2026

SUMMER SCIENCE & ENGINEERING SYMPOSIUM | 2026

7TH ANNUAL July 21st, 2026

SUMMER SCIENCE & ENGINEERING SYMPOSIUM| 2026

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. Scott Willard, Co-Chair
Dr. Wes Burger, Co-Chair
Dr. David Ford, Co-Chair
Dr. Daryl Sparks, Co-Chair
Mississippi State University

Dr. Ham Benghuzzi
MAS Divisional Advisor

Scientific Committee Coordinators
Dr. Jamie Larson, Chair
Dr. Raju Bheemanahalli, Co-chair
Dr. Shrinidhi Ambinakudige, Co-chair
Dr. Prakash Kumar Jha, Co-chair
Mississippi State University
Mississippi State, MS

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

Major Events

Time	Event
8:30-9:00 AM	Registration, poster set up and breakfast
9:00-9:15 AM	Opening of the event
9:15-10:15 AM	Opening Keynote
10:15-11:50 AM	3-minute oral presentations
12:00-1:00 PM	Lunch break
1:00-3:00 PM	Poster presentations and judging
3:00-3:15 PM	Coffee break
3:15-4:15 PM	Closing Keynote & Round Table Discussion
4:15-4:45 PM	Awards and recognitions
4:45 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 Biochemistry, 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

TABLE OF CONTENTS

PROGRAM

TIME	EVENT
8:30-9:00 AM	REGISTRATION, POSTER SET UP AND BREAKFAST
	Location: Bost Conference Center, Mississippi State University, Mississippi State, MS
9:00-10:15 AM	OPENING OF THE EVENT/ WELCOME SPEECHES/KEYNOTE
	Dr. K. Raja Reddy Symposium Chair & President, Mississippi Academy of Sciences, Mississippi State University *Dr. Ham Benghuzzi* Executive Director, Mississippi Academy of Sciences *Dr. Peter Ryan* Executive Vice Provost, Mississippi State University
	OPENING KEYNOTE *Topic:* **GenAI in Science & Engineering: Today & the Future** *Dr. Julie Jordan, Senior Advisor, AI and Data Governance, Mississippi State University*
10:15-11:50 AM	3-MINUTE ORAL PRESENTATIONS
	Moderators: Drs. Prakash Kumar Jha and Shrinidhi Ambinakudige Mississippi State University
12:00 -1:00 PM	LUNCH BREAK
1:00 -3:00 PM	POSTER PRESENTATIONS AND JUDGING
	Coordinator: Drs. Raju Bheemanahalli and Shrinidhi Ambinakudige Mississippi State University
3:00-3:15 PM	COFFEE BREAK
3:15-4:15 PM	CLOSING KEYNOTE SPEAKERS
	Moderator: Dr. Michelle Tucci JMAS, Editor, University of Mississippi Medical Center, Jackson
	Topic: AI and Robotics in Ag Research *Dr. Alex Thomasson, Director, Agriculture Autonomy Institute,* Mississippi State University **Topic: Fundamentals of Public Speaking** *Mrs. Cheryl Chambers, Director, The Speaking Institute,* Mississippi State University
4:15-4:45 PM	AWARDS AND RECOGNITIONS
	Dr. Michelle Tucci, JMAS, Editor University of Mississippi Medical Center *Dr. K. Raja Reddy,* Symposium Chair Mississippi Academy of Sciences
4:45 PM	CLOSING REMARKS *Dr. K. Raja Reddy,* Symposium Chair

msacad.org

SCIENTIFIC COMMITTEES AND JUDGES

Scientific Committee Coordinators

Jamie Larson, Chair
Raju Bheemanahalli, Co-chair
Shrinidhi Ambinakudige, Co-chair
Prakash Kumar Jha, Co-Chair

Judges		Local Arrangement Members
Abhro Shome Pias	Moses Ayoola	Alekhya Chakravaram
Amanul Hoque Chowdhury	Munirul Alam	Bala Subramanyam Sivarathri
Ardeshir Adeli	Namita Sinha	Bhawana Dc
Aswathy Rai	Prabhakar Pradhan	Chami Rampati Dewage
Bindu Nanduri	Rahel Mathews	David Brand
Bolugallu Padmayya	Rama Nannapaneni	Deekshitha Nimmagudem
Carley Morrison	Renee Clary	Dingiswayo Mwanza
Ethan Kang	Rodgers Kabenomuhangi	Evita Lopez
Fei Yu	Sandra Woolfolk	Fernando Ereno
Francis Kiemo	Santhana Boopalan	Gaurav Joshi
George Awuni	Sarah Lalk	Lekshmy Sankara Pillai
Hussein Gharakhani	Sayantan Samanta	Manoj Kumar Reddy Allam
Jesse Morrison	Shainy Sambyal	Mary-Margaret Fancher
Jhennys Becerra Ossa	Shien Lu	Mohan Kumar Bista
Jing Yang	Snehalatha Ballamoole	Naflath Thenveettil
Juan Silva	Vanessa Beeson	Nihal Nallapareddy
Karen Brasher	Vitor Martins	Renganathan V Gandhimeyyan
Kirandeep Kaur Gill	Wenliang Li	Sangeetha Govindareddy
Lauren Priddy	Xiaofe Li	Sujan Poudel
Madhav Dhakal	Xueyan Shan	Willie McGee
Maryam Mohammadi-Aragh	Yue Zhao	
Md Mehedi Hasan Khan Shaon		
Mohamed Naziq Sabeeulla		
Mohammad Nafe Assafi		

KEYNOTE SPEAKERS

Dr. Julie Jordan

Dr. Julie Jordan serves as Senior Advisor for AI and Data Governance at Mississippi State University, leading campus-wide strategy for responsible, high-impact adoption of artificial intelligence across teaching, research, and enterprise operations. She focuses on building internal capability, establishing clear data governance and stewardship frameworks, and advancing practical AI use cases that improve student success, research productivity, and operational effectiveness. Previously, she served as Vice President for Research and Economic Development until November 2025, overseeing MSU's research enterprise as it grew to more than $340 million and strengthening the university's role in innovation-driven economic development. Dr. Jordan also serves on the Mississippi AI Regulation Legislative Taskforce and the Mississippi AI Workforce Council. She holds degrees from Mississippi State University and a Ph.D. from the University of Southern Mississippi.

J. Alex Thomasson, Ph.D., P.E.

Dr. Alex Thomasson is the Founding Director of Mississippi State University's (MSU's) Agricultural Autonomy Institute, formed in 2023 to focus on autonomous machinery systems for agricultural production, post-harvest processing, and research. He served as Department Head, Professor, and Berry Endowed Chair in MSU's Department of Agricultural and Biological Engineering (ABE) from July 2020 to April 2026, and he previously held faculty positions at Texas A&M University (TAMU, 2005 to 2020) and MSU (1997 through 2004), after starting his career as a research engineer with USDA-ARS (1989 to 1997). From 2017 to 2020, he served as Professor and Endowed Chair in Cotton Ginning, Engineering, and Mechanization in TAMU's Department of Biological and Agricultural Engineering. He currently also serves as a professor in ABE and an adjunct professor at both TAMU and the University of Southern Queensland (Australia). He is a registered professional

engineer and earned his Ph.D. at the University of Kentucky, his M.S. at Louisiana State University, and his B.S. at Texas Tech University, all in agricultural engineering. Dr. Thomasson's expertise includes artificial intelligence in agriculture, ground-based robots and unmanned aerial vehicles for agriculture, precision agriculture, high-throughput phenotyping, remote and proximal sensing, and optoelectronic sensor development. His research has involved multiple crops, including cotton, sugar cane, sweetpotatoes, sorghum, corn, and catfish. He has authored or co-authored well over 100 refereed journal articles and four book chapters and holds a patent in sensors for determining crop yield. From October 2023 to October 2024, he served as President of CAST (Council for Agricultural Science and Technology), and from 2020 through 2025 he served on FCC's Precision-Agriculture Connectivity Task Force. Dr. Thomasson is a Fellow of both ASABE (American Society of Agricultural and Biological Engineers) and iAABE (International Academy of Agricultural and Biosystems Engineering), and a Senior Member of SPIE (Society for Optical Engineering). He also belongs to ISPA (International Society for Precision Agriculture), AUVSI (Association for Unmanned Vehicle Systems International), ASEE (American Society of Engineering Education), AAAS (American Association for the Advancement of Science), and Sigma Xi (The Scientific Research Honor Society).

