannic waters of the state. With a UAS platform, data can be collected quickly and safely, without the need for or with limited need for expensive and time-consuming, ground-based surveys or the use of specialized boats or aircraft. The main objective of my study is to test the relative capabilities of collecting UAS sonar/echo sounder-integrated bathymetric data in different water environments with variable water quality parameters and depths, validated using a suite of ground-based techniques. A secondary objective is to determine the best-performing interpolation method for deriving Digital Elevation Models (DEMs) from UAS echo sounder data collected at varying data survey methods. The results will lead to time and cost savings through increased inspection capabilities, improved mapping and models of water-logged and water-covered areas, and more robust measurements of drainage system capacities for a variety of monitoring and planning applications. Moreover, UAS echo sounder data can be a useful tool to provide insights for 3-D mapping to bridge the gap between terrestrial and marine surveys as well as between the mapping of specific morphological elements and entire landscapes.

#### U-3M05 Dynamic Monitoring of Phycocyanin Concentration in Western Mississippi Sound: Integrating Machine Learning Algorithms and Feature Selection Techniques with Uncrewed Aircraft Systems Imagery and Autonomous Surface Vessel Data

*Mohammad Shakiul Islam<sup>1</sup>, Padmanava Dash<sup>1</sup>*

<sup>1</sup>Mississippi State University, Mississippi State, MS, USA

Phycocyanin (PC) pigment is unique to cyanobacteria. Thus, measuring PC facilitates the monitoring of cyanobacterial blooms in aquatic environments. This paper evaluated ten machine learning algorithms (MLAs) for obtaining spatiotemporal variations of PC concentrations in the Western Mississippi Sound (WMS) using remotely sensed imagery from uncrewed aircraft systems and in situ PC concentrations measured by an autonomous surface vessel. Subsequently, the influence of river discharge and climatic variables on cyanobacterial concentrations were investigated by using a time-series of cyanobacteria maps. To derive the best PC retrieval model, a comprehensive list of 85 features was initially generated, including individual spectral bands, their band ratios, several vegetation indices, and three-band indices. To select the best feature subset for each MLA, the study adopted a combined approach utilizing two innovative feature selection techniques: Sequential Backward Floating Selection (SBFS) and Exhaustive Feature Selection (EFS). SBFS was employed initially to iteratively remove features to optimize model performance. Subsequently, EFS evaluated all combinations of features suggested by SBFS and selected the best subset. Among the ten MLAs, extreme gradient boosting performed the best ( $R^2 = 0.835$ , root mean square deviation =  $0.419 \mu\text{g/l}$ , unbiased mean absolute relative difference =  $0.176 \mu\text{g/l}$ , and average percentage difference =  $18.072\%$ ) in retrieving PC concentration. The time-series analysis revealed variations in PC concentration in WMS from 2018 to 2022. The highest average concentration was observed in 2019, attributed to the introduction of diverted Mississippi River water through the Bonnet Carre spillway, leading to an unprecedented cyanobacterial bloom. Additionally, the average PC concentration was consistently higher in summer than any other time of the year, likely due to elevated air temperatures and ample sunshine promoting cyanobacterial growth. The method formulated in this study enhances quantitative monitoring of PC

concentrations in coastal waters such as WMS and provides valuable insights for future water quality monitoring initiatives in other regions.

#### G-3M06 Serotype Classification Using Fine-Tuned Large Language Model

*Pelumi abimbola<sup>1</sup>, RamKumar Mahaligram<sup>1</sup>*

<sup>1</sup>Mississippi State University, Mississippi State, MS, USA

Serotype identification remains important in the epidemiological study and control of *Salmonella enterica* outbreaks. The traditional methods for serotype identification often rely on time and labor intensive laboratory techniques. In this study, we introduce an approach for classifying serotypes by fine-tuning a large language model (LLM), BERT, on a proposed natural language data. The method aims to use LLM integrated with computational biology techniques to accurately classify serotypes into their classes. We began by obtaining serotype samples as FASTQ files from NCBI. These raw sequencing reads are then assembled into a FASTA format using spade, after which they are then aligned against a reference genome (NC\_3197.fasta) using Bowtie2, a widely-used alignment tool known for its speed and accuracy, capturing comparable genomic variations across serotypes. The resulting alignment files are processed to extract relevant features that can serve as input to our LLM. These features include detailed descriptions of CIGAR strings, alignment scores, mismatch counts, and other alignment details, which are essential for capturing the nuances of genomic variations among the different serotypes. Taking large language models like BERT, we fine-tune them specifically for this task, by training on the alignment features from up to 18 different serotypes. This will allow the model to learn intricate patterns and relationships within the genomic data, enabling it to make precise classifications. The proposed LLM-based approach will not only enhance the accuracy of serotype classification but also significantly reduce the time and labor required for analysis compared to traditional methods.

#### G-3M07 Deep Learning System for Bruised Fruit Classification

*Ping Zhang<sup>1</sup>, Venkata Sir Sai Varun Bandi<sup>1</sup>, Babu Patlolla<sup>2</sup>*

<sup>1</sup>Department of Mathematics and Computer Science Alcorn State University Mississippi, United States. <sup>2</sup>College of Arts and Sciences Alcorn State University Mississippi, United States

Abstract: In this paper, we propose an algorithm for recognizing bruised apples based on surface shape information obtained by a 3D near-infrared (NIR) imaging system. The proposed algorithm comprises two parts: feature map construction and the classification of apples into bruised or unbruised categories. We propose a new algorithm to transfer 3D shape information into a 2D feature map. For classification, we propose to build a convolutional neural network to extract deep hierarchical features from the 2D feature map that are optimal for identifying bruised apples. Experimental results show that the proposed algorithm performs a higher classification than the algorithms developed previously, which indicates the proposed algorithm is promising for identifying bruised apples.

#### G-3M08 Quinoa Drought Tolerance: Morpho-physiological Responses During Flowering

*Sujan Poudel<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Quinoa (*Chenopodium quinoa* Willd.) is a  $C_3$  crop member of Amaranthaceae native to the Andean region. This is a highly nutritious annual pseudo-cereal species with a complete protein containing all

nine essential amino acids the human body cannot produce and hence called “golden grain”. Due to its health-benefiting values, quinoa cultivation has continuously increased in recent years, exhibiting its ability to grow in several climatic conditions. Quinoa cultivation in the United States is still in its early stages, but it has the potential to become a more significant crop. Although quinoa is known to be relatively tolerant to stress, like other field crops, it is also sensitive to drought during flowering. Here, two quinoa genotypes were subjected to different soil moisture conditions (full and low irrigation) during the flowering stage for 14 days to investigate the impact of moisture stress on gas exchange, leaf biophysical properties, reproductive fitness, and yield components. There were marked differences in physiology and pigments between treatments. Gas exchange parameters of both genotypes decreased under drought stress. For instance, exposure to 14 days of moisture stress led to a significant 74% reduction in stomatal conductance and a 60% decrease in transpiration. In addition, an 18% increase in chlorophyll and a 5% increase in anthocyanin were noted. Short-term drought stress affected the flowering and maturity traits, branching, panicle architecture, and yield components. These findings shed light on the genetic variability in quinoa responses to moisture stress, offering valuable insights for quinoa cultivation under diverse environmental conditions.

### G-3M09 Towards Resilience: Flood Risk and Social Vulnerability in Mississippi

*Udit Bhatta<sup>1</sup>, Narcisa Pricope<sup>1</sup>*

<sup>1</sup>Mississippi State University

The Southeast region of the United States has historically experienced the highest occurrence and cost of billion-dollar climate disasters, severely impacting coastal resources, human health, water resources, and agricultural and forest lands. Influenced by latitude, topography, and proximity to the Atlantic Ocean and Gulf of Mexico, the Southeastern US climate exhibits variability over seasons, years, and decades, with natural global cycles also playing a role. Climate change exacerbates droughts, floods, ice storms, hurricanes, tornadoes, and other severe weather events, increasing their frequency and severity. Flooding, in particular, is devastating, causing significant damage to lives and property in the US and around the world. Socio-economic factors like Poverty are shown to heighten flood risk, and Mississippi is prone to increased vulnerability as the poverty rate is 1.5 times higher than the national average of 12.6 percent, with the median household income 1.41 times below the national average. Among several initiatives to enhance community resilience, the Federal Emergency Management Agency (FEMA) has recently announced the Federal Flood Risk Management Standard (FFRMS), effective September 9, 2024, employs a Climate Informed Science Approach (CISA) and promotes strict floodplain standards. Prioritizing vulnerable and underserved communities in flood risk management and planning is crucial and has not always been effectively considered in the past. Using the Justice40 Initiative’s Climate and Economic Justice Screening Tool (CEJST, 2022) dataset, a spatial analysis of poverty rates and flood risk exposure in Mississippi over the next two decades revealed that 48% of census blocks (316 total) exceed the 75% federal poverty threshold, and 37% of areas (243 total) face a flood risk surpassing the 75% threshold. These findings underscore the urgent need to address social vulnerability for underserved communities in disaster planning and improve community resilience to flooding and other disasters.

### I-3M10 Peanut Responses to Elevated Temperatures, Water Stress, and Biochar

*Rajanna Adireddy<sup>1</sup>, Saseendran Anapalli<sup>2</sup>, Krishna Reddy<sup>2</sup>, Partson Mubvumba<sup>2</sup>, Heather Tyler<sup>2</sup>*

<sup>1</sup>ORISE-USDA, <sup>2</sup>USDA

Increasing greenhouse gases in the atmosphere from fossil fuel burning has resulted in global warming with increased extremes in temperatures, rainfall, and other related climate events. Enhancing carbon sequestered in the soil by applying biochar to soil in cropping systems has been gaining importance in mitigating the net greenhouse gas emitted into the air. However, how elevated temperatures can impact the responses of plants to biochar applications and the biochar per se have not been studied. Also, how different water availability scenarios modify the responses also need to be elucidated. In this context, we investigated the effects of different elevated temperature levels on the growth, phenology, and photosynthetic responses of peanut (*Arachis hypogaea* L.) under two irrigation levels with and without biochar. Peanut plants were grown in environment-controlled growth chambers (GC) where air temperature and light were controlled on day/night basis. The study consisted of three temperature levels (30/22, 35/27, and 40/32 °C) with two irrigation levels (100 and 50% field capacity, FC) and two biochar levels (0 and 5 t ha<sup>-1</sup>) in a split-plot design with four replications. Under 40/32 °C and 35/27 °C, seedlings emerged a day earlier than 30/22 °C. Irrespective of biochar and water levels, flowering, and peg initiation advanced, respectively, by 8 and 7 days under 40/32 °C and 4 and 5 days under 35/27 °C compared to 30/22 °C. At the flowering stage, plants with biochar maintained at 100% FC significantly reduced leaf area by 11, 33, and 79% under 30/22, 35/27, and 40/32 °C, respectively, compared to no-biochar control. Likewise, biochar application reduced nitrogen balance indices (NBI) by 4-8% under 35/27 and 40/32 °C compared to 30/22 °C. With biochar, photosynthesis rates were reduced by 4-10% in 100% FC and 12-19% in 50% FC under the elevated temperature conditions over control. However, the photosynthesis rate reduction was less under 40/32 °C compared to 30/22 °C. Root length at flowering under biochar, irrespective of irrigation levels, was reduced by 32-47% (30/22 °C) and 18-32% (35/27 °C), while 40/32 °C lessened the reduction in root length gap by 3-4%. To conclude, until flowering, biochar application in peanuts generally retard the growth process and phenological growth rates, possibly from microbe uptake-induced nitrogen immobilization in the soil but need more data analysis to confirm.



## POSTER (P)

## High School Poster (HS-P)

**HS-P01 Divergent Survival Patterns in Boar Spermatozoa Linked to Oxidative Stress during Prolonged Chilled Storage**Joe Yang<sup>1</sup>, Serge Kameni<sup>2</sup>, Notsile Dlamini<sup>2</sup>, Jean Feugang<sup>2</sup><sup>1</sup>Mississippi School for Mathematics and Science, <sup>2</sup>Mississippi State University

Artificial insemination relies on viable semen, the maintenance of which in the swine industry is a challenge due to the gradual decline in sperm quality during chilled storage. Previous studies have demonstrated the existence of Good and Poor preservation survival semen exhibiting divergent decreased sperm motility during storage. Identification of intracellular mechanisms associated with semen quality during storage is paramount for the potential prediction of Good and Poor survival of semen. This study investigates the underlying biochemical factors contributing to this variability. Extended single semen doses of fertile boars (n=25) were analyzed daily using a Computer-Assisted Sperm Analyzer for sperm motility and morphology during seven-day storage at 16-18°C. On Day 7, semen samples exhibiting extremely high and low sperm motility were identified as Good and Poor, respectively. These samples were further analyzed using commercial-grade biochemical assay kits (free radicals or ROS, total antioxidant capacity or TAC, and thiobarbituric acid or MDA) to evaluate the oxidative stress level of spermatozoa on Day 0 and Day 7. Data were statistically assessed with ANOVA, followed by the pairwise t-test. P<0.05 indicated significance. On Day 0 of semen collection and extension, all samples had comparable sperm motility and normal morphology parameters (P>0.05), but they were significantly decreased on Day 7 (vs. Day 0). However, Good samples maintained higher values than Poor counterparts (P<0.05). They exhibited higher TAC and lower MDA and ROS than Poor samples on both days. Findings indicate that a higher TOAC-to-MDA ratio may help identify good preservation survival boar semen.

**HS-P02 Applying Geospatial Analysis to Model Future Climate-Driven Bacterial Growth and Antimicrobial Resistance on a Global Scale**Pranav Reddy<sup>1</sup><sup>1</sup>St. Andrew's Episcopal School

Climate change is causally linked to escalating global infections, emphasizing the need for predictive models to identify infection hot spots. This three-part study, utilizing the K-12 strand of *Escherichia coli* on Muller-Hinton Agar Plates, aims to create a model to predict infection occurrences by correlating increasing temperatures with disease outbreaks on a global scale. Part one determines laboratory growth rates through incubation at temperatures increasing in 3-degree intervals from 37°C to 46°C over 4 tests over 24 hours by measuring percent surface area occupation. Part two determines the antimicrobial resistance rate: following the same method as part 1, at 24 hours, three plates are treated with a concentration of Amoxicillin while three remain as controls, replicated for each experimental temperature. Part 3 uses ArcGIS for predictive modeling of bacterial growth in 5-year intervals from 2030-2050, inputting empirical (pressure, humidity, population density) and laboratory data for an accurate growth map. An antimicrobial resistance map was generated in the same 5-year intervals from solely laboratory results. The growth rate, measured by a negative parabolic relationship peaks around 40°C. Conversely, the antimicrobial resistance rate, represented by a positive parabolic relationship is lowest at approximately 40°C. While bacterial growth peaks at 40°C, optimal conditions for resistance development occur at

higher temperatures due to increased horizontal gene transfer, despite suboptimal growth conditions. This study creates predictive maps by integrating multiple factors, enabling predictive measures to prevent bacterial infections on a global scale.

**HS-P03 Design and Synthesis of Plasmonic-Magnetic Nanoparticles for Chemotherapeutic Drug**Rohan Alamgir<sup>1</sup>, Sanchita Kundu<sup>2</sup>, Avijit Pramanik<sup>2</sup>, Olorunsola Praise Kolawole<sup>2</sup>, Kaelin Gates<sup>2</sup>, Shivangae Rai<sup>2</sup>, Paresh Chandra Ray<sup>2</sup><sup>1</sup>Madison Central High School, 1417 Highland Colony Pkwy, Madison, Mississippi, USA 39110, <sup>2</sup>Department of Chemistry, Physics and Atmospheric Science, Jackson State University, 1400 J.R. Lynch St., Jackson, Mississippi, USA 39217

Doxorubicin (DOX) is a one of most powerful chemotherapy drugs for the treatment of solid tumor in the United States. It kills or stops the growth of cancer cells via blocking a certain enzyme (topo isomerase 2) that is used in DNA replication and chromosome separation. However, this drug is highly toxic for healthy cells, leading to an irreversible heart muscle damage. The doxorubicin administration in human body can cause severe lethal adverse effects such as heart toxicity, nausea, vomiting and total hair loss. Untreated DOX waste that is discharged into the environment, has a significant impact on aquatic life and human health. During our study, we have synthesized plasmonic-magnetic nanoarchitecture using gold seeds and magnetic nanoparticles and explored them for the removal of DOX from environmental samples. We have investigated the interaction and binding mechanism of plasmonic-magnetic nanomaterials with doxorubicin by using spectroscopic and microscopic analysis, including UV-vis, Fluorescence, FT-IR, SEM and TEM.

**HS-P04 Simulating Lithium Breeding Materials for Nuclear Fusion**Roman Luckett<sup>1</sup><sup>1</sup>Author

Currently, fusion reactors run on deuterium, which is very abundant, and tritium, which is almost nonexistent on earth. Tritium's scarcity poses one of the greatest barriers to efficient fusion energy production. Lithium-tritium breeding is one proposed solution. Tritium can be produced by exposing lithium to the high energy neutrons created by nuclear fusion. If reactors can produce their own fuel, it could finally make fusion energy viable, producing almost limitless amounts of energy for the world. Several lithium "blanket" designs are being tested now by ITER, the leading organization in fusion energy. The blankets, which line the walls of the fusion reactor, are composed of varying lithium compounds. Alongside being tritium producers, these materials must be efficient neutron moderators. The more energy that can be captured, the more tritium can be produced. This experiment attempts to select a prime candidate for this material, comparing the moderation efficiency of lithium compounds proposed for use in fusion reactors. Using Geant4, a nuclear physics simulation software developed by CERN, neutrons are collided with the samples and the energy deposits are calculated. It was found that lithium oxide performed as the best neutron moderator. Future studies should consider the geometry of the blanket, as some materials may work better in liquid form, pebbles, or small bricks.

**UNDERGRADUATE POSTER (U-P)****U-P05 Deep Neural Networks for Predicting Soil Properties from Spectral Data**

*Will Heitman<sup>1</sup>, Abhinav Dhakal<sup>2</sup>, Callie Simon<sup>2</sup>, Gary Feng<sup>3</sup>, Jingdao Chen<sup>2</sup>*

<sup>1</sup>Carnegie Mellon University, <sup>2</sup>Mississippi State University, <sup>3</sup>USDA

Analyzing soil properties like carbon and nitrogen content and clay/silt/sand percentage has traditionally been time-consuming due to sophisticated lab equipment requirements. However, with the introduction of soil spectroscopy, this process has become more time- and cost-efficient. The challenge of using spectral data is its high dimensionality, non-linear nature, and lack of training labels for soil properties where lab data is not readily available. In particular, there is limited literature on predicting the permanent wilting point (PWP) and field capacity (FC). This research aims to use deep learning models to establish relationships between spectral data and these two soil properties using both labeled and unlabeled data. In this study, we use two different deep learning methods. The first method uses a neural network architecture with a series of fully connected layers and dropout regularization and is trained on only labeled soil samples. The second method uses a similar network architecture but also includes a secondary loss term to form a temporal ensemble model, allowing training on both labeled and unlabeled soil samples in a semi-supervised approach. Both networks are trained on 3000 soil samples collected from different regions in the state of Mississippi. We use the R<sup>2</sup> between the real and predicted values of the soil properties in our test set as our primary evaluation metric. Experimental results show that the proposed deep learning method achieves an R<sup>2</sup> value of 0.7 for wilting point prediction, compared to 0.54 from the baseline Cubist model.

**U-P06 POSS: Not Your Ordinary Bandage!!**

*Aiden Leise<sup>1</sup>, Michelle A. Tucci<sup>1</sup>, Hamed A. Benghuzzi<sup>2</sup>, Drew A. Hildebrandt<sup>1</sup>, Joseph D. Lichtenhan<sup>3</sup>*

<sup>1</sup>University of Mississippi Medical Center, Jackson, MS, <sup>2</sup>Jackson State University, Jackson, MS, <sup>3</sup>Hybrid Plastics, Inc., Hattiesburg, MS

Up to the present, autologous skin grafts or flaps have been widely used for repairing skin and soft tissue defects. However, improved reconstruction poses greater donor site problems. To resolve these problems, skin substitutes have been developed using tissue engineering. However, in order for skin substitutes to be applied to patients with full-thickness skin loss, the substitutes should function as an alternative to autologous skin, form an effective barrier against bacterial invasion, minimize inflammation and scar formation, improve fibrovascular tissue ingrowth, and have excellent reproducibility. Polyhedral oligomeric silsesquioxane (POSS), a class of compounds with a distinctive molecular cage structure consisting of an inner inorganic framework of silicon and oxygen atoms and an outer shell of organic functional groups, is a highly promising material for medical applications. Enhanced biocompatibility and physicochemical (material bulk and surface) properties have resulted in the development of a wide range of nanocomposite POSS copolymers for biomedical applications, such as the development of hemostatic agents, biomedical devices, drug delivery systems, dental applications, and tissue engineering scaffolds. The purpose of our experiment was to determine the short-term effects of applying POSS to a partial thickness skin wound using the pig as a model. Biopsies were taken after 3 and 7 days to determine the acute response to the material which was compared with wounds which were treated with traditional antibiotic cream or saline alone. The data show POSS was

able to induce early tissue formation and reduce inflammation and scar formation when compared to antibiotic wound coverage.

**U-P07 Innovation Hydrogel Composites for the Treatment of Craniofacial Defects in Adolescents**

*Almia Valentine<sup>1</sup>, Jonathan Lee<sup>2</sup>, Madisyn Avery<sup>1</sup>, Mabry Temple<sup>1</sup>, Amol Janorkar<sup>3</sup>, Chipu Chapusha<sup>3</sup>, William Farmer<sup>3</sup>, Chloe Batiste<sup>1</sup>, David Gordy<sup>4</sup>, Susana Marcho<sup>3</sup>, Bernadette Grayson<sup>5</sup>, Michelle Tucci<sup>3</sup>, Lir-Wan Fan<sup>2</sup>*

<sup>1</sup>Mississippi INBRE Research Scholar, University of Mississippi Medical Center, Jackson, MS 39216, USA. <sup>2</sup>Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA. <sup>3</sup>Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA. <sup>4</sup>Department of Radiology, University of Mississippi Medical Center, Jackson, MS 39216, USA. <sup>5</sup>Department of Population Health Science, University of Mississippi Medical Center, Jackson, MS 39216, USA. <sup>6</sup>Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA.

Pediatric head trauma often results in serious outcomes, frequently requiring cranioplasty to reduce brain swelling, and is linked to long-term inflammation and memory deficits. This study aimed to assess the healing and resorption rates of cranial defects with resorbable biopolymer composites, and evaluate the potential for inflammation-mediated changes in neurobehaviors and healing in juvenile rats. Four experimental groups of Sprague-Dawley adolescent rats were used in a 5-mm central critical-sized cranial defect model: (1) sham-operated, (2) empty defect, (3) autologous bone placement, and (4) hydrogel composite placement. Neurobehavioral assessment was determined biweekly, and characterization of bone remodeling performance was determined at the 8-week endpoint. Our data show that the empty defect group exhibited decreased short-term memory two, four, and six weeks after surgery, and the autograft (bone placement) group only decreased short-term memory two and four weeks followed by recovery six weeks post-surgery, but the hydrogel composite group showed no decreases in short-term memory two, four, and six weeks after surgery. In addition, bone remodeling results, as determined by dual-energy X-ray absorptiometry (DEXA) scan, showed that the hydrogel group achieved the most enhanced bone growth compared to composites lacking hydrogel eight weeks after surgery in both male and female rats. Our results suggest that the hydrogel composite-enhanced bone repair and neurobehavioral performance is superior to the autograft in our rat defect model.

**U-P08 Exploring a Novel Immune Modulation Approach for Monomeric Interferon Gamma (IFN $\gamma$ ) Design**

*April Guo-Yue<sup>1</sup>, Juan Mendoza<sup>2</sup>*

<sup>1</sup>Mississippi State University, <sup>2</sup>University of Chicago Pritzker School of Molecular Engineering

Interferon gamma (IFN $\gamma$ ), a key immune regulator, holds promise for therapeutic applications. However, its complex effects have hindered clinical success. Previous research shows mutating a dimeric structure can simplify immune responses. Simplification can be achieved by designing a monomeric form of IFN $\gamma$  to reduce complexity for more predictable and reproducible therapeutic outcomes. We reengineered the genetic sequence, unlocking partial agonist potential without dual polypeptide chains, based on Mendoza et al.'s (2019) findings. Helical rearrangements modulated expression as a monomer, enhancing therapeutic precision. We validated this design by amplifying the modified IFN $\gamma$  gene using polymerase chain reaction (PCR) and inserting it into a plasmid vector through Gibson assembly, a technique

for efficient DNA fragment integration to insert the designed sequence into a plasmid vector suitable for cellular uptake. This construct was transfected into yeast and insect cells. Yeast cells, single-celled organisms known for their ability to express complex proteins in a controlled environment, allowed for initial confirmation of successful protein production and facilitated analysis of expression levels. Transfection of High Five (Hi5) insect cells utilized mammalian-like folding machinery and post-translational modification capabilities, enhancing the potential of the engineered variant for therapeutic applications. Successful expression in yeast and Hi5 cells shows feasibility for diverse environments. This work paves the way for personalized treatments in cancer, autoimmune diseases, and infections. Future studies will assess its immune modulation ability in mouse studies will provide crucial preclinical insights for clinical development.

#### **U-P09 Neuropeptide Y Y1 Receptor Antagonist Attenuates Fetal Inflammation, Lipid Peroxidation, and Fetal Growth Restriction Following Maternal Inflammation and Reduced Uterine Perfusion Pressure in Rats**

*Ashya D. Richardson<sup>1</sup>, Jonathan W. Lee<sup>1</sup>, Madisyn Avery<sup>2</sup>, McKenzie S. Henson<sup>2</sup>, Madeline C. Harris<sup>2</sup>, Norma B. Ojeda<sup>3</sup>, Michelle A. Tucci<sup>4</sup>, Lir-Wan Fan<sup>1</sup>*

<sup>1</sup>Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA, <sup>2</sup>Mississippi INBRE Research Scholar, University of Mississippi Medical Center, Jackson, MS 39216, USA, <sup>3</sup>Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA, <sup>4</sup>Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA

Pregnancy increases uterine blood flow, which is necessary for normal fetal growth and development. Neuropeptide Y (NPY) mediates different biological effects, such as vasoconstriction, which might be associated with preeclampsia, a pregnancy complication usually resulting in persistent high blood pressure. Experimental studies have proposed a connection between reduced uterine perfusion pressure (RUPP), maternal inflammation, and increased NPY levels leading to reduced fetal development. The current study examined whether treatment of NPY Y1 receptor antagonist (Y1R-ANT) reduces maternal inflammation and RUPP-induced fetal inflammation, lipid peroxidation, and poor fetal development in rats. Lipopolysaccharide (LPS) (100 µg/kg) was administered intraperitoneally into pregnant rats on day 13 of gestation (G13), and RUPP surgery was performed on G14. G14 rats were treated with Y1R-ANT via intraperitoneal micro-osmotic pump infusion at 5 µg/kg/day for 6 days. On G20, placenta and fetal tissue were collected to assess fetal development. Our results showed that Y1R-ANT treatment reduced maternal inflammation and RUPP-induced reduction in placental efficiency and fetus weight. Y1R-ANT treatment also attenuated maternal inflammation and RUPP-induced increases in fetal proinflammatory cytokines and thiobarbituric acid reactive substances (TBARS) contents at embryonic day 20 (E20). These results suggest that Y1 receptor antagonization may reduce vasoconstriction-associated maternal LPS exposure and RUPP-induced fetal inflammation and lipid peroxidation. Additionally, normalized placental efficiency and fetal weight values may be useful for studying mechanisms involved in inflammation and RUPP-induced poor fetal development and have potential uses in the development of therapeutic strategies.

#### **U-P10 Blood Sodium Concentration Levels in Turtles Across Water Bodies in Oktibbeha**

*Avery Holt<sup>1</sup>, Scott Rush<sup>1</sup>*

<sup>1</sup>Mississippi State University, MS, USA

Waterbodies, in urbanized systems, to which human-derived discharge contributes, tend to show properties of materials of widespread human

use. This is true of sodium, an element that is used by people in food preparation. As compounds such as sodium accumulate in waterbodies so too do they manifest in aquatic organisms within those communities. High ambient sodium can be detrimental to these turtles, physiologically, but also propagate unique communities of microbiota within these animals. In our study we evaluated the concentration of sodium, as well as other elements and compounds in blood samples derived from the aquatic turtle (*Trachemys scripta*) across waterbodies within Oktibbeha County, MS. We also swabbed turtles so that we could evaluate microbial communities within their mouths and cloacal orifice. Collected blood samples show high levels of sodium, correlating with the concentration of anthropogenic discharge into these waterbodies as well as the landscape proximate to these waterbodies and the types of flow received (e.g. seasonal vs. permanent wetlands; riverine vs. lacustrine). This study provides insight into the influence of anthropogenic wastewater across various environments while also taking an additional step toward understanding the effect of urban systems on wildlife.

#### **U-P11 High-Resolution Characterization of Champion Sheep and Goat Gastrointestinal Microbiota Using Full-Length 16S Sequencing**

*Brandon Bernard<sup>1</sup>, Mackenzie Woody<sup>2</sup>, Himani Joshi<sup>3</sup>, Derris Devost-Burnett<sup>3</sup>, Chuan-Yu Hsu<sup>1</sup>, Peixin Fan<sup>3</sup>*

<sup>1</sup>Department of Biochemistry, Molecular Biology, Entomology & Plant Pathology, Mississippi State University, <sup>2</sup>Department of Biological Sciences, Mississippi State University, <sup>3</sup>Department of Animal & Dairy Sciences, Mississippi State University, <sup>4</sup>Institute for Genomics, Biocomputing & Biotechnology, Mississippi State University

Small ruminants are increasingly popular choices for livestock producers, particularly those with small farms or limited resources. They have a higher capacity to utilize lower-quality forages compared to large ruminants. The gastrointestinal tract of small ruminants harbors important microbes that contribute to digestion and pathogen prevention. In this study, we collected digesta samples from rumen and cecum, key fermentation sections, of 20 small ruminant animals at different locations in Mississippi State. The microbiota composition was analyzed using the full-length 16S amplicon sequencing with the Oxford Nanopore platform and Emu bioinformatic pipeline. We identified 270 and 344 bacterial species that were present in at least 10% of rumen and cecum samples, respectively. The 5 most abundant bacterial species in rumen included *Prevotella ruminicola* (13.4%), *Prevotella brevis* (4.9%), *Selenomonas ruminantium* (3.9%), *Bacteroidales bacterium CF* (3.9%), and *Succiniclasticum ruminis* (3.6%); while the top 5 bacterial species in cecum were *Bacteroidales bacterium CF* (19.2%), *Papillibacter cinnamivorans* (4.6%), *Dysosmobacter welbionis* (3.8%), *Lachnospiraceae bacterium GAM79* (3.3%), and *Oscillibacter valericigenes* (2.5%). Rumen and cecum bacterial species positively and negatively correlated with live animal body weight were identified. For example, relative abundance of the starch degrader *Ruminococcus bromii* in rumen was positively associated with body weight, while *Papillibacter cinnamivorans* in the cecum was negatively correlated with body weight. In conclusion, this study achieves a detailed species-level resolution of the bacterial population in the rumen and cecum of small ruminants, which will enhance our understanding of the relationship between gastrointestinal microbial ecosystem and growth performance of small ruminants.

#### **U-P12 SARS-CoV-2 RNA Detection by RT-qPCR in Millsaps College Wastewater**

*Elyssia Jones<sup>1</sup>, Aastha Banga<sup>1</sup>, Cory Toyota<sup>1</sup>*

<sup>1</sup>Millsaps College, MS, USA

This study presents an initial wastewater analysis conducted on Millsaps College campus in Jackson, MS to detect the presence of SARS-CoV-2 (COVID-19 RNA). Wastewater-based epidemiology has



emerged as a valuable tool for monitoring community health, offering early detection capabilities and aiding in proactively managing infectious disease outbreaks. Wastewater samples were collected from three sites across the sewage network, covering residential halls, academic buildings, and administrative facilities. Samples were processed using established total RNA extraction techniques followed by RT-qPCR analysis targeting three specific genetic markers (N1, N2, and E) of SARS-CoV-2. This analysis will inform a planning process currently considering implementing an infectious disease monitoring program on campus and/or inclusion as a component in student laboratory teaching courses.

#### U-P13 Adrenal Cortex Changes in Female Ovariectomized Rats

*Daxton Murphy<sup>1, 2</sup>, Prassana Guduru<sup>1, 2</sup>, Aiden Leise<sup>2, 3</sup>, Michelle Tucci<sup>2</sup>*

<sup>1</sup>Mississippi State University, Starkville, MS, <sup>2</sup>University of Mississippi Medical Center, Jackson, MS, <sup>3</sup>University of Southern Mississippi, Hattiesburg, MS

The adrenal glands are small, triangular-shaped endocrine glands located on top of the kidneys. The adrenal gland consists of two distinct regions, the adrenal cortex and adrenal medulla, which regulate several bodily functions, including metabolism, blood pressure, and the body's response to stress. During transition to menopause, females tend to experience significant changes in energy balance and stress which are symptoms of adrenal imbalance. The objectives of our study were: (1) to evaluate histological changes in the cortex and medulla of the adrenal glands in an ovariectomized rat and to determine if sustained delivery of either estrogen or an NPY 1 receptor antagonist (NPY-1RA) prevents histological changes of the gland, and (2) to determine if changes in the adrenal cortex are consistent with physiological changes at menopause such as weight gain and bone loss. Our results show that removal of ovaries (OVX) without treatment resulted in increased body weight, histological changes in the adrenal cortex zones, and resulted in significant bone loss within 8 weeks compared to ovary intact female rats. Treatment of OVX with either estrogen or an antagonist to NPY Y1 receptor reversed the metabolic and histological changes. The results suggests that estrogen loss impairs disrupts the zonation of the adrenal cortex and may be an important component of the metabolic changes associated with menopause.

#### U-P14 Enhancing Tree Genetic Diversity Assessment Using Linkage Disequilibrium

*Heidi Askeland<sup>1</sup>, Carlos Rivera<sup>1</sup>, Esteban Galeano<sup>1</sup>*

<sup>1</sup>Mississippi State University, MS, USA

Genetic diversity assessment in tree populations is crucial for understanding their adaptive potential amidst environmental challenges like climate change. Traditional methods, such as observed heterozygosity and Wright's fixation index ( $F_{ST}$ ), while informative, rely on assumptions that may not hold in dynamic ecological contexts. Effective population size ( $N_e$ ), a key parameter in genetic diversity studies, is conventionally estimated through labor-intensive field studies or molecular markers. The study of effective population size in plant species remains limited, presenting an opportunity to explore robust methodologies using linkage disequilibrium (LD). LD offers a snapshot of current population dynamics without requiring multiple temporal samples, potentially enhancing accuracy and practicality in genetic diversity assessments for tree populations. The objectives of our study are 1). to evaluate the accuracy and precision of LD-based  $N_e$  estimates compared to traditional methods in White Spruce, 2). to compare the performance of various LD equations under differing sample sizes and SNP densities, 3). to assess the influence of the number of loci and sample size on LD and  $N_e$  estimates, and 4). to identify optimal LD equations for different scenarios to enhance genetic diversity estimation in tree populations. The study assesses LD

and  $N_e$  using empirical data from White Spruce. LD-based  $N_e$  estimates are compared with traditional methods, considering varying sample sizes and SNP densities. Statistical analyses include comparison of LD equations and evaluating their performance under different scenarios. The research expects LD-based  $N_e$  estimates to demonstrate accuracy and stability in a conifer tree species, particularly under conditions where temporal sampling is challenging. Optimal LD equations are anticipated to vary based on sample sizes and SNP densities, providing insights into practical applications for genetic diversity studies in tree populations. Findings from this study contribute to refining methodologies for genetic diversity estimation in tree populations. LD emerges as a robust alternative for  $N_e$  estimation, offering practical advantages in accuracy and feasibility over traditional methods. These insights support sustainable forest management strategies amidst global environmental changes.

#### U-P15 Intra-Species Differences Impact Sperm Cryosurvival

*Jack Nelson<sup>1</sup>, Serge Kameni<sup>1</sup>, Notsile Dlamini<sup>1</sup>, Jean Feugang<sup>1</sup>*

<sup>1</sup>Department of Animal and Dairy Sciences, Mississippi State University, Starkville, MS USA

Semen cryopreservation is an invaluable technique for cryobanking both human and animal spermatozoa. Consequently, semen can be used for artificial insemination years after collection. In humans, it preserves couples' fertility, while in animals, it safeguards the genetic information of endangered species and advances agriculture by enabling the breeding of genetically superior animals. This study aimed to compare different bull breed responses to post-thaw survival of spermatozoa frozen under the same procedure. Following ten years of storage in liquid nitrogen, frozen straw semen ( $n=5$ ) from three breeds-Angus, Charolais, and Simmental-were thawed at 37°C water bath for 45 seconds. Frozen-thawed spermatozoa were then evaluated for motility and morphology using a computer-assisted sperm analyzer (CEROS II). All data were analyzed using SPSS expressed as mean±SEM. A significance threshold of  $P < 0.05$  was set. The total motility of the Charolais ( $59.3 \pm 2.7\%$ ) and Simmental ( $54.7 \pm 3.8\%$ ) samples was significantly higher than that of the Angus ( $33.0 \pm 7.9\%$ ). Additionally, the progressive motility of the Charolais samples ( $33.3 \pm 2.9\%$ ) was significantly higher than both the Simmental ( $19.8 \pm 1.2\%$ ) and Angus ( $16.6 \pm 4.5\%$ ) samples. There was no significant difference in normal morphology and specific sperm defects among the breeds. Furthermore, the Charolais bulls showed the highest VAP, VCL, and VSL ( $103.3 \pm 3.2$ ,  $190.1 \pm 7.5$ ,  $82.0 \pm 1.1$   $\mu\text{m/s}$ ) compared to the Simmental ( $89.5 \pm 3.2$ ,  $181.3 \pm 5.8$ ,  $62.0 \pm 3.9$   $\mu\text{m/s}$ ) and Angus ( $87.0 \pm 2.6$ ,  $159.9 \pm 2.9$ ,  $73.1 \pm 3.7$   $\mu\text{m/s}$ ). The linearity and straightness of Angus ( $46.0 \pm 2.2$  and  $81.4 \pm 1.7\%$ ) and Charolais ( $46.1 \pm 1.6$  and  $78.3 \pm 1.6\%$ ) were both significantly higher than Simmental ( $36.1 \pm 1.2$  and  $69.3 \pm 1.9\%$ ). In conclusion, Charolais semen exhibited the greatest cryotolerance, suggesting that differences within species influence the ability of semen to withstand cryopreservation. Work supported by USDA-ARS grant# 6066-31000-015-00D.