Cheryl Chambers

Cheryl Chambers is an Instructor II in the Department of Communication, where she is starting her 19th semester at MSU. Additionally, she is the founder and Director of The Speaking Center, whose mission is to help students and staff build their speaking skills.

PRESENTER INDEX

Time	Index
9:00 AM	3M: 3-Minute Oral Presentation
1:00 PM to 3:00 PM	H-P: High School Poster
	U-P: Undergraduate Poster
	G-P: Graduate Poster
	I-P: Investigator Poster

3-Minute Oral Presentation (3M)

Presenter Name	ID	Title
Anderson Chaney	H-3M1	*Centella asiatica* (L.): A New Specialty Superfood Crop for Mississippi
Bhawana DC	G-3M2	Balancing act: Impact of Heat and Drought on Soybean Yield and Nutrition
Dhruvil Solanki	G-3M3	Improving Early Cancer Detection: A Fourier-Transform Based Length Scale Study Using Finer-Focused Partial Wave Spectroscopy
Ehtasham Ali	G-3M4	Identification and Characterization of Antimicrobial Bacteria Associated with Charcoal Rot in Soybean
Elina Mukherjee	G-3M5	Benchmarking Federal Research Funding to Mississippi Higher Education: An Interactive, Validated Dashboard Across Six Agencies (FY2021–2026)
Faria Noshin	G-3M6	Management of *Rotylenchulus reniformis* in Sweetpotato Using Non-Fumigant Nematicides Integrated with Cover Crops
Fatimah Tabassum	G-3M7	GeoAI in Human Health: A Review of Applications and Spatially Explicit Artificial Intelligence Approaches
Harshal Nallapareddy	G-3M8	AI-Powered Cybersecurity Analytics and Threat Detection
Jephthah Nimoh Marfo	G-3M9	The Impact of Temperature and Water Stress on Cotton Planting Windows and Fiber Quality in Mississippi
Jobin Babu	G-3M10	Developmental Cell-Type Specific Alterations in MMP9 Expression in the Hippocampus of Prairie Voles Following Early-Life Sleep Disruption
Jocalyn Marie Cruz-Sanders	U-3M11	Basal ROS Levels May Indicate the Extent of Cellular Damage in Response to Fungal Pathogen Exposure in Select Hardwood Trees
Komal	G-3M12	From Curiosity to Habit: Psychological Factors Behind E-Cigarette Use
MD Mostafa Masud	G-3M13	Transcriptional Profiling of Aflatoxin Biosynthesis Genes and Aflatoxin Potential of *A. flavus* Isolates from Peanut Seeds
Md Shahnewaz Hossain	G-3M14	Multi-Hazard Socio-Ecological Vulnerability in the Yazoo-Mississippi Delta: A Scalable Framework for Environmental Justice and Resilience Planning
Mehadi Shawon	G-3M15	Distance, Trade Friction, and Commodity Leakage in Mississippi Agriculture and Forestry
Mohammad A. Ghanbari	G-3M16	Systems-Level Developmental Reprogramming Under Waterlogging Stress in Cowpea Revealed by Integrated Phenotypic, Physiological, and Transcriptomic Analysis
Mohammad Alizadeh Poshtiri	G-3M17	Development of Random Lasers for Applications in Biomedical Imaging
Mousa Alrubayan	G-3M18	Deep Learning-Based Classification of Multiple Cancer Types and Stages Using Brightfield Histopathological Images
Oluwafemi Oyedele	G-3M19	How Much Nitrogen Does Soybean Really Contribute? Lessons from 15 U.S. States
Rezwana Rahman Setu	G-3M20	Redox-Mediated Transcriptional Dynamics in *Arabidopsis* During Systemic Acquired Resistance
Santanu Maity	G-3M21	Fractal, Multifractal, and Fractal Functional Analysis of Tissue Characterization: Application to Cancer Detection
Trisa Das	G-3M22	Could Phenolic Bioherbicide Become a New Tool Against Resistant Palmer Amaranth?
Zakia Sultana Tithi	G-3M23	Optical Design Optimization of an In-Situ Laser Monitoring System for the ePIC pfRICH Detector

POSTER PRESENTATION

Presenter Name	ID	Title
H-P Series (High School Poster Presentations)		
Abigail McTaggart	H-P1	Cosmic Watch
Anderson Chaney	H-P2	*Centella asiatica* (L.): A New Specialty Superfood Crop for Mississippi
Antoniah Erves	H-P3	Radioactive Potassium (K-40) in Water Softeners
Armond Trevillion	H-P4	Radioactivity in Soils Collected in the Vicinity of a Nuclear Plant
Divya Sai	H-P5	Obstacle Detection and Safe Navigation with the Boston Dynamics Spot Robot
Maghan Rankin	H-P6	Radioactive Radon Concentrations in Underground Water Samples Collected from the Alcorn State University Campus
Yeshua Agyepong	H-P7	Linear-Attenuation Coefficients of Selected (Copper, Aluminum, and Lead) Shielding Materials
Willie McGee	H-P88	Impact of combined heat and drought stress on seed weight and number in soybean
U-P Series (Undergraduate Poster Presentations)		
Abigail Wiard	U-P8	Viscosity of Mars-Relevant Ternary Brines
Alex A. Bremond	U-P9	Photochemical Cyclization Reactions Involving the Saccharin Chromophores
Caleb Solangi	U-P10	Synthesis of Isoindolone Piperidines as Kinase Inhibitors: Preparation of Photochemical Starting Materials and Photoreactions
Clara Lee	U-P11	Innovative Hydrogel Composite Increases Bone Healing, Improves Neurobehavior Performance, and Decreases Chronic Inflammation Following Craniofacial Defects in Adolescent Rats
Dilber Annageldiyeva	U-P12	Functional Analysis of Human Retroviral-Like Protease Domains in Yeast Protein Quality Control and Secretion
Emily Snodgrass	U-P13	Using Yeast to Study How Human Proteases Control Vesicle Trafficking
Emma Morgan	U-P14	Human-Horse Cardiac Coupling on Student Perceived Stress Levels During a Collegiate-Based Equine-Assisted Interaction Program
Fernando Ereno	U-P15	Impact of Seed Size and Composition on Soybean Seedling Development
Jasmine Brewer	U-P16	Identification of Pulque Biomarkers: Comparison of Extraction Techniques
Jonathan W. Lee	U-P17	Application of Function-on-Scalar Regression to Chronic Motor Effects Following LPS Exposure in Neonatal Rats
Julius Culwell	U-P18	A Preliminary Investigation of Grooming-Based Equine-Assisted Experiences for Supporting College Student Emotional Well-Being
Kavya Gautam	U-P19	Research Intelligence Center: Mapping Critical and Emerging Technology Research
Kayla Bolden	U-P20	Chromosomal Aberrations Caused by *Echinochloa crus-galli* on *Lolium multiflorum*
Kelly E. Cantrell	U-P21	Azithromycin Reduces Hypoxia-Ischemia-Induced Sensorimotor Impairments, Brain Injury, Inflammation, and Oxidative Stress in Neonatal Rats
LirWan Fan	U-P22	Longitudinal Analysis of Neonatal Inflammation-Induced Sex-Specific Effects on Sleep in Adolescent Rats
Luke Carpenter	U-P23	Natural Antioxidants, Unnatural Outcomes: Thymoquinone and Epigallocatechin Gallate Suppress SKOV3 Ovarian Cancer Cell Viability
Megan Searcy	U-P24	LFHCAL Scintillator Tile Wrapping and Assembly Procedure at Mississippi State University
Mohnish Sao	U-P25	Restoration of a Mirror Reflectivity Test Stand with Modern Motion-Control Integration
Morgan Grace Sheffield	U-P26	Do Yeast Throw Out Their Trash? Testing if Loss of Ddi1 Increases Protein Secretion by Reducing Protein Degradation
Tyler D. Twedt	U-P27	Pyridine-Based HIV Integrase Inhibitors: Pyridine-Core Development
Vivian Jordan	U-P28	Ring-Expansion of Substituted Indoles
Ana C. Carneiro Leao	U-P89	Palmer Amaranth or Waterhemp? Phenotypic and Genotypic Identification of a Misidentified Pigweed Population from Florida
Felix Afiat	U-P90	Factors influencing understory plant species diversity in recently burned upland pine forests
G-P Series (Graduate Poster Presentations)		
Abhishek Panchadi	G-P29	Does Tabular Foundation Models Help Sample Efficient Soil Property Mapping Across Spectral and Environmental Covariate Frameworks?
Alekhya Chakravaram	G-P30	Whole-Plant Digital Phenotyping: Identifying Heat-Tolerant Rice Genotypes