#### U-P16 Optimization of a Two-Step Synthesis of Azomethine Imines for Use in Organocatalyzed Addition Reactions

*Jessica Bryant<sup>1</sup>, Francis Kekessie<sup>1</sup>, Julie Pigza<sup>1</sup>*

<sup>1</sup>The University of Southern Mississippi, MS, USA

Squaramide organocatalysts can catalyze a wide range of reactions by taking advantage of noncovalent interactions to activate one or both substrates. Azomethine imines are substrates containing a 1,3-dipole which can participate in various addition reactions and are compatible with squaramide organocatalysts. Products resulting from reactions of azomethine imines contain nitrogen heterocycles that exhibit biological activities relevant in the pharmaceutical and chemical industry. However, one limitation is the low yield of both steps to access the azomethine imines, which hinders the ability to study further reactions. This work describes our attempts to optimize the

yield of each step. The future goal is to extend the reactions to the use of chiral squaramide organocatalysts to produce enantiopure heterocycles.

#### U-P17 Using a Genetic Approach for the Identification and Phylogenetic Study of Larval Fish Species in the Seasonally Flooded Forests Alongside the Pascagoula River

*Ke'Daja Freelon<sup>1</sup>, Julia Null<sup>1</sup>, Grant Peterson<sup>1</sup>*

<sup>1</sup>*Department of Wildlife, Fisheries, and Aquaculture, Mississippi State University, MS, USA*

While research has shown that floodplain forests serve as critical habitat for adult freshwater fish, little is known about fish in their early life stages. Thus, determining the species composition of larval and juvenile fish communities in Southeastern flooded forests has important implications for further wetland and critical fish habitat conservation measures. Larval and juvenile fish species can be difficult to morphologically differentiate due to their underdeveloped pigmentation and lack of distinguishable characteristics. Molecular tools and techniques are emerging resources capable of identifying organisms at the species level. Our aim is to elucidate the identity of larval and juvenile fish species through DNA extraction and PCR amplification of mitochondrial DNA, which will illustrate the relationship between fish phylogeny, age class, and their geospatial patterns of habitat use and selection. The samples with less species identification confidence were categorized and ranked into three main priority groups, priority 1 being the least identifiable and priority 3 being the most identifiable by species. The 266 samples that were separated into priority groups 1 and 2 were then put through the DNA extraction process. The extracted DNA samples were tested for purity and PCR viability to ensure successful downstream PCR amplification of the mitochondrial DNA. 85 percent of our extracted samples proved adequate for the next steps in the PCR process, which will enable us to verify and analyze the varying identities of Southeastern fish species and their geospatial distributions in association with varying age classes in the seasonally flooded forests. This data will provide further implications for the conservation of vital larval and juvenile fish habitat and emphasize the importance of maintaining river ecosystem connectivity.

#### U-P18 TRAPS - A Visual Analytic Tool for Public Health Surveillance

*Kelsey Harmon<sup>1</sup>, Canon Sbravati<sup>1</sup>, Sujan Anreddy<sup>1</sup>*

<sup>1</sup>*Social Science Research Center, Mississippi State University, MS, USA*

The Tobacco Reporting and Progress System (TRAPS) is a visual analytic tool, developed by the Mississippi Tobacco Data Team, which has been actively used since 2014 to monitor and evaluate tobacco control programs in Mississippi. TRAPS supports public health professionals in managing programmatic activities. TRAPS provides insight for better planning of preventative health activities by integrating program specific data collection methods along with user-specific visualizations. The data collection abilities allow TRAPS to capture and validate statewide data to increase data quality. The reporting and interactive visualizations help users query data to aid in decision making. The tool's effectiveness for evaluating tobacco control programs has been validated through user logs and program evaluators' observations. Recent enhancements to TRAPS include an evaluation module that significantly improves evaluator's efficiency. Before TRAPS, programmatic activity data and evaluations were recorded on paper. Through the data portal and evaluation module, the time required to complete these tasks has drastically decreased. Additionally, a training module has been introduced which includes a comprehensive set of instructional videos meant to immediately assist TRAPS users to input data and record their activities. These additions and future updates will ensure that public health professionals are

well-equipped to make data-driven decisions to enhance public health outcomes. In the future, TRAPS could be used for monitoring and evaluating other preventative health programs pertaining to issues such as cancer, diabetes, oral hygiene, and nutrition.

#### U-P19 Perinatal Inflammation Involvement in Homeostatic Responses to Sleep Disturbances and Attention-Deficit/Hyperactivity Disorder (ADHD)-Like Behaviors in Adolescent Rats using Machine Learning-Based Pattern Analysis

*Charles L Matheny<sup>1</sup>, Jonathan W Lee<sup>1</sup>, Silu Lu<sup>1</sup>, Joseph C Crosby<sup>1</sup>, James P Shaffery<sup>2</sup>, Norma B Ojeda<sup>3</sup>, Haifeng Wang<sup>4</sup>, Zhiqian Chen<sup>5</sup>, Vignesh H Nayak<sup>6</sup>, Michelle A Tucci<sup>7</sup>, Lu-Tai Tien<sup>8</sup>, Lir-Wan Fan<sup>1</sup>*

<sup>1</sup>*Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA.* <sup>2</sup>*Department of Psychiatry and Human Behavior, Animal Behavior Core, University of Mississippi Medical Center, Jackson, MS 39216, USA.* <sup>3</sup>*Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA.* <sup>4</sup>*Department of Industrial and Systems Engineering, Mississippi State University, Mississippi State, MS 39762.* <sup>5</sup>*Department of Computer Science and Engineering, Mississippi State University, Mississippi State, MS 39762.* <sup>6</sup>*Department of Pediatrics, Division of Pediatric Pulmonary, University of Mississippi Medical Center, Jackson, MS 39216, USA.* <sup>7</sup>*Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA.* <sup>8</sup>*School of Medicine, Fu Jen Catholic University, Xinzhuang Dist, New Taipei City 24205, Taiwan.*

Perinatal exposure to inflammation may play an important role in the association between sleep disturbances and neurodevelopmental disorders such as attention-deficit/hyperactivity disorder (ADHD) development. This study aimed to examine whether machine learning-based pattern analysis identified sleep patterns associated with ADHD in juvenile rats exposed to perinatal inflammation and sleep disruptions. Intraperitoneal injections of lipopolysaccharide (LPS) (2 mg/kg) or saline were administered on postnatal day 5 (P5) to Sprague-Dawley male rat pups, followed by behavioral testing at P35, implantation of sleep recording electrode on P39, and exposure to sleep disruptions on P47. Baseline sleep, sleep disruption, and recovery sleep were recorded on P46, P47 and P48, respectively, for 24 hours. Four groups (n=5) were included in this study: Saline-Baseline, Saline-Recovery, LPS-Baseline, and LPS-Recovery. Our results showed that neonatal LPS treatment induced ADHD-like behaviors, including hyperactivity and inattention at P35. Neonatal LPS treatment interfered with REM sleep and sleep homeostatic responses (recovery sleep) to sleep disturbances in adolescent rats (P49). Six unsupervised machine learning models were applied to analyze the feature interaction patterns among the collected high-dimensional sleep data. Our approaches identified relative theta and spindle power as features significantly associated with ADHD and perinatal inflammation in this experimental model of sleep disruption. These results suggest that machine learning-based analysis could serve as a strong tool in identifying neurodevelopmental disorders utilizing sleep data in subjects exposed to perinatal inflammation and sleep disruptions. In addition, these results could help in developing new treatments for sleep disorders associated with ADHD.

#### U-P20 Agomelatine Reduces Systemic Lipopolysaccharide-Induced Attention-Deficit/Hyperactivity Disorder (ADHD)-Like Behaviors in Juvenile Rats.

*Mabry Temple<sup>1</sup>, Rachel Palmer<sup>2</sup>, Jonathan Lee<sup>2</sup>, Charles Matheny<sup>2</sup>, Selby Ireland<sup>2</sup>, Madison Klim<sup>2</sup>, Michelle Tuci<sup>3</sup>, Norma Objeda<sup>4</sup>, Mary Kosek<sup>2</sup>, Shuying Lin<sup>5</sup>, Lu-Tai Tien<sup>6</sup>, Lir-Wan Fan<sup>2</sup>*

<sup>1</sup>*Summer Undergraduate Research Experience Program (SURE), University of Mississippi Medical Center, Jackson, MS 39216, USA,* <sup>2</sup>*Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA,* <sup>3</sup>*Department of Anesthesiology, University of Mississippi Medical Center, Jackson,*

MS 39216, USA, <sup>4</sup>Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA, <sup>5</sup>Department of Physical Therapy, University of Mississippi Medical Center, Jackson, MS 39216, USA, <sup>6</sup>School of Medicine, Fu Jen Catholic University, Xinzhuang Dist, New Taipei City 24205, Taiwan

Inflammation and oxidative stress significantly contribute to brain injury in both neonatal humans and animal models. Our previous research demonstrated that neonatal systemic administration of lipopolysaccharide (LPS) causes brain damage and attention-deficit/hyperactivity disorder (ADHD)-like behaviors in juvenile and adolescent rats. Recent studies indicate that agomelatine, which can influence inflammation and microglia polarization, may act as a neuroprotective agent in adult animals. This study aimed to assess whether agomelatine, a melatonergic agonist with anti-inflammatory and antioxidative properties, could mitigate LPS-induced brain inflammation and ADHD-like behavior in neonatal and juvenile rats. Intraperitoneal (i.p.) injections of LPS (2 mg/kg) were administered in postnatal day 5 (P5) Sprague-Dawley rat pups, and agomelatine (20 mg/kg) or vehicle was administered (i.p.) 5 min after LPS injection and/or then every 24 hr for 3 days. Neurobehavioral tests were performed, and brain inflammation and injury were examined in P6 and P25 rats. Our results showed that agomelatine reduced LPS-induced reduction in pre-social interaction (ultrasonic vocalization) and LPS-induced brain injury, including a reduction in white matter oligodendrocyte numbers, increases in microglia numbers, and an increase in IL-1 $\beta$  and TBARS contents at P6, suggesting anti-inflammatory and antioxidative effects. Agomelatine also reduced neonatal LPS-induced brain injury and inflammation in P25 rats and ADHD-like behaviors, including hyperlocomotion activity, social interaction disturbances, and learning and memory deficits (P21-P25). These results indicate that agomelatine may protect against LPS exposure-induced brain injury, inflammation, lipid peroxidation, and ADHD-like behaviors and that the protective effects are associated with its ability to attenuate LPS-induced inflammation and oxidative stress.

#### **U-P21 Enhanced Susceptibility to Ischemic Stroke-Induced Brain Damage, Sensory, and Motor Dysfunction in Adult Rats Following Intrauterine Growth Restriction**

*Madeline Harris<sup>1</sup>, Jonathan Lee<sup>1</sup>, McKenzie Henson<sup>1</sup>, Aswin Arunachalam<sup>1</sup>, Valeria Quach<sup>1</sup>, Irene Arguello<sup>1</sup>, Michelle Tucci<sup>1</sup>, Lir-Wan Fan<sup>1</sup>, Norma Ojeda<sup>1</sup>*

<sup>1</sup>University of Mississippi Medical Center, Mississippi.

Epidemiological and experimental studies suggest that intrauterine growth restriction (IUGR) increases the risk of developing diseases later in life. However, susceptibility to ischemic brain injury in IUGR individuals is poorly understood. This study tested whether maternal inflammation or IUGR rats have greater ischemic brain injury compared to control rats. IUGR was induced in the rat offspring by using a reduced uterine perfusion pressure (RUPP) procedure during late gestation. At 5 months, middle cerebral artery occlusion (MCAO) was performed on the IUGR and control animals to induce stroke. Motor and sensory skills were tested 24 hours after the procedure, followed by euthanasia to collect brain tissue to assess the damage. Our results showed that the offspring of dams exposed to RUPP showed significant hypomotor activity and hyperalgesia with brain size alteration, as indicated by the reduction of total brain, cortical, and hippocampal volume, along with the dilation of ventricles compared to the control offspring. RUPP-induced IUGR rats showed greater motor and sensory deficits compared to control rats as assessed with the modified neurological severity score after the MCAO procedure. RUPP-induced IUGR also increased adult susceptibility to ischemic brain injury, including increases in brain damage volume and degenerating neurons (Jade C+), and the impairment of dendrites (MAP2+) and myelin (RIP+). These results suggest that RUPP-induced brain dysfunction in rats may enhance adult susceptibility to

ischemic brain injury. Our model may be useful for studying mechanisms involved in ischemic brain injury and developing potential therapeutic strategies.

#### **U-P22 Maternal Inflammation Exacerbates Intrauterine Growth Restriction-Induced Neonatal Oxidative Stress and Neurobehavioral Deficits in Juvenile Rats**

*Madisyn Avery<sup>1</sup>, Johnathan Lee<sup>2</sup>, Ashya Richardson<sup>2</sup>, Almia Valentine<sup>1</sup>, Michelle Tucci<sup>2</sup>, Lir-Wan Fan<sup>2</sup>, Norma Ojeda<sup>2</sup>*

<sup>1</sup>Mississippi INBRE Research Scholar, <sup>2</sup>University of Mississippi Medical Center

Epidemiological and experimental studies suggest that intrauterine growth restriction (IUGR) is associated with neurodevelopmental impairments. Previous studies demonstrated that systemic inflammation during pregnancy induces the priming activation of microglia and elevates levels of pro-inflammatory cytokines, which may contribute to behavioral dysfunction in rat offspring. This study further examines if maternal inflammation via lipopolysaccharide (LPS) exposure enhances neonatal inflammation and oxidative stress, and motor and cognitive deficits associated with IUGR in juvenile rats. LPS (100 g/kg) was administered intraperitoneally into pregnant rats on day 13 of gestation (E13) and the reduced uterine perfusion pressure (RUPP) surgery was performed on day 14 of gestation (E14) to induce IUGR. Sensorimotor and cognitive behavioral tests were conducted on postnatal day 8 (P8) and P21-P24, respectively. Our results show that maternal LPS exposure enhanced IUGR-induced sensorimotor dysfunctions at P8, and increased inflammatory cytokines and Thiobarbituric Acid Reactive Substances (TBARS) contents in P0 and P8 neonatal rats. Exposure to LPS during gestation also enhanced IUGR-associated motordisturbances, including increases in rearing events in juvenile rats, as well as cognitive deficits in short-term memory, learning, and long-term memory. The results also suggest that exposure to LPS during gestation enhances IUGR-associated inflammation, lipid peroxidation, and cognitive deficits, including learning and memory in neonatal and juvenile rats. This model may be useful for studying mechanisms involved in developing children's neurodevelopmental delays associated with exposure to inflammation and growth restriction during gestation and may help contribute to future potential therapeutic strategies.

#### **U-P23 Use of Y1 Receptor Antagonist Can Improve Bone Quality in Female Adult SLE mice**

*Daxton Murphy<sup>1</sup>, Michelle Tucci<sup>2</sup>, Aiden Leise<sup>1</sup>, Prasanna Guduru<sup>1</sup>*

<sup>1</sup>Student, <sup>2</sup>Researcher

Systemic lupus erythematosus (SLE) is a rheumatic disorder related to numerous organs damage, dysregulated autoantibodies production. Bone involvement such osteoporosis, avascular necrosis of bone, and osteomyelitis have been observed in higher rates in SLE compared to the general population. Lupus predominately occurs in females and alterations in proinflammatory cytokines with higher levels of NPY have been found in circulation of patients with SLE. Our previous in vivo studies found increases in circulating NPY following loss of estrogen in a rat model led to a decreased volume of cancellous bone and inhibition of the osteoblast cell activity, which was reversed using an antagonist to the Y1 receptor (NPY-IRA). Our objective was to determine if administering an NPY-IRA could protect bone loss in older SLE mice. Twenty SLE adult female mice were randomly divided into two groups. Group 1 animals received an osmotic pump containing vehicle, and animals in group 2 received an osmotic pump set to release NPY-IRA at a concentration of 5ug/kg/day for four weeks. At the end of four weeks, the animals were euthanized and the femurs were harvested and bone density, peak load, and histological assessments were determined. Our results antagonizing the Y1 receptor improves bone strength and bone quality compared with SLE animals receiving vehicle only.



**U-P24 AI Assisted Chatbot for Community Resources Referrals***Sadhan Ghimire<sup>1</sup>, Zeedan Khan<sup>1</sup>, Sujan Anreddy<sup>1</sup>*<sup>1</sup>Mississippi State University, Social Science Research Center, MS

Traditionally, community resource referral platforms provide referrals for older adults in need of resources and services in the community using centralized resource management platforms. Providing access to timely resources and services for older adults, including specialized medical care and social support, is challenging, particularly in rural states like Mississippi with high needs and low resources. Understanding rural aging population needs and providing reliable information can strengthen senior health systems and address critical needs. Recent advancements in artificial intelligence (AI) have triggered interest in its potential within public health communication. This abstract proposes an AI-assisted chatbot for older adults, offering assistance with inquiries about community programs and services. The proposed chatbot implementation aims to generate personalized responses and real-time visualizations of service locations. Implementation includes a question-answering pipeline supporting various input-output formats. User prompts are processed into vector embeddings using pre-trained Language Models (LLMs) from Hugging Face, and the chatbot continuously trains on input data to stay updated with real-time events. The LLMs are compared and evaluated for accuracy and reliability to align with the No Wrong Door (NWD) System initiatives, a collaborative effort of the Administration for Community Living (ACL) and the Center for Medicaid Services (CMS). This virtual assistant development aims to improve interactions with the geriatric health system and identify gaps based on social determinants of health, leading to cost-effective recommendations.

**U-P25 Studying the Impacts of Southern Pine Beetle on Loblolly Pine in the Homochitto National Forest using Remote Sensing***Sasha Goodnow<sup>1</sup>, Yun Yang<sup>2</sup>, Hui Liu<sup>2</sup>, Ashley N. Schulz<sup>2</sup>*<sup>1</sup>; Mississippi State University, Department of Forestry, Mississippi State, MS, 39762, USA; University of Missouri-Columbia, School of Natural Resources, Columbia, MO, 65211, <sup>2</sup>Mississippi State University, Department of Forestry, Mississippi State, MS, 39762, USA

The southern pine beetle (*Dendroctonus frontalis*) is a native pest of southern pine species, such as loblolly pine (*Pinus taeda*) and shortleaf pine (*Pinus echinata*), in the eastern United States. Typically, the beetle is drawn to the pheromones of stressed trees and quickly overcomes weakened defenses, resulting in individual tree mortality. When beetle populations grow rapidly, beetles can mass-attack healthy trees, resulting in widespread tree mortality that can have negative impact on many ecosystem functions, including tree canopy and evapotranspiration. Studies of the impact of bark beetle outbreaks using remote sensing data have been carried out in western forest ecosystems, but not in pine systems of the southeastern United States. Here, we analyzed the dynamics of remotely-sensed vegetation density and evapotranspiration over southern pine beetle detection spots within the Homochitto National Forest in southwestern Mississippi. We calculated the normalized difference vegetation index (NDVI) using Landsat satellite observations on Google Earth Engine at each USDA Forest Service documented beetle spot from 2012-2021. We also extracted evapotranspiration (ET) data at stand level from the OpenET platform over these infected spots. Results show a relationship between beetle infestations and NDVI and ET dynamics in loblolly pine forest systems. This analysis provides a look into the relationship between forest canopy and water use capability and southern pine beetle infestation, which provides important insights in understanding forest ecosystem function changes caused by outbreaks and further supports the importance of managing pine forests via mechanical thinning and/or prescribed fire to reduce future southern pine beetle risk.

**U-P26 Modeling Weather and Mycotoxin Contamination in Multi-State Field Trials***Soyab Karki<sup>1</sup>, Lina Castano-Duque<sup>2</sup>, Joshua Blackstock<sup>3,4,5</sup>, Hans E. Winzeler<sup>6</sup>, Jianzhong Su<sup>6</sup>, Xueyan Shan<sup>7</sup>*<sup>1</sup>Data Science Program, Mississippi State University, Mississippi State, MS, USA, <sup>2</sup>Food and Safety Research Unit, Southern Regional Research Center, Agriculture Research Service, United States Department of Agriculture, New Orleans, LA, USA, <sup>3</sup>Dale Bumpers Small Farms Research Center, Agriculture Research Service, United States Department of Agriculture, Booneville, AR, USA, <sup>4</sup>Center for Advanced Spatial Technologies, University of Arkansas, Fayetteville, AR, USA, <sup>5</sup>Department of Geosciences, University of Arkansas, Fayetteville, AR, USA, <sup>6</sup>Department of Mathematics, University of Texas at Arlington, Arlington, TX, USA, <sup>7</sup>Department of Biochemistry, Nutrition and Health Promotion, Mississippi State University, Mississippi State, MS, USA

Mycotoxin contamination in crops poses significant risks to human and animal health and leads to substantial economic losses globally. Leveraging data from nine field experimental stations across seven states in the USA (Iowa, Missouri, Kentucky, Wisconsin, Louisiana, Indiana, and Michigan), we are investigating the relationships among weather, soil properties and mycotoxin contamination (aflatoxin, fumonisin, and deoxynivalenol). We analyzed 1.5 years of time-series data (July 2022 - December 2023) on weather and soil properties, extracted using satellite acquire weather data set maps (NLDAS-2 and PRISM) via Google Earth Engine (GEE) and web scraping. Through data analysis and feature engineering, we generated a risk index for aflatoxin contamination by using Ratkowsky Growth equations. This aflatoxin risk index (ARI) connects field weather data with parameters to estimate fungal growth, aflatoxin production, spore dispersal, and insect damage. Given the dataset's size and multicollinearity among several weather properties, we employ numerous predictive models. Preliminary results indicate that the random forest regression model provides the most accurate predictions of mycotoxin contamination risk, identifying soil acidity (pH), calcium carbonate, pressure, relative humidity, and temperature as the most influential predictors. This research will enhance the understanding of environmental factors affecting mycotoxin contamination, providing valuable insights for mitigating risks in agricultural practices.

**U-P27 Synthesis of Isoindolone Piperidines as Kinase Inhibitors: Preparation of Photochemical Starting Materials***Elizabeth Hawkins<sup>1</sup>, Zoe Elder<sup>1</sup>, Tynai Bridges<sup>1</sup>, Caroline McKinney<sup>1</sup>, Matthew Donahue<sup>2</sup>, Wolfgang Kramer<sup>1</sup>*<sup>1</sup>Millsaps College, <sup>2</sup>The University of Southern Mississippi

In this project we report a novel synthesis of isoindolone piperidines. Our synthesis involves a photochemical key step that forms the piperidine moiety. Further transformation depends on the target molecule, but also on what substituents are tolerated during the photocyclization. The target structures, valmerins, are inhibitors to two key phosphorylating enzymes, glycogen synthase kinase-3 (GSK3) and cyclin-dependent kinases (CDKs). Inhibition of those enzymes leads to disruption of cancer cell metabolism and thus valmerins are used as cancer drugs. Valmerins contain an amino nitrogen on the isoindolone moiety which has to be introduced after the photoreaction because it is not tolerated during the cyclization. The use of nitro phthalimide has so far been not successful in the photodecarboxylative cyclization as reported in the literature. Reduction of the nitro group would yield the desired amine which can be transformed into the various substituents. An alternative is the formation of amide protected amino groups on the chromophore. Other syntheses of the photochemical starting materials are presented.

**U-P28 Photochemical Key Steps in the Synthesis of Isoindolone Piperidines as Kinase Inhibitors: Asymmetric Photochemical Cyclization**

*Kaydyn Carr-Turner<sup>1</sup>, Zoe Elder<sup>1</sup>, Tynai Bridges<sup>1</sup>, Matthew Donahue<sup>2</sup>, Wolfgang Kramer<sup>1</sup>*

<sup>1</sup>Millsaps College, <sup>2</sup>The University of Southern Mississippi

Cyclization reactions are used in many syntheses of medicinal compounds and control of the regio- and stereochemistry is vital to ensure efficient yields. Isoindolone piperidines are used as inhibitors to target two important enzymes in cancer cells, glycogen synthase kinase-3 (GSK3) and cyclin-dependent kinases (CDKs). Valmerins are isoindolone piperidines that have been shown to inhibit GSK3/CDK enzymes during cell proliferation. In this project we are using a photochemical key step to synthesize valmerin derivatives. To form the piperidine ring, the photodecarboxylative cyclization is employed and phthalimide is used as a chromophore to induce an electron transfer reaction with the terminal carboxylate. The syntheses are initiated from affordable building blocks and should culminate in the stereo-controlled synthesis of the target molecules. Variations in the substitution pattern of the chromophore lead to the formation of regioisomers, the control of which is important. Electron-donating and electron-withdrawing effects of the substituents might direct the cyclization to one side of the imide.

**U-P29 Pyridine-based HIV Integrase Inhibitors: Side-Chain Development**

*Tyler Twedt<sup>1</sup>, Christopher Bruni<sup>1</sup>, Brenna Macaluso<sup>1</sup>, Sharon Suffern<sup>1</sup>, Matthew Donahue<sup>2</sup>, Jacques Kessler<sup>2</sup>, Wolfgang Kramer<sup>1</sup>*

<sup>1</sup>Millsaps College, <sup>2</sup>The University of Southern Mississippi

Retroviruses employ three unique enzymes, reverse transcriptase, integrase and protease, that are essential for their life cycle. Antiviral therapy targets those enzymes preferably, as less side effects are expected. Human immunodeficiency virus (HIV), which causes acquired immunodeficiency syndrome (AIDS), is generally combated with triple therapy, consisting of usually two reverse transcriptase inhibitors and one integrase or protease inhibitor. As the high mutation rate of the virus causes resistance, HIV drugs are constantly optimized. HIV integrase incorporates the viral DNA into the host cell genome. HIV Integrase inhibitors are mostly based on aromatic heterocycles such as pyridine and quinoline. This project aims to synthesize new inhibitors based on the pyridine core. The heterocycle is generated by reaction of substituted malonic esters with an aminocrotonate ester. The development of the side chain in the 3-position which consists of a methine carbon carrying a tert-butoxy group and a carboxylic acid, is essential. Several methods have been attempted and are discussed. Further incorporation of substituents on the pyridine core will determine the efficiency of the inhibitors.

**GRADUATE POSTER (G-P)****G-P30 Integrating Autonomous Surface Vessel Data and UAS Imagery for Accurate Turbidity Estimation over the Oyster Reef in the Western Mississippi Sound: A Machine Learning Approach**

Abduselam M. Nur<sup>1</sup>, Padmanava Dash<sup>1</sup>, Jessica S. Wolfe<sup>2</sup>, Gray Turnage<sup>2</sup>, Lee Hathcock<sup>2</sup>, Gary D. Chesser Jr.<sup>3</sup>, Robert J. Moorhead<sup>2</sup>

<sup>1</sup>Department of Geosciences, Mississippi State University, Mississippi State, MS 39762, USA, <sup>2</sup>Geosystems Research Institute, Mississippi State University, Mississippi State, MS, USA, <sup>3</sup>Dept. of Ag. and Bio. Eng., Mississippi State University, Mississippi State, MS, USA

Turbidity is a crucial water quality parameter that impacts aquatic organisms, including fish and oysters, by disrupting food webs and creating low-oxygen zones. While satellite remote sensing has been widely used for monitoring coastal and inland waters, it faces limitations in spatial and temporal resolutions, and cloud cover can impede imagery availability. Recently, Unmanned Aircraft Systems (UAS) based remote sensing has emerged as a valuable alternative to overcome these challenges. This study leverages an Autonomous Surface Vessel (ASV) equipped with water quality sensors to automate traditional water sampling approach, enabling real-time data collection along predefined transects. The objective was to develop a robust turbidity estimation algorithm by integrating UAS-measured water-leaving remote sensing reflectance (Rrs), ASV-measured turbidity data, and machine learning models. Data were collected during four field campaigns across different seasons from over the Merrill Shell oyster reef in the western Mississippi Sound using the ASV. Concurrently, UAS flights in July 2021 and September 2022 captured imagery using a Micasense RedEdge-MX multispectral sensor with five spectral bands. Principal Component Analysis (PCA) was applied to reduce redundancy and extract significant information from the highly correlated spectral bands and derived indices. Seven machine learning algorithms were trained using the first five principal components out of 19 variables: Random Forest (RF), Support Vector Machine with Radial Kernel (SVM-RBF), Multiple Linear Regression (MLR), Gradient Boosting Decision Tree (GBDT), Extreme Gradient Boosting (XGBoost), Enhanced Adaptive Regression Through Hinges (EARTH), and Cubist. The SVM-RBF model demonstrated the highest performance with an  $R^2$  of 0.943, RMSE of 0.454, and MAE of 0.359, followed by Cubist and XGBoost. This study underscores the effectiveness of machine learning algorithms in generalizing turbidity data from ASV and highlights the potential of UAS imagery for continuous monitoring of small-scale water bodies, such as those over an oyster reef. It also demonstrates the feasibility of integrating ASV data with high-resolution imagery for large-scale machine learning algorithm development with extensive ASV datasets, offering a robust water quality monitoring and management approach.

**G-P31 Investigating the Biocontrol Activity of Root Endophytes against Fungal Pathogen *Xylaria necrophora* in Soybean**

Afra Anan Bhuiyan<sup>1</sup>, George Popescu<sup>1</sup>

<sup>1</sup>Mississippi State University, MS, USA

Microbial communities associated with soybean roots play a crucial role in plant health and defense mechanisms. Taproot decline (TRD) of soybean, caused by the pathogen *Xylaria necrophora*, has become a significant concern in soybean production, particularly in the southern United States. However, little is known about how TRD affects these microbial communities. To address this gap, a study was conducted previously to characterize the fungal and bacterial taxa associated with healthy and TRD-affected soybean plants at different disease stages. Inspired by the findings, we aim to understand the

diversity of root microorganisms responsible for specific soybean phenotypes. Additionally, our focus is to investigate the bacterial isolates for beneficial uses, such as improving plant growth and resistance against harmful pathogens. For the field trial, two different types of treatments were used against *Xylaria*: using a single bacterial isolate and using a cocktail of bacteria called synthetic community (syncomm). The roots (*Xylaria* infected and non-infected) were collected and cleaned, the root yield was checked by measuring the root mass, and the root yields were compared among different treatments. The DNA from the root samples was isolated and sent to the CosmosID® for 16S rRNA sequencing and ITS. The Microbiome Analyst will be used for raw sequence processing, statistical analysis, functional prediction, and meta-analysis for marker gene data, multiple approaches for shotgun data profiling, taxon set enrichment analysis, and integrative analysis of microbiome and metabolomics data. This research sheds light on the intricate interactions between soybean roots, their microbiota, and the TRD pathogen *Xylaria*, providing valuable insights for future disease management efforts.

**G-P32 Optimizing Baseline Distance in Stereo Vision**

Aldon Helmer<sup>1</sup>, John (Austin) Reed<sup>1</sup>

<sup>1</sup>Mississippi State University, MS, USA

Stereo vision is a recognized and efficient tool for depth perception in RGB-D applications. It is widely used in fields such as robotics, autonomous vehicles, and computer vision. This technology emulates human binocular vision with the use of two different sensors to view the same scene. Then by using the disparity between the two perspectives, this method can calculate the depth perception. There are many ways to optimize depth perception. These included using Machine Learning methods, advanced calibration techniques, and the latest camera technology. A different approach to improving depth perception is the baseline distance between the two sensors. When the sensors are closer to each other they are more optimal for finding depths at shorter ranges, but the further apart they are optimal for depths further from the sensor. As technology advances robotics and vehicles that use these sensors will be placed in a various domain of environments where finding the depth of a target could vary from close to the sensors to further away. Our solution to this problem of dynamic ranges is to simulate an adjustable baseline distance between the sensors for optimal depth perception. To do this we will calibrate the stereo cameras at multiple baseline distances and select the optimal one based on the target range. The calibrations and simulations will be done through apps in Matlab like stereo camera calibrator. To calibrate the stereo cameras we are using a checkerboard outline with the squares being 25mm. The application needs 20 pairs of images for the left and right cameras. To determine what is the optimal baseline, the goal is to measure the distance from the camera system and compare the true distance to the distance that each baseline provides. After determining what is the optimal distance conduct the test again with a different distance to determine how much of a change if any is in the accuracy. The results we are hoping to find are by how much suboptimal baselines affect the precision of depth perception whether is there a way to update the baseline and what effect it has on the accuracy. This application could be applied to a wide range of technologies ranging from drones that work collectively in a stereo vision manner to vehicles that can adjust the distance between their cameras. This would provide alternative solutions where implementing machine learning methods is not ideal. As drone technology is more readily available it allows users to take camera systems closer to their target and provides a stereo system that's baseline distance is unfixed. This allows drone systems and other

similar systems to optimize their accuracy by adjusting one variable. This solution could be implemented without the use of expensive camera equipment.

### **G-P33 Impact of Climate Change in the Productivity of Major Field Crops in Senegal using the DSSAT Simulation Model**

*Anitha Madapakula<sup>1</sup>, Prasanna Bayalusime<sup>1</sup>, Ruchita Bhattarai<sup>1</sup>, Prakash Kumar Jha<sup>1</sup>, Prakash K Jha<sup>2</sup>*

<sup>1</sup>Mississippi State University, <sup>2</sup>University of California, Merced.

Global agriculture faces a lot of challenges because of climate change, and Senegal's main field crops need to be carefully studied to determine how they might be affected. A study was performed to assess the extent of climate change and forecast the crop yield performance in changing climate situation in Senegal using DSSAT. For climate change impact assessment, three climate parameters were studied, and six different climate models were ensemble together to reduce the individual model biasness for future climate in two different RCP scenarios - RCP 2.6 and RCP 8.5. The ensemble suggests Senegal might see variations in rainfall between -7% and 15% and a maximum temperature might increase up to 1.2 °C under RCP 2.6 scenario, while rainfall will be in between -55% and -27% and a probable increment of 4.5 °C in temperature under RCP 8.5 scenario by 2100. It is likely that Senegal will suffer extreme drought and high temperature in future which is very critical for crop growth and development. Therefore, simulations were performed in DSSAT to estimate crop yields by integrating downscaled meteorological data from climate models and gridded soil data from Harvard Soil Data verse. The goal of this research is to improve resilience against the effects of climate change by strategically planning crop responses and yield measures. We aim to optimize Senegalese food production systems by analyzing climate-resilient technologies, thereby supporting sustainable agricultural practices.

### **G-P34 Weed Detection and Classification using YOLOv8: Enhancing Agricultural Efficiency with Machine Learning.**

*Ayman Almashwali<sup>1</sup>, Paul Tseng<sup>2</sup>*

<sup>1</sup>Mechtronics Engineering, Mississippi State University, <sup>2</sup>Mississippi State University

Weed management in modern agriculture is difficult since it competes for nutrients with crops, resulting in lower yields. While successful, traditional approaches based on physical labor and chemical pesticides are labor-intensive, costly, and ecologically hazardous and frequently fail to solve weed proliferation dynamics and agricultural issues. The rise of deep learning, particularly sophisticated models such as YOLOv8, holds promise for transforming weed identification and categorization. Weed detection in agriculture necessitates overcoming many significant difficulties. These include dataset imbalance and coverage, which need rigorous data collection and augmentation to represent weed species accurately and improve model performance. Weeds' diverse morphological characteristics, such as thin leaves and intricate structures that blend in with background vegetation, provide obstacles for identification algorithms. Advanced picture preprocessing approaches can improve feature extraction, reduce background noise, and increase detection accuracy. Effective model training, which focuses on subtle visual signals and strong optimization approaches like transfer learning, is critical for generalization across varied agricultural landscapes with changing lighting and soil conditions. We need better detection techniques and parallel processing technologies to effectively manage numerous weed instances in photos to maintain high accuracy and efficiency. This study aims to enhance the reliability and scalability of weed detection systems by combining various methods. It focuses on comprehensive

data collection, augmentation, and preprocessing to boost model resilience in different environmental conditions. Key priorities include refining detection algorithms and exploring hardware options like high-performance GPUs and edge computing for real-time agricultural use. Thus far, the suggested system's examination has yielded encouraging results, with a mean average accuracy (mAP) of 74%. This research aims to improve crop management strategies and sustainable agricultural practices by combining these components and increasing the efficacy and scalability of the weed detection system.

### **G-P35 Seed Priming with Biostimulants Boost Soybean Germination and Vigor**

*Bala Subramanyam Sivarathri<sup>1</sup>, Nisarga Kodadinne Narayana<sup>1</sup>, Mohan Bista<sup>1</sup>, Corey J. Bryant<sup>2</sup>, K. Raja Reddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, MS, <sup>2</sup>Delta Research and Extension Center, Mississippi State University, MS

Plant biostimulants in agriculture are gaining popularity for their sustainable and eco-friendly benefits. They are also known to mitigate the adverse impacts of stress on crops effectively. Seed treatment techniques such as priming are highly effective in enhancing germination under unfavorable environmental conditions and making the crop more tolerant to stress during their growing season. Therefore, we hypothesized that priming with biostimulants would augment the germination potential of soybean under chilling stress compared to seeds treated with and without biostimulants. The study investigated the impact of biostimulants applied through (i) seed treatment and (ii) priming on germination characteristics under both low (LT, 15°C) and optimum (OT, 25°C) temperatures. Priming demonstrated a superior effect among the two seed treatment strategies evaluated, significantly improving germination percentage and reducing the time required to achieve 50% germination by 24 hours. Further, priming with Zyro and Fertiactyl resulted in rapid germination by 3.48 and 4.34 hours under LT and OT, respectively. Hydropriming led to the shortest time to achieve 50% germination under both treatments. In conclusion, seed priming enhanced germination ability traits compared to seed treatment with biostimulants.