POSTER PRESENTATION

Presenter Name	ID	Title
Andrew Williams	G-P31	*Listeria monocytogenes* Persistence in High and Low Concentrations of Second Generation QAC, Ster-Bac in Water and Recovery of Small Colony Morphotypes
Anna Essel	G-P32	Detecting Phishing in the Era of Generative AI: A Machine Learning Analysis of Human-Written vs. AI-Generated Emails
Asifur Rahman	G-P33	Development and Field Evaluation of RTK GNSS Guided Waypoint Navigation for an Autonomous Soil Sampling UGV
Bala Subramanyam Sivarathri	G-P34	Heat Stress and Soybean: The Battle for Reproductive Success and Yield Potential
Bhavya Kaanadka Purushothama	G-P35	AI Prediction of the Impact of Traditional and Virtual Reality-Based STEAM Outreach Activities on Student Learning
Bhawana DC	G-P36	Balancing Act: Impact of Heat and Drought on Soybean Yield and Nutrition
Bipin Bastakoti	G-P37	Integrated Remote Sensing for Above-Ground Biomass Mapping Across Forest and Agricultural Systems
Chami Rampati Dewage	G-P38	From Vegetative to Reproductive: Salinity Tolerance of Soybean Across Growth Stages
Christian Capers	G-P39	Cafestol Attenuates the Proliferation, Migration and Clonogenic Survival of Breast Cancer Cells Through Modulating mTOR Signaling
Clever Nyengerai	G-P40	Obesity in Mississippi: Contributing Socioeconomic and Health Factors
Clifford Boateng	G-P41	Racial Disparities and Socioeconomic Factors in Compounded Air Pollution and Asthma Risk in U.S. Metropolitan Areas
Deekshitha Nimmagudem	G-P42	Genome-Wide Association Analysis of Agronomic Traits in Finger Millet
Denetrise S. Johnson	G-P43	Effects of *Echinochloa crus-galli*, *Lolium multiflorum*, and *Nicandra physalodes* on the Germination of the Maize Innvictis 1857 Double Pro
Denyoh Prince Mark Dela	G-P44	Oropouche Virus Infection Interrupts Fetal Neurodevelopment
Dingiswayo Mwanza	G-P45	Quantifying Morpho-Physiological Responses in Corn Hybrids to Waterlogging
Ehtasham Ali	G-P46	Identification and Characterization of Antimicrobial Bacteria Associated with Charcoal Rot in Soybean
Ester Goenaga	G-P47	Allelopathic Activity of Sweet Potato (*Ipomoea batatas*) Morado: Allelochemical Profiling and Phytotoxicity Against Three Weed Species
FNU Sweety	G-P48	Optical Spectroscopic Analysis of Biochemical Changes Using Infrared Spectral Discrimination of Transgenic Mice Serum to Study the Potential Correlation of the Nano-Structural Disorder Alterations for Neurological Diseases
Md Shahnewaz Hossain	G-P49	Multi-Hazard Socio-Ecological Vulnerability in the Yazoo-Mississippi Delta: A Scalable Framework for Environmental Justice and Resilience Planning
Ishini Sangarasekara	G-P50	Simultaneous Prediction of Plant Macro and Micronutrients from Mid-Infrared Reflectance Spectra Using Multi-Output Regression Models
Jakira Luckett	G-P51	Systematic Review of CRC in Mississippi: Perspective of Etiology, Clinical Presentation, Diagnosis, and Treatment Strategies
Jephthah Nimoh Marfo	G-P52	The Impact of Temperature and Water Stress on Cotton Planting Windows and Fiber Quality in Mississippi
Kenya Watson	G-P53	Systematic Review: Incidence of Hypertension Leading to Chronic Kidney Disease and Management Strategies
Kiranmai Kondeti	G-P54	Using Artificial Intelligence to Detect Plagiarism in AI-Generated Student Assignments
KymMiyiah Vernado	G-P55	A Systematic Overview of Type 2 Diabetes in Mississippi
Lucas Maltoni Andrade	G-P56	National-Scale Solar Radiation Estimation for Brazil via Remote Sensing and Artificial Intelligence
Manoj Kumar Reddy Allam	G-P57	Yield and Nutritional Responses of Rice Genotypes Under Salt Stress
Marionei Fomaca de Sousa Junior	G-P58	Integrated SWAT+ Machine Learning Framework for Continuous Nutrient Concentration Estimation
Minhazul Abedin	G-P59	Neighborhood Disadvantage as a Social Determinant of Adult Asthma Emergency Department Utilization in South Carolina, 2010–2019
Mohammad A. Ghanbari	G-P60	Systems-Level Developmental Reprogramming Under Waterlogging Stress in Cowpea Revealed by Integrated Phenotypic, Physiological, and Transcriptomic Analysis
Mohan K. Bista	G-P61	Beyond Leaves: Cotton Bracts Physiology Under Drought Stress

POSTER PRESENTATION

Presenter Name	ID	Title
Oluwafemi Oyedele	G-P62	Comparing GHG Emissions from Corn and Soybean Cropping Systems to a Bare Soil Control in the Blackbelt Soils of Mississippi
Prachi Pannu	G-P63	Development of Kartogenin-Loaded Electrospun PCL-PLGA Scaffolds for Enhanced Microfracture Repair
Prathiksha Raghava	G-P64	Integrated Remote Sensing Analysis of Irrigation Dynamics and Evapotranspiration for Agricultural Water Resource Assessment
Ramakrishna Nannapaneni	G-P65	Antimicrobial Efficacy of Potassium Ferrate Against *Listeria monocytogenes* Survival in Water
Raylon Reynolds	G-P66	AI-Assisted Suspicious Incident Classification for Emergency Dispatch and Security Operations
Rebecca Butz	G-P67	Nutrition Environment of SNAP Stores in Jackson, Mississippi Using NEMS
Rezwana Rahman Setu	G-P68	Analysis of Redox-Mediated Transcriptional Dynamics in *Arabidopsis* During Systemic Acquired Resistance
Sabin Shrestha	G-P69	Self-Amplifying mRNA Vaccine Against Chikungunya Virus (CHIKV)
Sachin Cooray	G-P70	A Multimodal 3D Point Cloud Fusion Pipeline for RGB-D, Thermal, and Hyperspectral Phenotyping of Soybean Under Drought and Heat Stress Conditions
Sadie Studdard	G-P71	Providing Universal School Meals Can Reduce Food Insecurity: A Policy Review of the Community Eligibility Provision in Mississippi
Salit Chakma	G-P72	Hotspot Analysis of Humid Heatwaves, the Silent Killer, in Mississippi
Samuel Ratan Bunga	G-P73	Evaluation of Soil-to-Plant Radioisotopic Transfer in Sweet Potatoes from Mississippi
Sk Nafiz Rahaman	G-P74	AEGIS: A Real-Time Geospatial Early-Warning System for Threats to United States Agriculture
Smruthi Sagarika Mahapatra	G-P75	Can Lignocellulolytic Fungi Improve the Sustainable Reuse of Paddy Straw?
Sujan Poudel	G-P76	Discovering Genomic Regions Associated with Yield Traits in Cowpea
Trisa Das	G-P77	Screening Commercial and Breeding Tomato Varieties for Tolerance to Heat and Herbicide Stress
Yehani Ekanayake	G-P78	Depth-Wise Distribution of Easily Extractable Glomalin-Related Soil Protein in Mississippi Benchmark Soils
Zonia Elizabeth Caro Carvajal	G-P79	Optimizing Harvest Time of Microgreens Through Metabolomic Profiling: A Species-Specific Approach to Enhancing Nutritional Value
Annyasha Mukherjee	G-P91	Addressing Behavioral Health Disparities in Mississippi
Lillian Butler	G-P92	Identification of Antifungal Metabolites in Maize Silk Using Liquid Chromatography-Mass Spectrometry