### **G-P36 Assessing Soil Health and Land-Use Sustainability in Vermilion-Teche Basin, Louisiana**

*Bipin Bastakoti<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University

It is estimated that nearly 2 billion ha of soil resources in the world have been degraded and the rate is accelerated due to a change in land use pattern. This study examines land-use land-cover changes in the Vermilion-Teche Basin from 2004 to 2022 and assesses soil health conditions. Land-use land-cover data from satellite (MODIS Land Cover-V6.1- MODIS MCD12Q1 V6.1) and ground observed data from the National Agricultural Statistics Service were used along with soil characteristics datasets from Web Soil Survey and Survey Geographic Database, and precipitation data from the National Oceanic and Atmospheric Administration. Our results suggested that the acreage of agricultural land in the Vermilion-Teche Basin had a downward trend, which declined from 29.36% in 2004 to 25.59% in 2022 of the total land area of the basin. Similarly, pastureland declined from 20.95% in 2004 to 15.02% in 2022. In contrast, the developed area increased from 1.85% in 2004 to 11.10% in 2022, indicating rapid urbanization and infrastructural development in the basin. Forested areas, wetlands, and water bodies remained relatively stable. An overlay analysis of the developed area and the soil map unit in the Vermilion-Teche Basin showed 17 out of a total of 332 soil map units accounting for one-third (31,685.56 ha) of the total developed area



(99,932.79 ha) in the basin in 2022. The impervious surfaces in the built-up area obstruct rainwater infiltration, thereby increasing runoff and possible flooding downstream. These results indicate that the policymakers, land managers, and other stakeholders in the Vermilion-Teche Basin need to consider sustainable land use and soil and water conservation practices, especially in the developed areas of the basin to enhance environmental sustainability.

### G-P37 Integrative Genomic Annotation of *Populus deltoides*

*Carlos Rivera<sup>1</sup>, Esteban Galeano<sup>1</sup>*

<sup>1</sup>*Department of Forestry, Mississippi State University, Starkville, MS.*

The availability of sequenced genomes on the web allows for a breakthrough in genetic research, providing a crucial basis for the genetic understanding of various species. *Populus deltoides* is a poplar species of great interest for its use in bioenergy and ecosystem restoration. Different groups of researchers in China and the USA have made essential contributions to the sequencing and annotation of the *Populus deltoides* genome. In addition to sequencing the nucleic DNA, the Chinese team sequenced the transcriptome to identify coding regions and annotate them within the genome. Yet, these annotations are only found in positions where a gene can hypothetically be located. On the other hand, the team from Florida, USA, sequenced a different clone and compared its genome with known species, such as *Populus trichocarpa* (the most closely related and best-annotated species), *Arabidopsis thaliana*, among others, trying to locate the genes within the genome. Despite these efforts, there are still significant gaps in the available information, including the absence of genes expected to be found in the *Populus deltoides* genome or the lack of information on the proteins that these genes encode. The objective of this project is to use the various genomic resources available to create a more complete and accurate annotation of the *Populus deltoides* genome. By integrating and comparing data from different investigations, we seek to fill existing gaps and enrich the genetic annotation of this species. This will improve our understanding of the *Populus deltoides* genome and provide a valuable tool for future genetic research and biotechnological applications.

### G-P38 Nonthermal Plasma Assisted Desorption and *in-situ* Conversion of Captured CO<sub>2</sub> from Atmospheric Air

*Xiang Yizhi<sup>1</sup>, Chinwendu Umeojiakor<sup>1</sup>*

<sup>1</sup>*Dave C. Swalm School of Chemical Engineering, Mississippi State University, Mississippi State, MS 39762, USA*

CO<sub>2</sub> capture and conversion are essential tools to mitigate the global climate crisis. However, sorbent regeneration frequently relies on the high-temperature thermal-driven process, making the integration of intermittent renewable energy into the process become an inherent challenge. Herein, by using lime-based sorbent as a model system, we show that an electrified process for the desorption and *in-situ* conversion of captured CO<sub>2</sub> (with tunable selectivity to CO or CH<sub>4</sub>) can be achieved through a non-thermal dielectric-barrier discharge plasma reactor. Specifically, up to 82% of captured CO<sub>2</sub> (by pure CaO from atmospheric air) can be converted into CO under the discharge of 10% H<sub>2</sub>/Ar. The reaction is able to be tuned for CH<sub>4</sub> production when a dual function material, Ni-Ru CaO/CeO<sub>2</sub>-Al<sub>2</sub>O<sub>3</sub>, or a physical mixture of CaO and a Ru/Al<sub>2</sub>O<sub>3</sub> methanation catalyst is employed. The kinetics of such a process are evaluated based on the nonsteady-state semi-batch reactor model. The reactions are identified to be first order for both CO<sub>2</sub> desorption and hydrogenation process.

### G-P39 Developing Decision Support Tools (DSTs) for enhancing participation in USDA's Conservation Reserve Program: What do stakeholders expect to see?

*Daniel Egerson<sup>1</sup>, Bradly Thornton<sup>2</sup>, Shannon Westlake<sup>3</sup>, Mark McConnell<sup>1</sup>, Sathishkumar Samiappan<sup>4</sup>, Amanda Sesser<sup>5</sup>, Diego Thompson<sup>1</sup>, Kristine Evans<sup>1</sup>*

<sup>1</sup>*Mississippi State University, <sup>2</sup>Nebraska Coop Fish & Wildlife Research Unit, <sup>3</sup>U.S. Fish and Wildlife Service Southeast Region, <sup>4</sup>Geosystems Research Institute, Mississippi State University, <sup>5</sup>US Fish & Wildlife Service*

Integrating DSTs into the Conservation Reserve Program (CRP) holds promise for enhancing conservation efforts, however existing tools have not effectively bridged knowledge gaps or engaged landowners as expected. To inform a CRP DST development for increased landowner understanding and engagement, we conducted 12 stakeholder workshops with 91 landowners and 145 practitioners across Mississippi, Missouri, and Illinois. Data from open and small group discussions were thematically analyzed using QDA Software, revealing six major themes. Stakeholders expect a CRP-DST to allow exploration of all conservation practices and payment rates, provide up-to-date enrollment information, outline management requirements, assess land and landowner eligibility, and enable scenario planning aligned with rental payment expectations. Desired features include filter options, a search function, report generation, etc. While landowners anticipate streamlined online signup, practitioners caution against this, citing the need for physical property verification. To mitigate conflicts, practitioners warn against providing inaccurate information, particularly regarding payment rates. Our thematic analysis offers valuable insights for the development of CRP DST to enhance engagement and decision-making for participating landowners.

### G-P40 Dissecting the Role of Cover Crops and Nitrogen Fertilization in Microbially-Mediated Nutrient Cycling in Corn Systems

*Durga P.M Chinthapudi<sup>1,2</sup>, Joshua White<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>, Shankar Ganapathi Shanmugam<sup>1,2</sup>*

<sup>1</sup>*Mississippi State University, Department of Plant and Soil Sciences., <sup>2</sup>Mississippi State University, Institute of Genomics, Biocomputing, and Biotechnology.*

Soil microbial communities are integral to part of soil ecosystem functions that respond to plant diversity and fertilization changes. However, the combined impact of these factors on microbial functional diversity and carbon/nitrogen (C/N) cycling in corn production systems remains underexplored. This study addresses this gap by examining the effects of various cover crops (CCs) and nitrogen (N) levels on soil microbial communities and C/N cycling in corn systems over two years (2022-23) using a strip plot design across two locations with distinct soil types: Starkville and Newton. The CC treatments included ryegrass (RY), Balansa (BL), a mix (ryegrass + radish + red clover), and a control (C), with N levels at 0 lb. and 100 lb. The Chao1 diversity index revealed higher bacterial ASV richness in 2022 compared to 2023 ( $p < 0.001$ ). Notably, plots receiving 100 lbs. of N exhibited elevated Shannon diversity compared to 0 lbs. N plots ( $p = 0.003$ ). Enzymatic assays for  $\beta$ -glucosidase (BG) and  $\beta$ -glucosaminidase (NAG), along with POXC, indicated variations across treatments. ANOVA results for BG activity showed significantly higher values in RY ( $3.47 \pm 0.22$ ) and Mix ( $3.43 \pm 0.25$ ) plots ( $p = 0.0021$ ). Similarly, NAG activity was elevated in RY ( $2.01 \pm 0.16$ ) and Mix ( $1.93 \pm 0.24$ ) plots ( $p < 0.001$ ). For POXC, RY plots recorded the highest value ( $724.6 \pm 9.60$ ), followed by Mix ( $713.92 \pm 8.32$ ). Additionally, the copy number of N-cycle genes *amoA*

and nifH varied significantly across CC treatments ( $p < 0.05$ ), highlighting the role of CCs in shaping soil N-cycling capabilities. Overall, ryegrass and mix treatments showed higher bacterial diversity, and their functions towards C/N cycling in corn production systems.

#### **G-P41 Effects of DL-methionine on the Growth Performance and Blood and Liver Antioxidant Status in Growing Pigs**

*Emmanuel Oladejo<sup>1</sup>, Susan Sotak<sup>1</sup>, James Brett<sup>1</sup>, John Htoo<sup>2</sup>, Shengfa Liao<sup>1</sup>*

<sup>1</sup>Mississippi State University, <sup>2</sup>Evonik Operations GmbH

Oxidative stress condition harms pigs' health and growth performance. This study investigated whether supplementing more DL-Methionine (Met) would exert an anti-oxidative effect in diquat-challenged pigs. Twenty pigs (average weight 21.5 kg) were divided into two groups and fed a corn-and-soybean-meal diet meeting or exceeding NRC (2012) standards. Group 1 received a basal diet (D1), while Group 2 received a DL-Met supplemented diet (D2) with 25% more SID Met+Cys than D1. After three weeks of feeding (Phase 1), pigs were injected with 10 mg/kg-BW diquat in 10 mL saline and fed for one more week (Phase 2). Growth performance (ADG, ADFI, G:F ratio) was measured at the end of each phase. Blood samples were collected on Days 1, 22, and 29, and liver samples on Day 29, which were assayed for the oxidative biomarkers that included MDA, GSH, SOD, CAT, GPX, and TAC. Statistical analysis was performed using Student's t-test. In Phase 1, no differences were observed between the two groups in initial and final BW, ADFI, ADG, and G:F ratio, or in serum and liver MDA, GPX, SOD, CAT, TAC, and GSH. By the end of Phase 2, there were no differences in ADFI, ADG, G:F ratio, and final BW between the two groups. However, Group 2 had a higher serum TAC ( $P < 0.05$ ), higher serum and liver GPX ( $P < 0.05$ ), and a higher liver SOD ( $P = 0.08$ ) comparing to Group 1. In conclusion, although additional DL-Met did not improve the growth performance of the oxidatively stressed pigs, their anti-oxidative status was improved.

#### **G-P42 An Effective Live-Attenuated Zika Vaccine Candidate with Modified 5' Untranslated Region**

*Farzana Nazneen<sup>1</sup>, Elizabeth Thompson<sup>1</sup>, Faqing Huang<sup>1</sup>, Fengwei Bai<sup>1</sup>*

<sup>1</sup>The University of Southern Mississippi, MS, USA

Zika virus (ZIKV) is a mosquito-transmitted flavivirus that caused devastating congenital Zika syndromes (CZS), including microcephaly, congenital malformation, and fetal demise in human newborns in recent epidemics. ZIKV infection also causes Guillain-Barré syndrome (GBS) and meningoencephalitis in adults. Despite intensive research in recent years, there is no approved vaccine or antiviral therapeutics against CZS and adult Zika diseases. We developed a novel live-attenuated ZIKV strain (named Z7) by inserting 50 RNA nucleotides (nt) into the 5' untranslated region (UTR) of a pre-epidemic ZIKV Cambodian strain, FSS13025, which is attenuated in neurovirulence, immune antagonism, and mosquito infectivity compared with the American epidemic isolates. Our data demonstrate that Z7 replicates efficiently and produces high titers without causing apparent cytopathic effects (CPE) on Vero cells or losing the insert sequence even after ten passages. Significantly, Z7 induces robust humoral and cellular immune responses that completely prevents viremia after a challenge with a high dose of an American epidemic strain (PRVABC59) in type I IFN receptor A deficient (*Ifnar1<sup>-/-</sup>*) mice. Moreover, adaptive transfer of plasma collected from Z7-immunized mice protects *Ifnar1<sup>-/-</sup>* mice from ZIKV infection. These results suggest that modifying the ZIKV 5'UTR is a

novel strategy to develop live-attenuated vaccine candidates for ZIKV and potentially for other flaviviruses.

#### **G-P43 Elucidating the Mechanism of Interleukin-17A Signaling in the Pathogenesis of West Nile Virus**

*Farzana Nazneen<sup>1</sup>, Biswas Nupane<sup>2</sup>, Shazeed Ul Karim<sup>1</sup>, Fengwei Bai<sup>1</sup>*

<sup>1</sup>The University of Southern Mississippi, <sup>2</sup>University of Pittsburgh, MS

West Nile Virus (WNV), a mosquito-borne neurotropic flavivirus, is considered as one of the leading causes of viral encephalitis. Since its detection in 1999 in the United States (US), 56,569 patients were diagnosed with WNV infection with 2,773 deaths due to various forms of neuroinvasive complications. As WNV is endemic to 48 states of the US, a constant threat of sudden WNV outbreak remains. But no vaccine or therapeutic is available against WNV infection. Our lab previously reported that interleukin-17A (IL-17A) promotes WNV clearance by facilitating the cytotoxicity of CD8<sup>+</sup> T cells. As IL-17A has therapeutic potential, it is important to understand the detailed mechanism of how IL-17A promotes cytotoxicity. Utilizing the IL-17A receptor C deficient (*Il17rc<sup>-/-</sup>*) mouse model, our preliminary studies showed that *Il17rc<sup>-/-</sup>* mice are more susceptible to WNV infection with higher viral load in brain and reduced cytotoxicity in WNV-specific CD8<sup>+</sup> T cells. Thus, it is inferred that IL-17RC subunit is important for protection against WNV infection and IL-17A initiates its signaling utilizing the IL-17RC subunit to promote the cytotoxicity of CD8<sup>+</sup> T cells. Data also showed that treatment with rIL-17A can increase the cytotoxicity in WNV-specific CD8<sup>+</sup> T cells. Interestingly, we found a novel role of IL-17A signaling in activating the phosphatidylinositol-3-kinase/mammalian target of rapamycin (PI3K/mTOR) signaling pathway in CD8<sup>+</sup> T cells in mRNA level which in turn increases metabolism in CD8<sup>+</sup> T cells to cope-up with the higher energy demand. Thus, our results demonstrated a novel mechanism of IL-17A signaling in the pathogenesis of WNV.

#### **G-P44 Method for In-situ Biomethanation of Biogas from the Anaerobic Digestion of Liquid Food Waste.**

*Froilan Aquino<sup>1</sup>*

<sup>1</sup>Mississippi State University, MS, USA

Small-scale anaerobic digestion (SSAD) systems, or digester systems processing between 200-5,000 tons of organic waste per year, typically generate less biogas which are often of lower quality. Biogas from SSAD systems typically consists of about 40%-60% vol. methane (CH<sub>4</sub>) with carbon dioxide (CO<sub>2</sub>) making up the balance. Oftentimes, it makes more economic sense for SSAD operators to either immediately flare the low-quality biogas or vent it directly into the atmosphere which contributes to higher carbon emissions. This research aimed to develop a technique for an "in-situ" upgrading of low-quality biogas from SSAD systems into close to pipeline-quality biomethane (i.e., with CH<sub>4</sub> content of 90% vol. or higher) using a new method for introducing hydrogen gas (H<sub>2</sub>) into the digester. Externally sourced H<sub>2</sub> was used to enhance the target biological processes for increasing CH<sub>4</sub> yield in the digester including acetogenesis and hydrogenotrophic methanogenesis. Our initial test results showed that the new H<sub>2</sub> delivery technique generated more CH<sub>4</sub> in the biogas during the digestion process (*in-situ*), thus improving the quality of the output biogas. The increase in methanogenic bacteria population indicated a positive response to the H<sub>2</sub> addition in the digester. Consequently, the CH<sub>4</sub>-content of the biogas also increased by approximately 46% compared to baseline biogas yield. However, the highest CH<sub>4</sub> content achieved was around 72% vol., suggesting other factors may have influenced the digester's performance during the *in-situ* biomethanation process.

**G-P45 Assessing Heat Responses of South Mississippi Grown Interspecific Hybrid Bunch Grapes***Haley Williams<sup>1</sup>, Eric Stafne<sup>1</sup>, Jenny Ryals<sup>1</sup>*<sup>1</sup>Mississippi State University, MS, USA

In Mississippi's challenging climate, with high heat, rainfall, and humidity, identifying resilient grape (*Vitis* spp.) cultivars is essential for sustainable viticulture. In 2023, the heat tolerance of nine interspecific hybrid bunch grape cultivars ('Ambulo Blanc', 'Black Spanish', 'Blanc du Bois', 'Lomanto', 'MidSouth', 'Miss Blanc', 'Muench', OK392, 'Victoria Red') were assessed at the Mississippi State University South Mississippi Branch Experiment Station in Poplarville, Mississippi. Stomatal density, conductance, transpiration, vapor pressure deficit, and chlorophyll fluorescence were evaluated in the field and via a 4-hour heat simulation, where leaf disks were heated from 25°C to 45°C at a rate of 5°C per hour. 'Miss Blanc' and OK392 had the highest stomatal density, while 'Black Spanish' had the lowest. Monthly in-field measurements showed no significant physiological differences among cultivars. In the heat simulation, 'Lomanto' had high stomatal conductance and transpiration, while OK392 had lower values. 'MidSouth' displayed high chlorophyll fluorescence, and 'Ambulo Blanc' had consistently lower levels. 'Miss Blanc' and OK392 exhibited high vapor pressure deficit, whereas 'MidSouth' showed low values. In 2023, 'MidSouth', with high chlorophyll fluorescence and low vapor pressure deficit, was characterized as the most heat-tolerant cultivar. Early 2024 results further corroborate these findings, with 'MidSouth' having high transpiration, relatively low vapor pressure deficit, and high chlorophyll fluorescence, suggesting that it manages heat stress by cooling itself through transpiration, avoiding excessive water loss, and maintaining photosynthetic efficiency. These findings enhance the understanding of grapevine physiological responses to heat and assist in the selection of resilient cultivars for production in challenging environments.

**G-P46 Rumen Microbiome Signature-Based Machine Learning Model for Heat Stress Prediction***Himani Joshi<sup>1</sup>, Michael Caprio<sup>2</sup>, Lindsey Reon<sup>1</sup>, Peixin Fan<sup>1</sup>*<sup>1</sup>Department of Animal and Dairy Sciences, Mississippi State University, <sup>2</sup>Department of Biochemistry, Molecular Biology, Entomology and Plant Pathology, Mississippi State University, MS, USA

Heat stress has a huge negative impact on the global dairy industry, leading to huge loss in milk production, reproduction, and alteration of rumen microbiota, affecting rumen fermentation functions in dairy animals. Until now, none of the microbiome studies reported consistent heat-stress-associated rumen microbes in cattle. Therefore, to evaluate specific rumen microbiota markers in dairy cattle, we collected 16S sequencing data of 96 rumen samples of dairy cows from eight published studies and built machine learning models with the rumen microbiota profile to predict the heat stress. All the raw sequencing data was re-analyzed with QIIME2 software and Silva 138.1 database. The sequencing depth and matrix of absence/presence of the 988 bacterial taxa served as independent variables to predict heat stress as the response. The important independent variables were firstly selected using Burota package of R. The feature-selected dataset containing 11 important bacterial signatures was further trained using algorithms, i.e. Random Forest (RF), and Support Vector Machines (SVMs). The trained models predicted heat stress with an area under the receiver operating characteristic curve (AUROC) of 0.86-0.95. SVMs outperformed RF with a mean accuracy of 86% and a specificity of 93%. Moreover, it has been found that model selected features, such as *Bacteroidales* BS11 and *Bacillus*, have also been reported to be enriched in heat-stressed cattle in multiple studies,

suggesting their potential association with heat stress. In conclusion, the unique rumen microbiota feature obtained from this model can be used to develop mitigation strategies targeting heat stress responses in dairy cows.