INVESTIGATOR POSTER (I-P)

Amrit Shrestha	I-P80	Transferability of Stable Quadrant Between Soybean and Corn
Emran Ali	I-P81	Deploying Advanced On-Site Technologies for Vegetable Disease Detection and Extension Education
Gaurav Joshi	I-P82	Unlocking the Genetic Secrets of Stay-Green Trait in Rice Under Heat Stress
Hassan Ebrahim	I-P83	Olibanum as a Novel Source of Bioactive Metabolites for the Control of Triple-Negative Breast Cancer
Lekshmy V. Sankarapillai	I-P84	Natural Variation and Genetic Regulation of Leaf Architecture and Leaf Physiology in Soybean
Lir-Wan Fan	I-P85	Association of Nurses' Hand Hygiene Knowledge, Attitudes, Practices, and Hand Hygiene Methods on Bacterial Hand Contamination
Naflath Thenveettil	I-P86	Upland and Pima Cotton Responses to Drought and Salinity Stress Under Ambient and Elevated CO_2 Levels
Renganathan Vellaichamy Gandhimeyyan	I-P87	Physiological and Agronomic Responses of Finger Millet to Heat and Drought Stress

ABSTRACTS

3-MINUTE ORAL PRESENTATION (3-M)

H-3M1/H-P2 *Centella asiatica* (L.): A New Specialty Superfood Crop for Mississippi

Anderson Chaney[1], Naflath Thenveettil[2], Navneet Kaur[2], and K. Raja Reddy[1]

[1]Mississippi School of Mathematics and Science, Columbus, MS, [2]Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Centella asiatica (L.), commonly known as Gotu Kola, is a medicinal herb renowned for its wound-healing, anti-inflammatory, and cognitive-enhancing properties. It is widely used in the cosmetic, nutraceutical, and pharmaceutical industries. To establish Centella as a promising new crop in Mississippi, it is essential to optimize cultivation practices for successful production. Harvesting Centella at the wrong time, either too early or too late, can significantly reduce marketable yield. This greenhouse study aimed to evaluate the growth performance and biomass yield of Centella asiatica under different harvesting intervals in two separate experimental trials. In each trial, fifteen stolons, each with 3 to 5 adventitious roots, were transplanted into 15-liter pots (31 cm in diameter and 22 cm in height). The growth medium consisted of a 1:3 mixture of fine sand and commercial growing mix. The plants were irrigated to maintain optimal soil moisture, and Osmocote fertilizer was applied biweekly to meet their nutrient needs. After a 31-day establishment period, the plants were harvested weekly for up to six weeks, with above-ground parts, including petioles and leaf blades, being cut. Significant differences in petiole length and biomass accumulation were observed in both experiments. Chlorophyll content in mature leaves increased by 82% from week 2 to week 5. During this time, the concentrations of other pigments, such as flavonoids and anthocyanins, remained stable, helping ensure the crop's antioxidant value. Petiole lengths grew consistently, reaching 16.7 cm in experiment 1 and 21 cm in experiment 2 by week 6. Although the areas of mature leaves remained relatively unchanged throughout the harvesting period, the number of leaves per plant steadily increased. Both marketable fresh and dry biomass also grew each week. In experiment 1, fresh leaf weight increased from 0.5 kg/m^2 at week 2 to 8 kg/m^2 at week 6, while dry weight rose from 0.08 kg/m^2 to 0.99 kg/m^2. Similar trends were observed in experiment 2. On average, the crop produced over 1.5 kg m-2 of fresh weight and 0.2 kg m-^{2} of dry weight weekly. These findings suggest that Centella asiatica has strong potential as a specialty superfood crop in Mississippi, particularly with frequent harvesting and promoting continual production of marketable fresh and dry biomass."

G-3M2/G-P36 Balancing Act: Impact of Heat and Drought on Soybean Yield and Nutrition

Bhawana DC[1], Sadikshya Poudel[1], Mary Love Tagert[2], Raju Bheemanahalli[1]

[1]Department of Plant and Soil Sciences, Mississippi State University, [2]Agricultural and Biological Engineering, Mississippi State University

Soybeans (*Glycine max* L.) are often exposed to drought and heat stress during seed development, leading to significant yield and mineral losses. Previous studies on drought (DS) or heat stress (HS) have focused on growth, physiological, and reproductive mechanisms that affect yield-related parameters. However, little is known about the extent of damage these stressors cause to grain nutritional parameters. To address this gap, two-year experiments were conducted to assess the potential effects of individual and combined HS+DS on grain yield and mineral composition across 10 high-yielding genotypes grown in the southern US. Soybean genotypes were grown under four contrasting growing environments from full bloom to maturity: control (CNT), HS, DS, and combined. These conditions during the reproductive stages led to the largest yield losses (seed weight by 51% and seed number by 54%) compared with CNT. In addition, among the macronutrients, nitrogen and phosphorus decreased under all stress treatments, with the greatest decrease noted under HS or HS+DS. Potassium levels increased under combined stress compared with the CNT. Similarly, sulfur, boron, and zinc increased across all stress treatments, while calcium showed the most significant increase under combined stress. These findings suggested that a higher seed mineral concentration under stressors may be due to smaller seed size rather than better overall performance. Principal component analysis revealed a shift in the yield-nutrition relationship under stress and identified the genotype with high nutrition under individual and combined stress. These findings highlight the importance of selecting for both yield and seed nutrition to maintain yield and nutritional security under hot, dry growing conditions.

G-3M3 Improving early cancer detection: a Fourier-transform based length scale study using finer-focused Partial Wave Spectroscopy

Prakash Adhikari, Ishmael Apachigawo, Fatemah Alharthi, Prabhakar Pradhan

Mississippi State University, MS, USA

Early-stage cancer alters the ultrastructure within cells and tissues at the nanoto submicron scale, disrupting key macromolecules, including DNA, RNA, proteins, and other cellular components. We employed a finer-focused, highly sensitive spectroscopic technique's Finer-Focused Partial Wave Spectroscopy (ff-PWS) to detect changes in different types of cancer and with stage progression. These structural changes are invisible to conventional optical methods due to the diffraction limit. The ff-PWS enables us to detect minute structural changes at the nanoscale level inside cells/tissues. We further employed Fourier transform (FT) analysis of spectral intensity data obtained by ff-PWS images to further explore the hierarchical organization of these changes. This process provides us with precise length scale distributions of intracellular structural changes, which exhibit spatial patterns of cancer onset. The changes in length scale distributions are likely to reflect stage-specific alterations in organelles. The dual-modality approach holds promise for earlier and more precise detection of different stages of cancer."

G-3M4/G-P46 Identification and Characterization of Antimicrobial Bacteria Associated with Charcoal Rot in Soybean

Ehtasham Ali

Department of Agricultural Science and Plant Protection, Mississippi State University

Soybean is the major row crop in Mississippi, but its production is threatened by fungal diseases such as charcoal rot, caused by the soil-borne pathogen Macrophomina phaseolina, which thrives under hot, dry conditions. Currently, no resistant varieties or chemical controls are available, making preventive measures the primary means of disease management. Biological control using plant growth-promoting bacteria offers an environmentally sustainable alternative. Endophytic Burkholderia strains MS455 and MS389, isolated from soybean plants in charcoal rot-diseased patches, showed strong antifungal activity against multiple plant pathogens. MS455 has previously been reported to harbor a gene cluster responsible for the synthesis of the antifungal compound occidiofungin. In a 2025 greenhouse trial, both strains enhanced plant growth, with MS455 showing pronounced improvements in stem height, pod number, and dry biomass. Treatments T2 (drenching with MS455) and T5 (priming with MS389) significantly reduced disease incidence from 32% in the control to 4.97% and 7.5%, respectively; and drench applications at seeding and R1 growth stages were more effective than seed priming alone. Additionally, new isolates of the genera Paenibacillus and Pseudomonas with antifungal potential are under investigation. Current efforts focus on isolating and characterizing more antimicrobial bacteria and investigating host-microbe interactions in the soybean production system. The goal of this research is to develop a microbial package to prevent soybean diseases.