**G-P47 Characterizing Frass Associated Microbiome for Enhancing Plant Growth***Jasmine Sahota<sup>1, 2</sup>, Jagman Dhillon<sup>1</sup>, Shankar Ganapathi Shanmugam<sup>1, 2</sup>*<sup>1</sup>Mississippi State University, Department of Plant and Soil Sciences,<sup>2</sup>Mississippi State University, Institute of Genomics, Biocomputing and Biotechnology, MS, USA

The insect breeding for feed and food generates a significant amount of frass, which comprises a diverse community of microorganisms that can serve as an effective biofertilizer. Applying insect frass as a soil amendment can play a pivotal role in nutrient cycling and soil health. However, the compositional dynamics of frass and the associated microbiome have received little attention. To bridge this gap, we studied the microbiome related to insect frass and its potential use as a biofertilizer. We collected insect frass samples from various insect species fed on different diet sources that were subjected to different industrial treatments. Genomic DNA was extracted from these samples, followed by amplicon sequencing to target 16S-V4 region (bacterial) and ITS2 (fungal) to characterize the microbial communities present in insect frass. Microbial abundance in cricket frass samples exhibited the highest alpha diversity, which varied significantly according to different diet sources and industrial treatments. Beta diversity showed distinct microbial community structures influenced by insect species and diet. The bacterial phylum *Firmicutes* was the most abundant across all frass samples with the relative abundance ranging from 45-80% across different diet sources. These findings contribute to understanding the ecological significance of insect frass and its associated microbial communities. Further, analyses using Biolog Ecoplates and functional prediction tools such as PICRUST2 revealed the metabolic capabilities of microbial communities in frass, highlighting their role in carbon and nitrogen cycling.

**G-P48 Improving Stem Cutting Propagation of Grapevine Species***Jenny Ryals<sup>1</sup>, Haley Williams<sup>1</sup>, Patricia Knight<sup>1</sup>, Eric Stafne<sup>1</sup>, Scott Langlois<sup>1</sup>*<sup>1</sup>Mississippi State University, MS, USA

Improving stem cutting propagation of grapevine species holds immense importance with the growing interest in grapevine cultivation in the region. Propagating these plants from stem cuttings can be a challenging endeavor. As a result, this research initiative seeks to address this issue by exploring methods to enhance the success rate of stem cutting propagation. By developing more efficient and reliable techniques, nurseries can increase their ability to supply grapevine plants to local growers, which not only expands the availability of grapevines in the market, but also plays a pivotal role in bolstering the wine industry in Mississippi. By facilitating the growth of this industry, improved grapevine propagation methods contribute to economic development, agricultural diversification, and ultimately benefiting the local economy and wine enthusiasts. Hardwood cuttings of four bunch grape varieties: 'Miss Blanc', 'Mid-South', 'Norton' and OK392 were subjected to 10 hormone treatments of indole-3-butyric acid (IBA) alone and in combination with ascorbic acid. These treatments were applied as a basal quick dip. Sixty days after treating, rooting percentage, growth index (new shoots), cutting quality (0-5, with 0 = dead and 5 = transplant-ready cutting), total root number, average root length (of three longest roots), and root quality (0-5, with

0=no roots and 5=healthy, vigorous root system) data were collected. Of the four varieties trialed, 'Miss Blanc' and OK392 performed the best with the greatest rooting percentages of 95% and 52.5%, respectively. Both rooted successfully regardless of treatment applied.

#### **G-P49 Evaluating the Impact of Cover crop and Nitrogen treatments on Soil Microbial dynamics in Sweet Potato production system**

*Lahari Nekkalapudi<sup>1, 2</sup>, Shankar Ganapathi Shanmugam<sup>1, 2</sup>, Mark Shankle<sup>1</sup>, Lorin Harvey<sup>1</sup>, Michael Cox<sup>1</sup>*

<sup>1</sup>Mississippi State University, Department of Plant and Soil Sciences,

<sup>2</sup>Mississippi State University, Institute of Genomics, Biocomputing and Biotechnology, MS, USA

Mississippi is the third-largest, sweet potato producer in the U.S. Sweet potato requires adequate nitrogen for sustainable yields. Microorganisms mediate nitrogen transformations from fertilizers, organic matter, and crop residues. Limited research exists on studying soil health implications of soil microorganisms in cover crop - sweet potato systems. Field study was initiated at Pontotoc Ridge-Flatwoods Branch Experiment Station, Pontotoc, Mississippi to assess the effects of cover crops on nitrogen availability in sweet potato. This study was implemented in a randomized block design following a split block arrangement and replicated four times. Three N treatments (0, 50, 100 lb/acre) and three cover crop treatments (no cover crop, winter wheat, and clover) were adopted. Cover crops were planted in fall and terminated in spring before planting sweet potato. Soil samples were collected at the time of planting, after harvesting of sweet potato and at the termination of cover crop. Changes in soil microbiome were characterized by sequencing the amplicons targeting the bacteria (16s) and fungal (ITS). DNA sequence data was analyzed using QIIME (Quantitative insights into microbial ecology). R statistical software was used for sequence data analysis. Cover crop treatments showed significant difference in measured soil permanganate-oxidizable carbon (PoXC). Specifically, cover crop treatment showed significantly higher soil PoXC levels than control treatment. Sequencing data revealed a significant difference (p-value:0.02) in microbial alpha diversity among nitrogen treatments. Beta diversity analysis indicated a significant difference in soil microbial community composition influenced by both cover crop (p-value: 0.04) and N treatments (p-value: 0.02).

#### **G-P50 Identifying Trends in Racial and Ethnic Disparities in Labor Neuraxial Use**

*Landry Smtih<sup>1</sup>, Michelle Tucci<sup>1</sup>, Chawla Mason<sup>1</sup>*

<sup>1</sup>Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216

Neuraxial anesthesia, which includes epidural and spinal analgesia, is widely used for pain management during labor. In the US, the literature shows estimates between 60%- 75% of women utilize neuraxial analgesia during labor. However, the literature also shows lower utilization rates among marginalized racial and ethnic groups. The objective of our study was to evaluate the trend in neuraxial analgesia use for vaginal delivery from January 1-31, 2024 at the University of Mississippi Medical Center, Wiser Hospital. Labor and Delivery logs from the labor and delivery ward at Wiser hospital were evaluated for live births during the Month of January, 2024. Race and Hispanic ethnicity were recorded, along with type of delivery and use of neuraxial analgesia. The data were further placed into a REDCap database and exported into Microsoft Excel in order to evaluate the data. The rate of neuraxial analgesia was 61.8% among 214 births. At our institution, the percent of vaginal deliveries by race were 60% for black individuals and 57% for white and Hispanic individuals. In

assessing epidural use for vaginal delivery, it was found that 38% of Hispanic individual utilized neuraxial analgesia, while greater than 90% of black and white individuals. Our data suggests the need for better communication with our Hispanic women to understand if the lack of utilization or resistance of use is due to cultural myths, financial burden of self-pay, or lack of education.

#### **G-P51 Chilling Tolerance of Diverse Soybean Genotypes during Seedling Emergence**

*Vijaykumar Hosahalli<sup>1</sup>, Bikash Adhikari<sup>1</sup>, Sujan Poudel<sup>1</sup>, K. Raja Reddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, MS, 39762

Soybean yields are greatly affected by moisture and temperature stress during the growing season. Historical data from the US Midsouth, including Mississippi, shows that soybeans are often exposed to unfavorable conditions, resulting in significant yield losses. Therefore, adopting an early-season planting approach similar to corn (*Zea mays*) could offer an opportunity to escape some drought and heat stress damages during the flowering and seed-filling period and efficiently utilize late spring and early summer rainfall for soybean growth and development. Soybean requires average soil temperatures of 25°C for uniform seedling emergence percentage and to maintain post-emergence seedling vigor and health. No systematic studies have explored the genetic potential of soybean cultivar responses to chilling tolerance. To address this knowledge gap, seventeen high-yielding soybean genotypes from diverse sources were evaluated for chilling (15°C) tolerance using an incubator, growth chamber, and field-like conditions. Under chilling stress, the average germination rate decreased, and the time required to reach 50% germination or emergence was prolonged compared to conditions at 25°C. Furthermore, significant differences in the levels were noted for photosynthetic pigments among the soybean genotypes under chilling stress. Our findings suggest that the soybean genotypes exhibit varied responses to chilling stress, with some genotypes displaying higher seedling vigor under chilling conditions. Based on three different experiments, chilling-tolerant genotypes with greater germination or emergence and high vigor were identified. Findings indicate significant genetic variability in chilling stress and could be explored for breeding tolerant genotypes.

#### **G-P52 Numerical Evaluation of Engineered Wood Beams with Honeycomb Core**

*Manikanta Thati<sup>1</sup>, Aadarsha Lamichhane<sup>2</sup>, Mostafa Mohammadabadi<sup>2</sup>*

<sup>1</sup>Computational Engineering Graduate Program, Mississippi State University, Starkville, MS 39762, <sup>2</sup>Department of Sustainable Bioproducts, Mississippi State University, Starkville, MS 39762

Mass timber products, which can compete with steel and concrete in the construction of tall buildings, are gaining popularity in North America due to their sustainability and structural performance. The question that arises here is how small-diameter trees, often underutilized due to the lack of a high-value market, can be used to develop high-structural performance products. Such achievement creates a high-value market for small-diameter trees, which in turn promotes sustainable forest management practices, resulting in improved forest health and reduced wildfire risk. In this study, corrugated geometries, resulting in significant advancements in the aerospace and automotive industries, were adopted to convert small-diameter trees into high-performance engineered wood products. Wood strands mixed with phenol formaldehyde adhesive were hot-pressed between the halves of a matched-die mold to produce wood-



based corrugated panels. However, corrugated panels with different geometries and honeycomb cores with different orientations can be designed to develop engineered beams. Since it is costly and time-consuming to fabricate and experimentally evaluate all these geometries and orientations, this study developed a Finite Element (FE) model for wood beams with honeycomb core. Evaluation of these beams in the virtual environment of Abaqus FE model provided insight into the effect of honeycomb core orientation on beam structural performance. To verify the accuracy of this FE model, these beams were manufactured and will be experimentally tested. An accurate FE model enables us to modify the geometry of the corrugated panels and the orientation of the honeycomb core to optimize the engineered beams' structural performance for different applications.

#### **G-P53 Do Multiple Abiotic Stresses Affect the Early Growth and Development of Cotton Differently in Current and Future CO<sub>2</sub> Levels?**

*Mohan Kumar Bista<sup>1</sup>, Purushothaman Ramamoorthy<sup>1</sup>, Ranadheer Reddy Vennam<sup>1</sup>, Sadikshya Poudel<sup>1</sup>, K. Raja Raddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, USA

Projected temperature, precipitation, and soil quality changes will impact cotton production. Reports suggest that elevated CO<sub>2</sub> (eCO<sub>2</sub>) may negate the damage caused by stressors through improved physiological performance. Although multiple studies reported the impact of single stress on the morpho physiology of cotton under ambient CO<sub>2</sub> (aCO<sub>2</sub>, 420 ppm; current) and eCO<sub>2</sub> (700 ppm; future) levels, limited studies have explored the responses of cotton to multiple stressors with eCO<sub>2</sub> during the vegetative stage. This study quantified low (LT, 22/14°C, day/night) and high temperature (HT, 33/30°C, day/night), drought stress (DS, 50% irrigation of the control), and salt stress (SS, 8 dS<sup>-1</sup>) impact on pigments, physiology, growth, and development using fourteen cotton genotypes under contrasting CO<sub>2</sub> levels during the vegetative stage. The eCO<sub>2</sub> negated the effects of all stresses on most of the physiological traits. For example, HT at the aCO<sub>2</sub> significantly increased stomatal conductance by 36% compared to the control. Conversely, a combination of HT+eCO<sub>2</sub> decreased stomatal conductance by 18% compared to HT+aCO<sub>2</sub>. The first square development was delayed by one day under SS+aCO<sub>2</sub> and advanced by two days under SS+eCO<sub>2</sub> than control-grown plants. Leaf area, shoot, and root dry weights increased higher under all stresses, except for LT+eCO<sub>2</sub>, than other combinations. The root-to-shoot ratio increased under DS and LT and *vice versa* under HT and SS compared to the control. Among the evaluated genotypes, PhytoGen PSC355 exhibited greater stress resilience to aCO<sub>2</sub> and eCO<sub>2</sub> levels, indicating its potential use as a recurrent donor in stress-tolerance breeding programs. Morpho-physiological adaptation of tolerant cotton genotypes to multiple stressors compared to sensitive ones under aCO<sub>2</sub> and eCO<sub>2</sub> levels will be discussed.

#### **G-P54 Effect of Corn Hybrid, Plant Population and Nitrogen Rate on Grain Yield and Quality**

*Namita Sinha<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>, Vaughn Reed<sup>1</sup>, Daniel Jeffers<sup>2</sup>, Brian Henry<sup>1</sup>, Jagman Dhillon<sup>1</sup>*

<sup>1</sup>Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, 39762, <sup>2</sup>USDA-ARS, Mississippi State University, Mississippi State

Corn (*Zea mays* L.) is a staple food and feed worldwide, providing starch as the major nutrient, in addition to fiber, protein, and oil. Consumption of corn has several health benefits such as lowering the risk of cardiovascular diseases, type II diabetes, and obesity. However,

ingestion of ear rot infected corn can lead to various diseases such as hepatocellular carcinoma in humans, and oesophageal cancer, equine leukoencephalomalacia (ELEM) in horses (*Equus caballus*), and porcine pulmonary edema in pigs (*Sus scrofa domesticus*). Moreover, corn diseases such as Aspergillus ear rot, Fusarium stalk rot, Fusarium ear rot, gray leaf spot, and southern rust, produced by different fungi (*Aspergillus flavus*, *Fusarium verticilloides*, *Cercospora zea maydis*, *Puccinia polysora*) cause substantial yield and quality loss. Therefore, a two-year multi-site study was conducted to analyze the effect of different plant population, corn hybrid and nitrogen rates on grain yield and quality. The factors tested includes four plant populations (75,000, 87,500, 100,000 and 112,500 plants ha<sup>-1</sup>), N rates (0, 112, 224, and 336 kg N ha<sup>-1</sup>) and corn hybrids with and without *Bt* traits (DKC 70-27 and DKC 70-25, respectively) in a split-plot design. Higher N rates and lower plant population are hypothesized to have better grain yield and quality. The overarching aim is to determine agronomic optimum plant population (AOPP) and agronomic optimum nitrogen rate (AONR) to improve the corn yield and quality. Preliminary results will be presented.

#### **G-P55 Persistent Extreme Heat Exposure Among Socially Vulnerable Communities in the Contiguous United States: A Two-Decade Analysis**

*Nishat Shermin<sup>1</sup>, Narcisa Pricope<sup>2</sup>, Sk Nafiz Rahaman<sup>3</sup>*

<sup>1</sup>Graduate Student, Department of Geosciences, Mississippi State University, <sup>2</sup>Associate Vice President for Research and Professor, Department of Geosciences, Mississippi State University, <sup>3</sup>Graduate Student, Department of Geosciences, Auburn University, USA

Socio-economically disadvantaged communities in the United States, often comprising minority groups, children, and the elderly, face heightened exposure and reduced resilience to extreme heat events. These households typically lack health insurance and live in crowded conditions, exacerbating their vulnerability. Despite national and local initiatives for extreme heat planning and urban heat management, the trajectory of heat exposure among these socially vulnerable groups remains underexplored. In this study, we analyze county-level Social Vulnerability Index (SVI) data from the Agency for Toxic Substances and Disease Registry (ATSDR) alongside average Land Surface Temperature (LST) data from the Parameter-elevation Regressions on Independent Slopes Model (PRISM) dataset from 2000 to 2020. Employing advanced geostatistical techniques such as Geographically Weighted Regression (GWR), we examine the evolution of heat exposure among socially vulnerable populations in the conterminous USA over the past two decades. Our findings reveal a consistent correlation between SVI and LST (ranging from 0.5 to 0.6) across the years, indicating persistent heat exposure zones in the southwestern United States, notably California, Nevada, and Colorado. These regions are recognized for high homeless populations and recurrent droughts, posing significant health risks. The results underscore enduring inequities in heat exposure among socio-economically vulnerable populations, emphasizing the urgent need for targeted and sustained intervention strategies to shield these at-risk communities from the escalating impacts of extreme heat.

#### **G-P56 MicroRNA Profiles of Seminal Plasma Extracellular Vesicles Reflect Boar Sperm Quality**

*Notsile Dlamini<sup>1,2</sup>, Scott Willard<sup>1,2</sup>, Peter Ryan<sup>2</sup>, Jean Feugang<sup>1,2</sup>*

<sup>1</sup>Department of Animal and Dairy Sciences, <sup>2</sup>Mississippi State University, MS, USA

Boar fertility hinges on high-quality semen doses to optimize reproductive efficiency. Seminal plasma (SP), the primary environment for sperm, contains extracellular vesicles (EVs) that carry

microRNAs that influence sperm function. SP-EV miRNAs could be used to detect potential biomarkers for semen quality. We hypothesized that the microRNA profiles of SP-EVs could indicate the quality status of boar semen. This study aimed to analyze SP-EV microRNAs isolated from accepted (Passed) or rejected (Failed) boar semen samples. Over eight weeks, raw semen ( $n = 83$ ) was collected from sexually mature Duroc boars at Prestage Farms, MS. Samples were analyzed for sperm motility and morphology and classified as Passed ( $\geq 70\%$ ) or Failed ( $< 70\%$ ) based on predefined criteria ( $\geq 70\%$  and  $< 70\%$ , respectively). SP-EVs were isolated using differential centrifugation and characterized by transmission electron microscopy (TEM) and nanoparticle tracking analysis (NTA). Illumina NextSeq sequencing was used to identify SP-EV miRNAs. Data analysis was conducted using SPSS, with significance set at  $P < 0.05$ . TEM and NTA confirmed spherical EV structures with a size of 50-300 nm. Passed SP-EVs expressed 443 miRNAs, while Failed SP-EVs expressed 437 miRNAs. MiRNA differential analysis identified 28 downregulated and two upregulated miRNAs in Passed vs. Failed groups. Lastly, miRNA gene targets were associated with biological functions such as Ub1 conjugation, acetylation and RNA binding, suggesting SP-EVs' potential in influencing boar sperm quality.