G-3M5 Benchmarking Federal Research Funding to Mississippi Higher Education: An Interactive, Validated Dashboard Across Six Agencies (FY2021-2026)

Elina Mukherjee[1], Narcisa Pricope[2], Seungdeog Choi[1]

[1]Electrical and Computer Engineering, Mississippi State University, Mississippi State, MS, [2]Associate Vice President for Research, Professor of Geography and Geospatial Science, Mississippi State University, Mississippi State, MS

Federal research funding is a primary driver of university research capacity and is widely associated with regional economic development, yet states differ sharply in the support their institutions receive. This work presents an interactive, openly reproducible dashboard that benchmarks Mississippi's position against the nation. Using the live USAspending.gov API, we pulled federal obligations for fiscal years 2021-2026 from six agencies (DoD, DOE, HHS, DHS, NSF, and NASA) to higher-education recipients- public, private, and minority-serving institutions- restricted to grants and contracts and attributed by recipient location (the institution's home state). Obligations were normalized per capita using 2023 Census population estimates and compared to a population-weighted national benchmark (total national obligations divided by the combined population of the 50 states and DC). Across most agencies, Mississippi's per-capita higher-education funding falls below the national benchmark, with HHS, DOE, and NASA showing persistent gaps; agency-level patterns vary, however, with DHS exceeding the national rate and NSF nearly converging. Within Mississippi, obligations concentrate among a small number of research institutions. All figures were validated against USAspending.gov. Because federal research investment is linked to research capacity and economic growth, Mississippi's persistent per-capita shortfall warrants attention from institutions and policymakers. The dashboard generalizes to any state, providing a transparent, reproducible tool for monitoring federal research investment.

G-3M6 MANAGEMENT OF ROTYLENCHULUS RENIFORMIS IN SWEETPOTATO USING NON-FUMIGANT NEMATICIDES INTEGRATED WITH COVER CROPS

Faria Noshin[1], Chang Liu[1], Lorin Harvey[2]

[1]Mississippi State University, Dept. of Agricultural Science and Plant Protection, Starkville, MS 39759, [2]Mississippi State University, North Mississippi Research and Extension Center, Pontotoc, MS 38863.

Reniform nematode (Rotylenchulus reniformis) is one of the most significant plant-parasitic nematodes that restricts the production of sweetpotato (Ipomoea batatas [L]. Sweetpotato is an economically important crop in the US, especially in Mississippi, whereby soil borne pests often reduce the yield and root quality. The reniform nematodes can cause losses of yield up to 70 percent, but there are few management options available due to the lack of resistant cultivars and the increasing restrictions on fumigant nematicides. Therefore, to ensure sustainable management of reniform nematodes, there is a need to have integrated management strategies that involve the integration of cultural practices and non-fumigant nematicides. A field experiment was conducted at the Pontotoc Ridge- Flatwoods Branch Experiment Station in Mississippi in a field that was naturally infested field with R. reniformis. This study evaluated the combined effects of winter cover crops and non-fumigant nematicides on suppressing nematodes and the yield of sweetpotatoes. This experiment followed a split-plot randomized complete block design with four replications. Cover crop treatments included fallow, wheat (Triticum aestivum), winter pea (Pisum sativum), canola (Brassica napus), and a mixture of wheat, winter pea, and canola. The treatments of nematicides were of fluopyram (Velum Prime), oxamyl (Vydate), and an untreated control. Soil samples were collected before planting, at mid-season, and at harvest to quantify reniform nematode populations using the sucrose-centrifugal flotation technique. Agronomic measurements, including storage root grading and total and marketable yields, were also recorded during harvesting. Cover crop selection significantly influenced reniform nematode populations. Treatments with winter pea, canola, and mixed cover crops significantly reduced reniform nematode density compared with fallow and wheat. Mid-season observations indicated a strong interaction between cover crops and nematicide treatments, with significant nematode suppression by fluopyram and oxamyl primarily occurring in plots previously planted with mixed cover crops. The effects of nematicides on nematode populations were reduced by harvest, while cover crop-mediated suppression remained evident. Mixed cover crops maintained the lowest population of nematodes, whereas the fallow plots had the greatest population. Yield trends reflected nematode pressure across treatments. Mixed cover crops and winter pea numerically produced higher sweetpotato yields than fallow and wheat. Nematicide applications improved yield primarily in higher nematode pressure systems. These results demonstrate that cover crop selection strongly influences R. reniformis population dynamics and can affect the performance of non-fumigant nematicides. Integrating biologically suppressive cover crops with non-fumigant nematicide applications may provide a sustainable strategy for managing reniform nematodes and improving sweetpotato productivity.

G-3M7 GeoAI in Human Health: A Review of Applications and Spatially Explicit Artificial Intelligence Approaches

Fatimah Tabassum, Mei Yang

Department of Geosciences, Mississippi State University, Mississippi State, MS

Geospatial Artificial Intelligence (GeoAI) has evolved as an effective framework for studying complicated spatial patterns in human health by combining geospatial data with machine learning (ML) and deep learning (DL) techniques. This study aimed to systematically review and critically evaluate heterogeneous data sources and GeoAI applications in human health research while examining how GeoAI captures spatial heterogeneity, spatial dependence, and temporal dynamics. Five major scientific databases, including PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar, were searched for peer-reviewed, English-language articles published between January 1, 2015, and April 2, 2026, to capture recent advances in GeoAI-based health research. Of the 280 studies identified, 88 met the inclusion criteria and were included for in-depth analysis. Various and complex data sources have been used in GeoAI health research, and the major applications include disease surveillance, environmental exposure assessment, health disparities research, urban health and built environment analysis, healthcare access and resource optimization, and digital health, mobility, and behavioral modeling. GeoAI enables spatially explicit and data-driven modeling that captures spatial and temporal dynamics, improving health outcome prediction, visualization, and understanding compared with traditional techniques. However, several challenges remain, including data heterogeneity, spatial and sampling bias, model interpretability limitations, measurement error and uncertainty, and privacy and ethical considerations.The results suggest potential pathways for developing more geographically robust GeoAI frameworks. Future research should aim to address the aforementioned challenges to advance health analyses, improve public health outcomes, and support evidence-based policymaking."

G-3M8 AI-Powered Cybersecurity Analytics and Threat Detection

Harshal Nallapareddy[1], Chandrababu Nallapareddy[2]

[1]Georgia Institute of Technology, [2]Capital One Financial Services LLC

The rapid evolution of cyber threats, coupled with the increasing complexity of digital ecosystems, has necessitated more intelligent and adaptive security solutions. Artificial Intelligence (AI) and Machine Learning (ML) have emerged as transformative technologies in the cybersecurity landscape, enabling organizations to proactively detect, prevent, and respond to malicious activities with greater speed and precision. This paper explores the integration of AI and ML algorithms in various cybersecurity applications, including threat detection, incident response, vulnerability management, and user behavior analytics. It also examines the alignment of these technologies with established cybersecurity frameworks and standards such as NIST CSF, ISO/IEC 27001, and the NIST AI Risk Management Framework to ensure ethical, secure, and effective implementation. By evaluating real-world use cases and current challenges, the paper underscores the critical role of AI/ML in building resilient, future-ready cyber defense strategies.