#### **G-P57 Macrofauna Accelerates Nutrient Cycling Through Litterfall in Cocoa**

*O. Oyedele<sup>1</sup>, Michael J. Mulvaney<sup>1</sup>, D-G.J.M Houghn<sup>2</sup>, S. Hauser<sup>3</sup>, A. G. T Schut<sup>4</sup>, L. S Woittiez<sup>4</sup>, L. Rusinamhodzi<sup>5</sup>, M. Ogunlade<sup>6</sup>, K. E. Giller<sup>4</sup>*

<sup>1</sup>Plant and Soil Science, Mississippi State University, <sup>2</sup>International Maize and Wheat Improvement Center, <sup>3</sup>International Institute of Tropical Agriculture, <sup>4</sup>Plant Production Systems, Wageningen University and Research, Wageningen, the Netherlands, <sup>5</sup>International Institute of Tropical Agriculture, Accra, Ghana, <sup>6</sup>Cocoa Research Institute of Nigeria

Nutrient cycling in cocoa (*Theobroma cacao* L.) systems is poorly understood, but is critical to understand in order to design improved nutrient management strategies. This study aimed to understand better N, P, and K cycling through litterfall in smallholder cocoa fields and to assess if these nutrient flows can be measured with standard litterbags. Annual litter production, relative mass loss and nutrient loss rates from cocoa leaf litter were evaluated at three farms in South-Western Nigeria with and without macrofauna access. Litterfall was measured fortnightly close to the base of the cocoa tree and at the edge of the tree canopies from January 2020 to December 2021. Leaf litter decomposition rates were determined over 388 days in 2 mm mesh litterbags to exclude macrofauna and in frames open to the soil surface to allow macrofauna access. Concentrations of C, N, P, and K were measured in the remaining litter at 180, 244, 314, and 388 days after incubation. Annual estimates of litterfall (10.62 Mg DM ha<sup>-1</sup>) did not significantly differ between the traps close to and away from the cocoa tree trunk. Nutrient cycling from litter was roughly estimated at 101 kg N, 5 kg P and 89 kg K ha<sup>-1</sup> year<sup>-1</sup>. Relative litter decomposition rates (k) significantly differed between frames and litterbags. Macrofauna access significantly reduced the C: N ratio in the remaining litter and increased N and P loss from the litter layer by 28 and 69%, respectively. In conclusion, nutrient flows through litterfall are considerable, and N and P transfer rates to soil are likely underestimated in litterbag experiments that exclude macrofauna.

#### **G-P58 Climate Change Impact Assessment and Adaptation and Mitigation Measures for Major Field Crops in Guatemala and Honduras: Feed the Future Countries**

*Prasanna Bayalusime<sup>1</sup>, Ruchita Bhattarai<sup>1</sup>, Anitha Madapakula<sup>1</sup>, Prakash Kumar Jha<sup>2</sup>, Prakash Kumar Jha<sup>2</sup>*

<sup>1</sup>Mississippi State University, <sup>2</sup>University of California - Merced

Climate change poses a formidable threat to global agriculture, prompting research into its potential impacts based on the IPCC sixth assessment and various Representation Concentration Pathway (RCP) scenarios in Guatemala and Honduras. The primary goal of the research is to develop effective adaptation and mitigation strategies to counter the adverse effects of climate change under different climatic models for major crops in Guatemala and Honduras. First, the study was conducted on assessing impact of climate parameters under historical (1970-2000) and future (2025-2100) RCP 2.6 and RCP 8.5 climate change scenarios. We found that ensembling multiple climate models led to robust understanding of future climate conditions. Our ensemble climate model studies highlighted that for RCP 8.5 scenario rainfall had ranged from -28 % to 12 % and maximum temperature increased up to 6° C in Guatemala. Similarly, Honduras rainfall ranged from -28 % to 8 % and maximum temperature may increase up to 4 ° C from 2071 to 2100 in comparisons with historical data from 1970-2000. To assess the impact of climate change on major field crops, the DSSAT crop model was used to simulate crop growth and yield. The gridded soil database from Harvard data base and downscaled weather data from climate model were used to run DSSAT for each grid to estimate crop yields. These yields reflect the impact of climate change on major crops in Guatemala and Honduras. This research aims in strategizing adaptation and mitigating measures to minimize the adverse effects of climate change and evaluating climate resilient technologies for food production system.

#### **G-P59 GWAS Reveals Genetic Regions Associated with Chilling Tolerance in Rice**

*Raveendra Chandavarapu<sup>1</sup>, K. Raja Reddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Rice is a staple food for over half of the world's population. Originating from the tropics, rice is significantly impacted by low temperatures ( $< 15$  °C), especially during germination and seedling establishment. To decode the genetic basis of rice chilling tolerance, the *japonica* diversity panel ( $n = 233$ ) was phenotyped, and genetic loci were mapped using a genome-wide association study (GWAS). Phenotyping was conducted in controlled growth chambers (control: 30/ 22 °C, day/night temperatures, and chilling, 22/ 14 °C) and field-like conditions. Chilling-induced genetic variability in aboveground (seedling height, leaf number, shoot weight, and plant vigor) and belowground (root length and weight) were recorded 14 days after stress. Significant phenotypic variation was observed for all the parameters in response to treatment. Chilling stress induced a significant reduction in the number of leaves (54%), shoot length (57%), root length (7%), shoot biomass (133%), root biomass (109%), and vigor index (33%) compared to the control. In contrast, chilling stress increased the root-shoot ratio by 15%. Pearson correlation revealed a significant correlation between shoot and root weights ( $r = 0.74$ ). Root-to-shoot ratio showed significant correlations with root biomass ( $r = 0.51$ ) and root length ( $r = 0.36$ ). Single-locus (GLM and MLM) and multi-locus (FarmCPU and BLINK) models-based GWAS identified 12 significant genomic regions ( $p < 1.146 \times 10^{-8}$ ) associated with the following traits: leaf number (1), shoot weight (4), root weight (4), and root-to-shoot ratio (3). Further, *in silico* analysis of genes housed within these regions revealed their prior reported expression of candidate genes in root and shoot tissues under chilling stress. These findings provide valuable insights into chilling stress tolerance and candidate genes that could be used to develop the KASP assay for improving chilling tolerance in rice breeding programs.

**G-P60 Agricultural Yield Prediction Under Changing Climate in USAID - Feed the Future Countries: A Case Study of Cambodia***Ruchita Bhattarai<sup>1</sup>, Anitha Madapakula<sup>1</sup>, Prasanna Bayalusime<sup>1</sup>, Prakash Kumar Jha<sup>2</sup>, Prakash Kumar Jha<sup>1</sup>*<sup>1</sup>Mississippi State University, <sup>2</sup>University of California - Merced

Global agricultural crop production is undoubtedly affected by climate change, making farming communities extremely vulnerable. Three-fourth of farmers in Cambodia are smallholders and such farming communities face critical challenges of climate extreme during crop growth season. Moreover, several future climate studies have shown serious impact on food production system. A study was conducted to assess the changes in climatic parameters such as precipitation, maximum and minimum temperature in near future (2026 - 2055) and far future (2071 - 2100) for RCP 2.6 and RCP 8.5 scenarios in Cambodia as Feed the Future countries. Three climate models, namely MOHC, MPI and NCC were ensembled together to reduce the model biasness and calculate the change in climate parameters. The ensembled suggests there will be divergent change in precipitation; some part of countries will experience 11% decline in rainfall while other regions might experience 12% increase in rainfall by 2100 for RCP 2.6. The increase in rainfall is even higher for RCP 8.5, around 24% than the historical average. The maximum temperature will increase by 1 °C in RCP 2.6 while it might increase by 3 °C in RCP 8.5. Based on these, we conclude that the change in climate is evident in Cambodia which will impact the yield of field crops. Therefore, we simulated the yield of major cereal crops - rice and maize under two different RCPs using DSSAT for Cambodia. Gridded soil data from Harvard Soil Database was downscaled to create a country soil map which was then combined with daily weather data from different climate models to run DSSAT CERES model grid by grid. The focus of the research is to help decision makers design climate risk management for food production systems in Cambodia under USAID Feed the Future Program and assist other associated missions.

**G-P61 Determine optimum planting window and increase soybean production in eastern MS***Rui Peng<sup>1</sup>, Gary Feng<sup>2</sup>, Guihong Bi<sup>1</sup>*<sup>1</sup>Mississippi State University, <sup>2</sup>USDA Genetics and Sustainable Agriculture Research Unit

Soybean is the most important crop in MS, covering 2.13 million harvested acres valued at \$1.60 billion in 2023. The majority of the annual precipitation occurs during the off-growing season, particularly in the wet months of March and April. Frequent rainfall events usually led to flooding and waterlogging in poorly-drained croplands, which resulted in the delayed planting and reduced crop yields. The objective of this research was to evaluate the field workability during wet springs and determine optimum planting window under various drainage systems for the dominant soil and local weather conditions. We conducted DRAINMOD simulations for various combinations of three drain depths and a range of drain spacing from 5 to 50 m. These simulations calculated daily water content dynamics at different soil depths over the past century. Moreover, we identified suitable drainage systems for timely spring planting based on predicted workable days. Furthermore, the relative crop yield was simulated by adjusting planting dates to determine the optimal date for planting during dry, normal, and wet April. This study will provide valuable guidance for farmers to determine windows of spring fieldwork in Mississippi.

**G-P62 Design Subsurface Drainage Systems for Spring Field Operations in Mississippi State***Rui Peng<sup>1</sup>, Gary Feng<sup>2</sup>, Guihong Bi<sup>1</sup>*<sup>1</sup>Mississippi State University, <sup>2</sup>USDA Genetics and Sustainable Agriculture Research Unit

The past 100-years records showed annual precipitation approached 1350 mm in MS, with approximately 60% occurring during the fallow season. Excessive wetness and waterlogging during this period prevented timely tilling, fertilizing and planting, potentially impacting soybean yield. While installing subsurface drain tiles have been widely recognized as an effective method for removing excess soil water from the profile, few studies have specifically assessed the effectiveness of drainage systems under dominant soil type and weather conditions in eastern MS. The research aimed to optimize drainage system designs for timely field operations during wet springs. We conducted DRAINMOD simulations to evaluate the effects of various drain depths and spacing on the drainage efficiency and soil surface water content. Additionally, we calculated the number of workdays supporting agricultural vehicle traffic and field operations across different drainage systems, aiming to identify the optimal drainage design meeting the minimum required work days. The results suggested that installing shallow drains (75 cm) with the spacing of less than 15 m is suitable and

cost-effective for achieving the desired field operations.

**G-P63 Association Between Food Security, Dietary Quality, and Diagnosed Periodontitis: Analysis of NHANES 2015-2018***Sharon Samuel<sup>1</sup>, Rahel Mathews<sup>1</sup>, Joel Komakech<sup>1</sup>*<sup>1</sup>Mississippi State University

Food insecurity, inadequate dietary quality, and periodontal disease pose significant challenges to the United States adult population. This study examined the association between food security, dietary quality, and diagnosed periodontitis among U.S. adults using NHANES 2015-2018 data. The sample was 9,486 individuals aged 30 and older. The dependent variable was diagnosed periodontitis, and the independent variables were food security as defined by USDA and dietary quality measured using the Healthy Eating Index (HEI 2015). Multivariable logistic regression models were adjusted for demographics including race, gender, age, marital status, smoking status, income ( $p < 0.05$ ). About 51.7% were female, and 48.3% male, with mean age 55.1 and 55.8 years respectively. Most were non-Hispanic White (34.4%), while 26.3% identified Hispanic, and 22.1% non-Hispanic Black. Most participants reported full food security (60.4%) and a mean HEI of 54 (out of 100). Households with very low food security were about 1.5 times more likely to report diagnosed periodontitis [AOR=1.57, 95% CI(1.28, 1.93)]. Households with low [AOR=1.29, 95% CI(0.89, 1.43)], and marginal [AOR=1.36, 95% CI(1.07, 1.73)] had high odds of reporting diagnosed periodontitis than households with full food security. Dietary quality was not significantly associated with diagnosed periodontitis [AOR=0.99, 95% CI(0.99, 1.00)]. Non-Hispanic Asian [AOR=1.99, 95% CI(1.60, 2.46)], Hispanic [AOR=1.89, 95% CI(1.53, 2.35)], non-Hispanic Black [AOR=1.44, 95% CI(1.21, 1.69)] were more than 1.4 times more likely to report diagnosed periodontitis compared to non-Hispanic Whites. Public health initiatives should advocate for improved food security and healthy lifestyles to improve oral health outcomes among U.S. adults.

**G-P64 Develop an Animal Model for Chikungunya Virus (CHIKV) Infection in Heart***Shazeed-Ul Karim<sup>1</sup>, Farzana Nazneen<sup>1</sup>, Fengwei Bai<sup>1</sup>*<sup>1</sup>University of Southern Mississippi

In 2022, various regions across the Americas reported a total of 273,685 cases of Chikungunya virus (CHIKV), with documented involvement of cardiovascular diseases (CVD). The pathogenesis of



cardiovascular disease (CVD) caused by Chikungunya virus is not well studied and there are no specific treatments for CHIKV infection. The study involved working with live Chikungunya virus (CHIKV) in Biosafety Level 3 (BSL3) facilities. RNA was extracted from CHIKV infected cells and tissues, followed by quantitative real-time PCR (QPCR) to detect CHIKV and inflammatory cytokines. Flow-cytometry and immunohistochemistry were performed to evaluate pathology of heart. This study investigates the susceptibility of Chikungunya virus (CHIKV) in heart of C57BL/6 mice of varying ages and interferon (IFN) statuses. Wild-type (WT) mice heart displaying resistance to CHIKV beyond 7 weeks, low susceptibility at 3 to 7 weeks, and notable susceptibility at 1 week of age. Severity of infection in young WT (3 weeks old) mice were further investigated and rapid decline in viral load was observed in heart and spleen of young mice from 2-day post-infection (dpi) onwards, emphasizing an efficient rapid viral clearance in WT young mice. Both interferon  $\alpha/\beta$  receptor deficient homozygous (*ifnar1<sup>-/-</sup>*) and interferon  $\alpha/\beta/\gamma$  receptor deficient homozygous (*ifnag<sup>-/-</sup>*)

<sup>/-</sup>) mice displayed heightening viral severity in the heart, while heterozygous counterparts (*ifnar1<sup>+/-</sup>* and *ifnag<sup>+/-</sup>*) exhibited restored immunity after 1 dpi, indicating the crucial role of IFN in CHIKV protection. Survival analysis underscored the significance of IFN in preventing CHIK-induced mortality with the 100% mortality in both *ifnar1<sup>-/-</sup>* and *ifnag<sup>-/-</sup>* mice by 3 dpi and 100% survivality in WT, *ifnar1<sup>+/-</sup>* and *ifnag<sup>+/-</sup>* mice. Heart tropism revealed no significant differences in heart weight-to-body weight ratio at earliest time point (1 dpi) amongst different group of mice. Flow cytometry results revealed the presence of highest immune cell infiltrates, particularly neutrophils, monocytes, and leukocytes in *ifnar1<sup>-/-</sup>* mice, followed by *ifnag<sup>+/-</sup>*, compared to WT, highlighting the crucial role of immune cells in determining the cardiac diseases severity. The presence of pro-inflammatory cytokines suggests possible immune cell mediated damage in the heart. This study sheds light on age-related susceptibility, IFN mediated protection, and role of innate immunity during CHIKV infection in mice model.

#### G-P65 The Sre Ambel Floodplain of Southwest Cambodia: Analysis of Forest Cover, Plant Species Composition, and Ecosystem Services for Sustainable Forest Management

*Sitha Som<sup>1</sup>, Sandra Correa<sup>1</sup>, Joshua Granger<sup>2</sup>, Vitor Souza Martins<sup>3</sup>*

<sup>1</sup>Dept of Wildlife, Fisheries, and Aquaculture, <sup>2</sup>Dept. of Forestry, <sup>3</sup>Dept. of Agricultural and Biological Engineering

The Sre Ambel River floodplain in southwest Cambodia is considered one of the richest biodiversity hotspots in the coastal region of Cambodia. It supports several globally threatened species of waterbirds, reptiles, mammals, and fishes. The rich floodplain ecosystem provides a great economic opportunity for more than 3000 households to support their livelihoods. Although the Cambodian Forest Service recently included the Sre Ambel floodplain in a newly established Protected Area, it faces unsustainable utilization from illegal logging of the flooded forests, riparian forests, and mangroves for agriculture, construction, charcoal, and new settlements. Furthermore, little is known about the floodplain forest community and how the plant composition in the floodplain contributes to

maintaining ecosystem services for local livelihoods. As of 2023, the Department of Wildlife, Fisheries, and Aquaculture of Mississippi State University partnered with the Wildlife Conservation Society-Cambodia Program to establish a collaborative project entitled “The Sre Ambel floodplain of southwest Cambodia: analysis of forest cover, plant species composition, and ecosystem services for sustainable forest management” aiming to 1) evaluate the extent, vegetation cover, and plant composition within the floodplain; 2) assess the floodplain forest ecosystem services for local livelihoods; and 3) map the forest products across seasonal harvest within the floodplain for sustainable forest management. This abstract will present preliminary results from the first objective, where forest plots were surveyed from March to June 2024.

#### G-P66 Effects of Water Deficit on Cowpea: Physiology, Yield, and Quality

*Sujan Poudel<sup>1</sup>, Lekshmy V. Sankarapillai<sup>1</sup>, Vijaykumar Hosahalli<sup>1</sup>, K. Raja Reddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Cowpea (*Vigna unguiculata*) is a popular grain legume crop known for its adaptability to various environmental conditions. Low rainfall and increased evaporation during the crop growing season have become a major concern for sustaining the yield of crops grown under rainfed conditions, including cowpeas. However, resilience to water deficit (WD) at different growth stages has been overlooked. Two experiments were carried out in greenhouse conditions using 2-10 cowpea genotypes to investigate the impact of reduced soil moisture during the V2, V4, R1, and R4 stages. Physiological (stomatal conductance, photosynthetic efficiency, and pigment), morphology (node number and biomass), and yield component traits were measured. Two cowpea genotypes were grown in contrasting conditions: well-watered (WW) and WD during the vegetative (V2 and V4) and reproductive (R1 and R4) stages for 14 days. The results showed a significant reduction in carbon assimilation, stomatal conductance, biomass, and yield across all growth stages. Among all growth stages, the R1 (flowering) showed the most sensitivity to WD conditions. In experiment II, ten cowpea genotypes were exposed to two water regimes to study genetic variability in resilience to stress during the reproductive stage and identify WD-resilient genotypes. Physiological parameters such as conductance, transpiration, canopy temperature, and chlorophyll content displayed significant variation ( $p < 0.05$  to  $p < 0.001$ ) among the cultivars and between the treatments. Under WD, chlorophyll content decreased by 23%, stomatal conductance decreased by 94%, and canopy temperature increased by 4.7 °C compared to the WW. Moisture stress reduced the stem diameter by 6% and increased the specific leaf area by 34% compared to the control. Our study assessed the variability in drought tolerance and identified traits or genotypes resilient to drought stress during the reproductive stage.

## INVESTIGATOR POSTER (I-P)

### I-P67 Row Crops Response to Waterlogging During Vegetative and Reproductive Stages

*Bikash Adhikari<sup>1</sup>, Lekshmy V Sankarapillai<sup>1</sup>, Jagmandeep Dhillon<sup>1</sup>, Krishna N. Reddy<sup>2</sup>, K. Raja Reddy<sup>1</sup>, Raju B Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, Mississippi, USA, <sup>2</sup>USDA-ARS, Crop Production Systems Research Unit, Stoneville, Mississippi, USA

Short-term waterlogging (WL) during seedling emergence and reproductive stages severely compromises crop productivity by causing hypoxia, triggering a cascade of morphological and metabolic alterations in roots and leaves, thus inhibiting the full genetic potential of a crop. Identifying WL-resilient genotypes is crucial for sustainable production in unpredictable climates. We hypothesized that high-yielding genotypes might inherently tolerate WL, allowing them to thrive in such conditions. However, there is little information on multi-crop, multi-stage, and genotype-specific responses to WL during the early and reproductive stages. Five genotypes of three commercially important row crops (corn, cotton, and soybean) were subjected to 7 days of WL and 11 days of recovery at the vegetative and reproductive stages to bridge this gap. Results indicated that WL significantly lowered stomatal conductance ( $g_{sw}$ ) and transpiration in all crops, with partial recovery evident during the early vegetative stage. For instance,  $g_{sw}$  was reduced by 64% during WL, with a partial recovery of 41.3% below control. Biomass reduced significantly in corn (66%), cotton (65%), and soybean (55%) during seedling stage. During the reproductive stage, biomass reduced from 3% (corn) to 56% (cotton), with no physiological recovery. Soybean yield declined by an average of 52% at both stages of WL, while corn and cotton yields dropped by 84%, and the decline was 84% in corn and cotton. Overall, soybean demonstrated a relatively higher tolerance to WL across multiple growth stages than cotton and corn. These findings highlight the need for genetic and molecular research to identify WL-tolerant genotypes and genes.

### I-P68 Role of Peptides in Regulating Rice Responses to Drought

*Taiwo Abifarin<sup>1</sup>, K. Raja Reddy<sup>1</sup>, Jiaxu Li<sup>1</sup>*

<sup>1</sup>Mississippi State University

Abiotic stresses such as drought and salinity are the main factors limiting crop production. Improving plant resilience to stress is key to sustainable and future agricultural productivity. A significant part of the cell-to-cell communication in plants is mediated by small signaling peptides. Recently, small signaling peptides have emerged as an important class of regulatory molecules in plants involved in the control of plant growth and development. However, the involvement of small peptides as regulatory molecules in abiotic stress responses remains to be determined. In this study, we examined the effects of drought stress on the expression of small proteins/peptides. Small proteins/peptides were extracted from the leaves and roots of rice plants subjected to drought stress as well as from the control plants. The extracted proteins/peptides were separated by tricine-sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Two peptides were found to be upregulated by drought stress. The amino acid sequences of the up-regulated drought-responsive peptides were analyzed by mass spectrometry-based de novo sequencing. These results suggest that drought-responsive peptides may play an important role in drought stress perception and response. Further functional analysis of the drought-responsive peptides will elucidate their roles in drought adaptation and tolerance in rice.

### I-P69 Warmer Nighttime Disrupts the Day-Night Assimilate Utilization and Yield Potential in Soybean

*Lekshmy Valsala Sankara Pillai<sup>1</sup>, Bikash Adhikari<sup>1</sup>, Salliana R. Stetina<sup>2</sup>, K. Raja Reddy<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, MS, USA, <sup>2</sup>USDA-ARS Crop Genetics Research Unit, Stoneville, MS, USA

With the current projections for global warming, it is predicted that extreme heat events, both day and night, will become more common during the soybean growing season. In the southeastern US, historical data shows night temperatures rose about twice as fast as day temperatures. The negative effects of high daytime temperatures on soybean yield during flowering are well-documented. Limited studies quantified genetic diversity in tolerance to high night temperature (HNT) during peak flowering and grain filling. This study quantified the impact of HNT on photosynthesis ( $A$ ) and night respiration ( $R_d$ ) and their relationship with yield components. Seventeen soybean genotypes were subjected to control ( $23 \pm 2.3^\circ\text{C}$ ) and HNT ( $27.8 \pm 0.6^\circ\text{C}$ ) with a consistent daytime temperature of  $\sim 32^\circ\text{C}$  from peak flowering (R2) until physiological maturity (R8). Among the diurnal and nocturnal gas exchange parameters, nocturnal stomatal conductance was decreased by 54%, followed by a 38% decrease in nocturnal transpiration. A  $4.8^\circ\text{C}$  increase in nighttime temperature decreased  $A$  by 17% reduction and increased  $R_d$  by 29%. On average, each  $1^\circ\text{C}$  rise in nocturnal temperature resulted in a 2.8% reduction in yield. The efficiency of assimilate utilization ( $R_d/A$ ) showed a stronger negative association with seed yield under HNT. Genotypes with higher tolerance to HNT maintained low  $R_d/A$  and higher yields. The study highlights the potential impacts of warmer nights on soybean physiology and yield, suggesting a need to select or breed beans with improved tolerance to day and night temperature stress in legumes.

### I-P70 Elevated Air Temperatures Damage the Reproductive Behavior of Cotton under Current and Future CO<sub>2</sub>

*Naflath Thenveetil<sup>1</sup>, Krishna N Reddy<sup>2</sup>, K. Raja Reddy<sup>1</sup>*

<sup>1</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, <sup>2</sup>USDA-ARS, Crop Production Systems Research Unit, 141 Experimental Station Road, P.O. Box 350, Stoneville, MS

The increased risk of warmer temperatures has raised the attention of agriculture producers and policymakers to adopt mitigation strategies to stabilize crop yields. However, the rising CO<sub>2</sub> concentrations over the years can enhance crop yields. The study was carried out in sunlit plant growth chambers using four day/night temperature combinations: optimum (OT;  $33/21^\circ\text{C}$  day/night), high daytime (HDT;  $36/24^\circ\text{C}$  day/night), high nighttime (HNT;  $33/24^\circ\text{C}$  day/night), and high day/night temperature (HDNT;  $36/28^\circ\text{C}$  day/night) under ambient ( $a\text{CO}_2$ , 425 ppm) and elevated ( $e\text{CO}_2$ , 725 ppm) CO<sub>2</sub> environments in cotton. The flower morphology and seed yield traits were monitored under each experimental condition. All the floral characteristics were modified ( $p < 0.001$ ) under temperature treatments except sepal and stigma length, while the  $e\text{CO}_2$  only influenced the flowering to boll opening days, pedicel, and anther column length. Under HDNT, HDT, and HNT, the pollen number per anther reduced to 186, 232, and 266, as compared to 307 under OT. The flowering to boll opening date was reduced under HDNT (38 days) and HDT (42 days) conditions compared to 45 days in HNT and 47 days in OT. The increased flower drops under HDNT and HDT decreased the boll number by 85% and 43% compared to OT. This ultimately resulted in

lower seed cotton weight under HDNT (12 g plant<sup>-1</sup>) and HDT (47 g plant<sup>-1</sup>) compared to 90 g plant<sup>-1</sup> under HNT and 105 g plant<sup>-1</sup> under OT. Similarly, the lint (%) under HDNT drastically reduced by 26% compared to OT. A rise in daytime temperature and its combination with nighttime temperature causes a severe impact on cotton reproduction and yields.

#### **I-P71 Quantifying Temperature Effects on Sorghum Grain Yield and Quality**

*Navneet Kaur<sup>1</sup>, Naflath Thenveetil<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>, K. Raja Reddy<sup>1</sup>*

<sup>1</sup>*Plant and Soil Sciences, Mississippi State University*

Sorghum, the fourth most important staple food, forage, and biofuel crop globally, tolerates hotter and dryer climates than other grain crops. Quantifying the impact of projected temperature changes on sorghum yield potential is essential for future food security. An experiment was conducted with varying day/night temperatures (27.4/15.4 °C to 36.4/24.4 °C) imposed at flowering using sunlit plant growth chamber facilities. Two sorghum genotypes, Macia and RTx430, were evaluated for growth, development, yield, and grain quality under optimum water and nutrient conditions. The two genotypes differed in their response to temperature treatments in terms of plant height, tiller number, grain maturing duration, and grain weight. The seed index, 100 seed weight, was not different between the two genotypes across the temperature treatments. Both genotypes matured faster at higher temperatures and produced lesser grain weight. The maximum seed index (7.72 g) was observed at 22 °C average temperature and declined linearly with an increase in temperature. The grain mass per unit total weight declined with an increase in temperature in both the genotypes; the decline was less in Macia compared to RTx430. The seed starch content declined with an increase in temperature in both genotypes. The leaf minerals (N, Ca, S, B, and Zn) increased with an increase in temperature, and the response was more prominent in RTx430 than in Macia. The functional relationships between temperature and grain yield and quality will be helpful in optimizing management decisions and improving the functionality of the crop models. The data also indicates that any upward changes in temperature will have implications for sorghum yield and quality. Efforts are needed to develop heat-tolerant genotypes for sustained sorghum production.

#### **I-P72 Deciphering Crop Responses to Water Deficit Stress During the Vegetative Stage**

*Nisarga Kodadinne Narayana<sup>1</sup>, Mohan Bista<sup>1</sup>, Bala Subramanyam Sivarathri<sup>1</sup>, Ardeshir Adeli<sup>2</sup>, Darrin Dodds<sup>1</sup>, Raju Bheemanahalli<sup>1</sup>*

<sup>1</sup>*Department of Plant and Soil Sciences, Mississippi State University, MS 39762, USA,*

<sup>2</sup>*USDA-ARS, Genetics and Sustainable Agriculture Research Unit, Mississippi State, MS 39762, USA*

Sustaining global food security in the face of rapidly changing climate conditions, particularly the projected increase in drought stress frequency, duration, and severity, has become increasingly challenging. Various management and crop improvement approaches have enhanced crop production under low-water regimes. However, diverse crops' adaptation responses to water deficit stress during specific growth stages have been overlooked, which is crucial for developing tools to mitigate drought stress. In this investigation, we subjected four crops (corn, cowpea, cotton, and soybean) to water-deficit and well-watered conditions during the vegetative stage to elucidate their physiological, leaf biophysical, and whole plant (shoot and root morphology) responses. Substantial reductions in gas exchange traits and biomass were observed under water deficit stress across all crops, with cotton exhibiting the most pronounced reductions, followed by cowpea. All crops adopted a water-conserving

strategy by reducing stomatal conductance and transpiration. Notably, corn and cowpea displayed the least reduction in stomatal conductance compared to cotton and soybean under water deficit stress. Moreover, under water deficit stress, cotton and soybean experienced a significant increase in leaf temperature. Significant differences in root morphological traits, including total root length, surface area, and diameter, were evident among crops and stress treatments. Moreover, the crop-level analysis revealed variations in the root-to-shoot ratio but no significant biomass partitioning between shoot and root under water deficit stress. In addition, to examine the ability of proximal sensing in differing crops and stress streams, several vegetation indices linked to chlorophyll content, leaf area index, and biomass exhibited significant decreases in response to water deficit stress. Overall, corn demonstrated a greater water acquisition potential through greater root length and surface and higher biomass accumulation than other crops under water deficit stress. This comprehensive analysis of divergent crops adapted to upland conditions allowed us to demonstrate crop trait's plasticity under water deficit stress.

#### **I-P73 Reviewing the Literature on Machine Learning Techniques in Maize and Soybean Yield Prediction**

*Ramandeep Kumar Sharma<sup>1</sup>, Jasleen Kaur<sup>2</sup>, Gary Feng<sup>3</sup>, Yanbo Huang<sup>3</sup>, Chandan Kumar<sup>4</sup>, Yi Wang<sup>5</sup>, Sandhir Sharma<sup>2</sup>, Johnie Jenkins<sup>3</sup>, Jagmandeep Dhillon<sup>4</sup>*

<sup>1</sup>*Orise Oak Ridge, Tennessee, USA,* <sup>2</sup>*Chitkara University,* <sup>3</sup>*USDA,* <sup>4</sup>*Mississippi State University,* <sup>5</sup>*University of Wisconsin*

In-season crop yield prediction is a challenging task due to the intertwined nature of numerous variables. However, today's agronomy is data-rich, and machine learning (ML) provides the

ability to efficiently predict crop yields, utilizing high-volume data to optimize agricultural decision-making. Numerous ML models are employed in yield prediction research, yet systemized know-how on its crop-targeted utilizations is lacking, specifically for soybean and maize, world's vital crops. Henceforth, this systematic literature review (SLR) is performed to retrieve and consolidate the ML techniques and key features utilized in maize and soybean yield prediction research. Study's search criteria utilized four electronic databases including ProQuest, Wiley, Science direct, and EBSCOhost, totally producing 1859 related articles, which were finally reduced to 82 articles following SLR's inclusion and exclusion criteria. Aligning with the study objectives, all papers were thoroughly analyzed for generating common consensus and future research recommendations. The SLR analysis noted that ML is gaining popularity in the studied domain with a significant increase in its adoption after 2019. This study revealed the temperature, precipitation, historical crop yield, normalized difference vegetation index (NDVI), and soil pH to be the most utilized variables in ML for yield prediction research. The Random Forest (RF), Artificial Neural Networks (ANN), Support Vector Machines (SVM), and Extreme Gradient Boosting (XG-Boost) were identified as the mostly used ML algorithms. Most often applied deep learning (DL) techniques include long short-term memory (LSTM) and convolutional neural network (CNN). In the utilized models, the most used performance assessment measures were noted as the coefficient of determination (R<sup>2</sup>), root absolute error (RAE), root mean square error (RMSE), and mean absolute error (MAE). Most applied software's for building ML models include Python, MATLAB, Weka, R, and SPSS. Altogether, there is a rising trend among ML researchers towards leveraging ensemble techniques in for the betterment of model performance and reliability.

#### **I-P74 County-level Estimation of Optimal Planting Dates to Maximize Cotton Fiber Quality in The U.S.**

*Sahila Beegum<sup>1</sup>, K. Raja Reddy<sup>2</sup>, Vangimalla Reddy<sup>1</sup>, Shrinidhi Ambinakudige<sup>3</sup>*

<sup>1</sup>*Adaptive Cropping System Laboratory, USDA-ARS, Beltsville, MD 20705, USA, <sup>2</sup>Department of Plant and Soil Sciences, Mississippi State University, Mississippi, MS 39762, USA, <sup>3</sup>Department of Geosciences, Mississippi State University, Mississippi, MS 39762, USA*

Cotton quality is as crucial as cotton quantity. Despite considerable efforts to enhance cotton yield, there has been limited focus on maximizing fiber quality. The temperature experienced from flowering to boll opening becomes the critical factor affecting fiber quality when cotton is cultivated under optimum water and nutrient conditions. This depends on the planting date for a specific location and cultivar. Therefore, fiber quality can be improved by optimizing the planting date for a specific geographic location and cultivar. The study aims to develop a methodology for optimizing planting dates to maximize fiber quality, considering location-specific weather and cultivar details. A methodology is developed and demonstrated for the cotton belt in the USA. The methodology accounts for temperature, planting intervals, cotton varieties (early, mid, and late-season), and four major fiber quality indicators (fiber length, strength, micronaire, and uniformity). Based on the average of the last 15 years of weather data and different cotton cultivars, spatial maps depicting the best planting dates and associated fiber quality are analyzed for 765 cotton-growing counties in the USA. The study also explores variability in the optimum planting date and fiber quality with climate change in these counties. Results indicate that planting cotton at the optimum planting date can improve all fiber quality features. Fiber length can range from medium (25-29 mm) to long (30-34.5 mm), fiber strength from strong (29 to 30 g/tex) to very strong (>31 g/tex), micronaire from the discount range ( $\leq 3.4$  and  $\geq 5.0$ ) to the base range (3.5 to 3.6 and 4.3 to 4.9), and uniformity can be high (>85). Applying the methodology with consideration of future climate projections shows a 19% decline in micronaire - the most affected trait, followed by 8.4% and 1.6% decreases in length and uniformity, respectively. In contrast, fiber strength is expected to increase by 5% in the future. Results indicate that optimizing the planting date with the developed methodology can enhance fiber quality. Additionally, the methodology can predict variations in fiber quality due to future climatic conditions. The developed methodology can be valuable for farmers and growers seeking to enhance fiber quality. It is standard and applicable to any location and cultivar. A similar approach can be adopted for other locations and crops, such as soybeans, rice, and wheat, to optimize their quality.

#### **I-P75 Semen Quality Decline During 7-Day Storage: Mechanistic Determinants in Boar Sperm**

*Serge L. Kameni<sup>1</sup>, Notsile H. Dlamini<sup>1</sup>, Jean M. Feugang<sup>1</sup>*

<sup>1</sup>*Department of Animal and Dairy Sciences, Mississippi State University*

Artificial insemination (AI) is a tool of excellence in farming, ensuring reproductive efficiency, genetic improvement, herd health, and economic benefits. In the hog industry, AI relies on extended semen that can be chill-stored for up to 10 days. However, semen quality deteriorates over time, affecting fertility. Herein, by monitoring sperm parameters, we investigated the mechanistic determinants of boar

sperm quality decline during 7-day storage at 17°C. Semen doses (n=25) from fertile Duroc boars were evaluated on the collection day (D0) and after 7 days (D7) of storage for motion and morphology using CASA, apoptosis, viability, and intracellular ROS using flow cytometry, and antioxidant and lipid peroxidation using bioassays. Data were analyzed using SPSS and  $P < 0.05$  was considered significant. Results are presented as means  $\pm$  SEM. Total motility (TM), progressive motility (PM), and normal morphology (NM) significantly decreased from D0 to D7 (TM: 78.87 $\pm$ 1.37% to 73.19 $\pm$ 1.98%). On D7, high motility (HM, n=6) and low motility (LM, n=6) semen doses were identified according to the difference in maintaining sperm motility during storage. HM doses retained higher TM (83.73 $\pm$ 1.17%), PM (36.07 $\pm$ 1.11%), and NM (89.45 $\pm$ 2.30%) compared to LM doses (TM: 59.40 $\pm$ 3.35%, PM: 16.57 $\pm$ 3.25%, NM: 79.93 $\pm$ 2.61%). Compared to HM doses, LM doses had higher apoptotic, dead cells, and intracellular ROS levels on D0. In contrast, HM doses exhibited a higher oxidative stress index (TAOC/MDA) than LM on days 0 and 7 of storage. In conclusion, semen with similar initial characteristics displayed differential storage responses, with oxidative stress and apoptosis markers influencing long-term survival.

#### **I-P76 Aggregation Variations in a No-Till Corn System with Combined Soil Amendments and Cover Cropping Practices**

*Wei Dai<sup>1</sup>, Gray Feng<sup>1</sup>, Yanbo Huang<sup>1</sup>, Ardeshir Adeli<sup>1</sup>, Johnnie N Jenkins<sup>1</sup>*

<sup>1</sup>*USDA Genetics and Sustainable Agriculture Research Unit*

A four-field experiment was conducted near Pontotoc, Mississippi, to study the integration effects of poultry litter and inorganic fertilizer N with soil amendments and winter cover crop on soil aggregate stability and erodibility in Falkner silt loam upland soil under a no-till corn system. The winter cover crop treatments included cover crop and no cover crop and soil amendments with fertilization treatments included poultry litter and inorganic fertilizer N alone and in combination with flue gas desulfurization gypsum and lignite, and an unfertilized control in a split-plot design. Soil aggregate stability indices were determined at the conclusion of the study. The 0.25-0.053 mm aggregates was the most prevalent among treatments. The winter cover crop resulted in the highest values of mean weight diameter and geometric mean diameter (1.4 mm and 0.57 mm, respectively), while fractal dimension and soil erodibility factor K were the lowest. Among the fertilization treatments, poultry litter alone exhibited the highest mean weight diameter and the lowest fractal dimension and soil erodibility factor K. Mean weight diameter and geometric mean diameter were significantly negatively correlated with fractal dimension and soil erodibility factor K. Spearman's correlation analysis and Random Forest modeling jointly demonstrated that > 2 mm aggregates was the major domination of the stability of aggregates and erodibility, indicating their significant role in influencing soil aggregate stability. Overall, the results highlighted that integrating winter cover crop with poultry litter increased soil aggregate stability and erosion resistance in upland soils under a no-till corn system.



# SPONSORS & EXHIBITORS