G-3M9/G-P52 The Impact of Temperature and Water Stress on Cotton Planting Windows and Fiber Quality in Mississippi

Jephthah Nimoh Marfo[1], Shrinidhi Ambinakudige[1], Sahila Beegum[2], Kambham Raja Reddy[3]

[1]Department of Geosciences, Mississippi State University, Mississippi State, MS, [2]Nebraska Water Center, Robert B. Daugherty Water for Food Global Institute, 2021 Transformation Drive, University of Nebraska, Lincoln, NE, [3]Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

The quality of cotton fibers is a critical factor in determining the price farmers receive for their cotton. Planting date influences the temperature and water conditions experienced during fiber development and, therefore, significantly impacts fiber quality. Current methods for optimizing cotton planting dates to improve fiber quality typically assume ideal water availability throughout the growing period and do not account for interactions between temperature and water status. This study presents a modeling framework that combines long-term PRISM temperature data, leaf water potential (LWP), and a genetic algorithm to optimize planting dates and evaluate fiber quality in Mississippi. The methodology accounts for temperature, LWP, planting intervals, cotton varieties (early, mid, and late-season), and four major fiber quality indicators (fiber length, strength, micronaire, and uniformity). Three scenarios (temperature-only, temperature and LWP, and sensitivity) were developed to evaluate the suitability of planting windows under varying temperatures and LWP conditions. Spatial maps showing the best planting dates and fiber quality for 66 cotton-growing counties in Mississippi were produced. The results indicate that rising temperatures expand the planting window by accelerating the accumulation of growing degree days, particularly benefiting mid- and late-season cultivars. However, this expansion does not translate into improved fiber quality. When water stress is incorporated, the proportion of counties producing long-fiber cotton decreased from 100% under baseline conditions to zero under water-stress conditions, representing a complete loss of long-fiber classification and highlighting water availability as the dominant constraint on cotton fiber quality. Under warmer, drier conditions, all counties transition to lower-quality fiber classifications, indicating a potential loss of high-quality fiber classifications across the region. This study presents a county-level geospatial framework that integrates satellite-derived crop water stress indices and leaf water potential into a genetic algorithm optimization of cotton planting dates, an advance over prior approaches that assume non-limiting water availability. The results demonstrate that while temperature broadens planting flexibility, water stress is the dominant constraint on fiber quality, underscoring the need for region-specific adaptation strategies, including optimized planting windows, cultivar maturity selection, and irrigation management to minimize reproductive-stage water stress.

G-3M10 Developmental Cell-Type Specific Alterations in MMP9 Expression in the Hippocampus of Prairie Voles Following Early-Life Sleep Disruption

Jobin Babu

University of Mississippi Medical Center

Early-life sleep disruption (ELSD) is a significant environmental risk factor for autism spectrum disorders (ASD). Previous studies from our group demonstrated that ELSD resulted in impaired behaviors in adult prairie voles, including reduced partner preference and novel object recognition, a hippocampal-

dependent behavior. Spatial memory deficits are also common in people with ASD. Prior work from our lab demonstrated decreased perineuronal nets (PNNs) in the hippocampal sector CA1 of ELSD prairie voles and elevated MMP9 expression in the hippocampus of children with ASD. MMP9, a matrix metalloproteinase, modulates synaptic plasticity and degrades extracellular matrix structures, including PNNs. PNNs are ECM structures composed of chondroitin sulphate proteoglycans (CSPGs) involved in neuronal maturation and synaptic plasticity implicated in neurodevelopmental disorders. Here, we tested the hypothesis that ELSD alters the developmental trajectory and cellular specificity of MMP9 expression in hippocampal CA1 in prairie voles. We analyzed hippocampal sections from juvenile (P17-P20) and adult (P150-160) male and female prairie voles with and without ELSD (n = 24). Immunohistochemistry for MMP9 was performed, and stereological microscopy was used to quantify labeled neurons, glia, and PNNs across CA1 subregions (stratum oriens and pyramidale). In adult CA1, most MMP9+ cells were neurons (80.5% in stratum oriens, 89% in stratum pyramidale), with smaller proportions of MMP9+ glia (17.7% in stratum oriens, 8.9% in stratum pyramidale. We also observed unexpected MMP9 labeling in PNNs, which colocalized with wisteria floribunda-positive PNNs surrounding parvalbumin neurons. Analysis of the data collected thus far revealed that adult ELSD voles exhibit significantly reduced densities of MMP9+ neurons in both the stratum oriens and the stratum pyramidale (p<0.03). In comparison, MMP9+ PNNs are increased in the stratum oriens (p<0.05) of adult ELSD voles. Across development, MMP9+ PNNs increased with age in both groups, while MMP9+ neurons remained stable in control voles but declined sharply in ELSD voles. These findings represent the first cellular-level mapping of MMP9 expression in the prairie vole hippocampus and demonstrate unexpected MMP9 labeling within PNNs. Furthermore, ELSD disrupts normal MMP9 developmental patterns, potentially impairing hippocampal ECM remodeling and synaptic integrity, which has been implicated in children with ASD. These data support a mechanism by which ELSD contributes to neurodevelopmental vulnerability through cell-type-specific ECM dysregulation.

U-3M11 Basal ROS Levels May Indicate the Extent of Cellular Damage in Response to Fungal Pathogen Exposure in Select Hardwood Trees

Jocalyn Marie Cruz-Sanders[1], Ryan Williams[1], and Richard Baird[2]

[1]Mississippi State University, [2]Agriculture. Science and Plant Protection Department, Mississippi State University, Mississippi State, MS

Cryphonectria parasitica is commonly referred to as the chestnut blight fungus. First identified in New York City, NY, in 1904, and, within the span of 50 years, nearly eradicated the entire American chestnut (Castanea dentata) population. Just prior to the disease epidemic, the Appalachian Mountains contained 25% American chestnut trees. This exotic Asian disease, introduced from Asia via Chinese chestnut logs, causes necrotic lesions to form on damaged branches and girdles the main trunk, cutting off the nutrient and water supply above the soil line and killing these highly susceptible trees in mere months. Over a 60-year period, reforestation efforts have led to the crossbreeding of the American chestnut and the Chinese chestnut, both of which are tolerant of the pathogen. After 3 generations, B3F3, the hybrid of these two types of trees, remains undetermined regarding its tolerance to the pathogen. B3F3 has been planted at 11 sites from Virginia to Georgia. The six-year-old saplings in Nantahala National Forest near Sky Valley, Georgia, include native American chestnut, Chinese chestnut, and B3F3. In this study, leaves were sampled to evaluate whether disease tolerance (biomarkers) could be identified using ROS-based testing. Reactive Oxygen Species (ROS) is the response to biological or environmental stressors. ROS can increase damage or preserve a species, depending on the biochemical signals induced by the stressor. Lipid peroxidation can increase the risk of developing various diseases and lead to cell death. In this study, the goal is to determine whether lipid peroxidation in foliar samples from varying American chestnut (B3F3) and Chinese chestnut genotypes can serve as a biomarker of oxidative stress, aiding future reforestation efforts.

G-3M12 From Curiosity to Habit: Psychological Factors Behind E-Cigarette Use

Komal

Mississippi State University, Mississippi, USA

E-cigarette use has become increasingly common among adolescents and young adults, making it an important public health issue. Although many young adults try e-cigarettes, not everyone continues using them. This suggests that different psychological factors may influence different stages of e-cigarette use. Previous studies have found that people with higher sensation seeking are more likely to be curious about e-cigarettes and try them for the first time. However, the role of self-esteem is less clear. Some studies suggest that people with lower self-esteem may be more likely to continue using e-cigarettes, while others have found no relationship. Most of this research has focused on the early stages of e-cigarette use, and very few studies have looked at whether self-esteem is related to established e-cigarette use, which is an important gap that this study aims to address. This study will recruit participants through the Psychology Research Program (PRP) at Mississippi State University and collect data using an online survey. Participants will complete questionnaires measuring sensation seeking, self-esteem, e-cigarette dependence, mental health, and nicotine dependence. It is hypothesized that sensation seeking will be more strongly related to the early stages of e-cigarette use, such as susceptibility and initiation, while lower self-esteem will be more strongly related to current and established e-cigarette use. Understanding how these psychological factors influence different stages of e-cigarette use may help researchers and healthcare professionals develop more effective prevention and intervention programs for young adults.

G-3M13 Transcriptional Profiling of Aflatoxin Biosynthesis Genes and Aflatoxin Potential of *A. Flavus* Isolates from Peanut Seeds

MD Mostafa Masud, Sumyya Waliullah, Dr. Emran Ali

Alcorn State University, MS, USA

Aflatoxin contamination is a major threat in the United States, which is caused by one of the major species, Aspergillus flavus. It infects peanuts in both pre and post-harvest stages, leading to significant yield loss. This pathogen possesses a complex aflatoxin biosynthesis gene cluster that is responsible for producing toxins. Accurate identification of toxigenic A. flavus and subsequent aflatoxin production largely depends on the transcriptional regulation of biosynthesis genes. To address this, we isolated A. flavus from the peanut samples and performed morphological and molecular identification along with aflatoxin quantification through ELISA. We combined molecular identification and aflatoxin quantification techniques to get better insights for detecting toxin-producing isolates, focusing on structural and regulatory genes (aflR, aflP, aflD, aflQ) from the

gene cluster. Our RT-PCR and RT-qPCR revealed differential gene expression of four genes throughout our isolates. Aflatoxin quantification analysis revealed that out of 24 isolates, only 11 isolates produced aflatoxin. Our correlation study between the biosynthesis gene and aflatoxin accumulation showed that there is a negative correlation between overall gene expression and aflatoxin production, indicating that other factors are involved. However, the correlation between the four genes themselves showed a positive correlation. Moreover, a positive correlation was observed between the aflR gene and the other genes (aflP, aflQ, aflD), particularly between aflR and aflQ gene. Overall, our study highlights the transcriptional regulation of four biosynthesis genes to understand the aflatoxigenic potential of A. flavus isolates, along with the use of molecular markers for differentiation between toxigenic and atoxigenic isolates.

G-3M14/G-P49 Multi-Hazard Socio-Ecological Vulnerability in the Yazoo-Mississippi Delta: A Scalable Framework for Environmental Justice and Resilience Planning

Md Shahnewaz Hossain, Shrinidhi Ambinakudige

Department of Geosciences, Mississippi State University, Mississippi State, MS

The Yazoo-Mississippi Delta (YMD) faces an intricate set of multi-hazard risks, including flooding, drought, tornadoes, and severe winter events, compounded by entrenched socio-economic inequalities. This study introduces a novel multi-hazard, socio-ecological vulnerability framework that leverages the Global Delta Risk Index (GDRI) to integrate social, ecological, and hazard-exposure dynamics across multiple scales. Using census tract-level socio-economic data and watershed-scale ecological metrics (HUC12), vulnerability is assessed across dimensions of susceptibility and adaptive capacity/resilience. Hazard exposure, incorporating flooding, drought, tornadoes, and winter events, is mapped using spatial datasets on event frequency and intensity. The framework synthesizes these components into a composite vulnerability index, followed by spatial hotspot analysis to identify critical clusters of elevated risk. A key innovation is the explicit examination of the convergence and divergence between socio-economic and ecological vulnerability surfaces. Preliminary results reveal hotspots in counties like Washington, Leflore, and Bolivar, where high socio-economic susceptibility converges with ecological degradation and frequent hazard exposure, exacerbating risks. In contrast, areas of divergence highlight regions where social and ecological vulnerabilities do not spatially align, challenging traditional risk assumptions and revealing pockets of resilience. These findings challenge the limitations of conventional, single-hazard or single-domain vulnerability assessments. By offering a multi-dimensional, scale-sensitive framework, this research provides actionable insights into more targeted adaptation strategies. It further supports environmental justice-oriented decision-making, enabling more equitable and effective resilience planning for vulnerable regions like the YMD.

G-3M15 Distance, Trade Friction, and Commodity Leakage in Mississippi Agriculture and Forestry

Mehadi Shawon

Mississippi State University, Mississippi, USA

Mississippi generates billions of dollars annually in agricultural and forestry commodities, yet most of this value leaves the state. This paper quantifies how much leaves, why, and whether external shocks alter the pattern. Using the Freight Analysis Framework (FAF5.7.1) €" a federal dataset tracking state-to-state commodity flows from 2017 to 2022 €" we estimate a structural gravity model of agricultural and forestry trade across all 48 contiguous states. The distance elasticity of trade is ˆ'1.16, indicating that a 10% difference in bilateral distance between otherwise identical state pairs is associated with a 13% difference in trade volume. Forestry sectors are significantly more distance-sensitive than agriculture ($p = 0.004$), consistent with the higher transportation burden of bulk forest products such as lumber and paper. An event-study analysis identifies a 6.3% reduction in Crop Production trade flows following the 2018 retaliatory tariffs, with a temporal pattern €" larger effects in 2019 and 2022, smaller in 2020-2021 €" consistent with Phase One Agreement purchase commitments providing partial offset. Applied to Mississippi, the 2022 IMPLAN Social Accounting Matrix reveals that 67.3% of the state's agricultural and forestry output flows outside Mississippi, rising to 78.8% for forestry. Food and Beverage Processing has the highest outflow share (81.8%), while Livestock and Dairy is lowest (23.7%), driven by local broiler production. These sector-specific estimates provide a quantitative foundation for evaluating infrastructure investments and local processing policies aimed at retaining commodity value within Mississippi.

G-3M16/G-P60 Systems-Level Developmental Reprogramming Under Waterlogging Stress in Cowpea Revealed by Integrated Phenotypic, Physiological, and Transcriptomic Analysis

Mohammad A. Ghanbari[1], Omolayo J. Olorunwa[2], Mohit Verma[3], Sorina C. Popescu[4], Ainong Shi[5], T. Casey Barickman[6], George V. Popescu[1]

[1]Institute for Genomics, Biocomputing & Biotechnology, Mississippi State, Mississippi, USA, [2]Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, Mississippi, USA, [3]Department of Biomedical Sciences, Joan C. Edwards School of Medicine, Marshall University, Huntington,West Virginia, USA, [4]Department of Biochemistry, Nutrition, and Health Promotion, Mississippi State University, Mississippi State, Mississippi, USA, [5]Department of Horticulture, University of Arkansas, Fayetteville, Arkansas, USA, [6]School of Integrative Plant Science, Horticulture Section, Cornell University, Ithaca, New York, USA

Cowpea (*Vigna unguiculata* (L.) Walp.) is a climate-resilient grain legume that contributes to nutritional and food safety in a variety of production regions around the world; however, many of these regions are becoming more vulnerable to climate-driven flooding and waterlogging, endangering productivity and seed quality. In this study, we used RNA-seq to assess transcriptional responses to waterlogging in different cowpea genotypes during the vegetative, flowering, and maturity stages. Using measured phenotypic/physiological, biochemical, yield, and seed-quality traits, RNA-seq expression profiles were combined with differential expression analysis, KEGG pathway enrichment/Pathview mapping, transcription factor profiling, weighted gene co-expression network analysis (WGCNA), and XGBoost-based machine-learning prediction. The tolerant genotype UCR369 demonstrated stronger physiological recovery and more dynamic transcriptional adjustment than EpicSelect.4, whereas flowering and maturity exhibited the clearest divergence in waterlogging responses, which were strongly stage- and genotype-dependent. Waterlogging caused stage-dependent alterations to soluble sugars, phenolics, flavonoids and seed-quality traits while decreasing pigment status, gas exchange, chlorophyll fluorescence, membrane stability, and yield components. Pathway analysis revealed four prominent response axes: phenylpropanoid biosynthesis, flavonoid/isoflavonoid biosynthesis, starch and sucrose metabolism, and

cutin/suberin/wax biosynthesis. KEGG pathway and Pathview analyses revealed activation of antioxidant and wall-associated phenolic metabolism, carbohydrate reallocation, and surface-lipid/barrier remodelling in UCR369, with a stronger integration of these responses, particularly during flowering and maturation. Transcription factor expression dynamics exhibited stage-specific activation of the MYB, bHLH, ERF/AP2, WRKY, HD-ZIP, and HSF families, which is compatible with redox buffering, hormone-linked stress signalling, and membrane/cuticle protection. WGCNA detected 35 co-expression modules, with the top five modules as the most closely linked to phenolics/starch, sucrose, plastid/pigment functions, and membrane stability. These transcriptome-scale patterns were condensed by XGBoost into a compact collection of trait-linked predictors, with the strongest cross-layer support centred on LTP3, CER1/CER22, and CASPL1D1 for cuticle/barrier remodelling, NIA2/NR2, ICL, and SAG12 for carbohydrate and redox reprogramming, HSP21 for plastid protection, and ACS6 for ethylene-associated stress signalling. Additional recurrent predictors, such as Vigun07g271600 and Vigun08g155100, point to cytochrome P450 and HSP20-related stress-protective activities. These findings establish a trait-anchored, systems-level framework for cowpea waterlogging tolerance, as well as biologically grounded targets for marker development, functional validation, and breeding in waterlogging-prone regions.

G-3M17 Development of Random Lasers for applications in biomedical imaging

Mohammad Alizadeh Poshtiri, Suprabhat Paramanick ,Wisdom Koku Evadzi, Mahesh K Gangishetty, Prabhakar Pradhan

Department of Physics and Astronomy, Mississippi State University, Mississippi State, MS

Laser-based biomedical imaging is widely valued for its high brightness and directional illumination; however, it is fundamentally constrained by speckle noise, a consequence of the high spatial coherence inherent to laser light. These speckle artifacts degrade image contrast, obscure fine structural details, and reduce quantitative accuracy. Such limitations are particularly pronounced in wide field and deep tissue imaging contexts. Random lasers (RLs) have the potential to transform applications into disease diagnostics, tissue imaging, and BioNanoPhotonic technologies by providing laser level brightness with low spatial coherence, resulting in speckle free, label-free biomedical imaging. Conventional incoherent sources, such as LED lamps, can reduce speckle but fall short of the brightness required for high resolution biological imaging due to their low Photon Degeneracy and Spectral Radiance. Unlike conventional lasers, RLs do not rely on a defined optical cavity; instead, light amplification is achieved through coherent feedback from multiple scattering events within a disordered gain medium, making them effectively mirrorless laser sources. Through an ongoing interdisciplinary collaboration between the Physics and Chemistry Departments, random lasing has been successfully demonstrated across several disordered gain media, including dye doped polymer bead systems and CsPbBr,f based platforms in both liquid and fiber configurations. High contrast, speckle free imaging of biological cells/tissues has also been confirmed, providing strong proof of concept for RL based biomedical illumination."

G-3M18 Deep Learning-Based Classification of Multiple Cancer Types and Stages Using Brightfield Histopathological Images

Mousa Alrubayan

Mississippi State University, Mississippi State, MS

Cancer diagnosis relies heavily on histopathological examination, but distinguishing between different cancer stages can be difficult because the visual differences are often very subtle. Recent advances in deep learning have shown great potential in analyzing histopathological images and supporting cancer diagnosis. In this study, we investigated whether deep learning models can distinguish between different cancer stages using conventional brightfield microscopic images obtained from Tissue Microarray (TMA) samples. Eighteen deep learning models were evaluated using the same methodology across six different cancer types. The models were compared using standard classification metrics. Overall, the results showed that deep learning models were able to identify subtle differences between cancer stages and achieved high classification performance across the studied datasets. These findings demonstrate that conventional brightfield histopathological images contain sufficient information for deep learning models to distinguish between different cancer stages and support computer-aided pathology.

G-3M19 How Much Nitrogen Does Soybean Really Contribute? Lessons from 15 U.S. States

Oyedele Oluwafemi[1], Reed Vaughn[1], Calhoun Justin S., Lindsey Laura E.[2], Plumblee Thomas Michael[3], Conley Shawn P.[4], Vann Rachel A.[5], Licht Mark A[6]., Reis Andre[7], Singh Maninder P[8]., Casteel Shawn[9], Francisco Eros[10], Cafaro La Menza Nicolas[11], Ross Jeremy[12], Jake McNeal[13], Moseley David O.[14], Ortel Carrie[15], Prakash Kumah Jha[1], Fiorellino N. M.[16], Carrijo Daniella[17], Edmisten K.[18], Olomitutu Emmanuel O.[1], Wallace John[1], Mulvaney Michael J.[1]

[1]Mississippi State University, [2]Ohio State University, [3]Clemson University, [4]University of Wisconsin, [5]University of Illinois, [6]Iowa State University, [7]University of Missouri, [8]Michigan State University, [9]Purdue University, [10]Auburn University, [11]University of Nebraska, [12]University of Arkansas, [13]University of Tennessee, [14] LSU AgCenter, [15] Virginia Tech, [16]University of Maryland, [17]Penn State University, [18]North Carolina State University

Cooperative Extension Services across the United States often provide fertilizer recommendations for row crops, with nitrogen (N) recommendations being arguably the most important, as N is the most commonly yield-limiting nutrient in non-legume crop production systems. Across major soybean (*Glycine max* L.) growing regions, some Extension services recommend an N credit of 22-70 kg N to subsequent non-legume crops following soybean, based on the assumption that soybean, being a legume, contributes biologically fixed N to subsequent non-legume crops. However, the actual magnitude of these N contributions remains poorly quantified under field conditions due to variability in weather and soil properties and the absence of fallow controls in most study designs, making it difficult to distinguish whether observed yield differences result from N immobilization by non-legume residues or from N mineralization by legume residues. To address this knowledge gap, a sixteen-site-year experiment was conducted across 15 U.S. states to quantify N contributions from soybean residues to subsequent corn (*Zea mays* L.) across diverse growing environments. The experimental design was a split-plot factorial in which crop history (corn, soybean, and weed-free fallow) served as the main plot factor, and N rate (0, 84, 168, 224, 280, and 336 kg N) applied to subsequent corn served as the sub-plot factor. Accurately quantifying N credits from soybean residue could reduce N application rates to subsequent non-legume crops, providing evidence of the economic and environmental value of soybean as a sustainable rotational crop.

G-3M20 Redox-Mediated Transcriptional Dynamics in Arabidopsis During Systemic Acquired Resistance

Rezwana Rahman Setu[1], Sargis Karapetyan[2], Mohammad A. Ghanbari[3], George V. Popescu[4], Sorina C. Popescu[5]

[1]Department of Biochemistry, Nutrition and Health Promotion, Mississippi State University, Mississippi State, MS 39762, [2]Department of Biology, Duke University, PO Box 90338, Durham, NC., [3]Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University, Mississippi State, MS 39762, [4]Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University, Mississippi State, MS 39762, [5]Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology (BCH-EPP)

In plants, systemic acquired resistance (SAR) provides long-lasting, broad-spectrum protection against pathogens through priming mechanisms involving redox and phytohormonal signaling. Despite its importance, transcriptional dynamics during SAR onset and the role of redox signaling in SAR maintenance remain poorly understood. Here, we investigated these dynamics by analyzing GRXS13 (Glutaredoxin 13, At1g03850), a CC-type glutaredoxin strongly inducible by salicylic acid; NUDT6 (Nudix hydrolase 6, At2g04450), a gene implicated in SAR-associated nucleotide/redox signaling; and PAD4 (Phytoalexin-deficient 4, At3g52430), a third-cluster SAR-upregulated gene that works with EDS1 and is essential for full SAR establishment. To track in vivo transcriptional dynamics, promoter regions of GRXS13, NUDT6, and PAD4 were fused to luciferase reporters using Gateway cloning and transformed into Arabidopsis thaliana wild type and the SAR-defective top2 mutant via Agrobacterium-mediated floral dip. T2 plants were infiltrated with Pseudomonas syringae pv. tomato DC3000 expressing avrRPT2 to induce SAR, and promoter activity was monitored by bioluminescence at two-hour intervals over four days under 12 h light and 12 h dark cycles. In parallel, in vitro qPCR time-course analyses of additional SAR marker genes like PR1 (Pathogenesis-Related 1, At2g14610), ICS1 (Isochorismate Synthase 1, At1g74710), including GRXS13 and NUDT6, were conducted to obtain precise, quantitative measurements of transcriptional responses. Oscillatory expression patterns of GRXS13 and NUDT6 were observed, and comparisons with known SAR driver genes revealed distinct differences between WT and top2 mutants, reflecting the impact of dysregulated redox and nucleotide signaling on SAR onset. Together, these in vivo and in vitro analyses define key temporal control points of SAR-associated transcription, revealing how redox signaling coordinates systemic immunity and establishing a framework to improve disease resistance strategies in plants.

G-3M21 Fractal, Multifractal, And Fractal Functional Analysis Of Tissue Characterization: Application to Cancer Detection

Santanu Maity, Mousa Alrubayan, Ishmael Apachigawo, Dhruvil Solanki, Prabhakar Pradhan

Mississippi State University, *Mississippi, USA*

The light scattering experiment establishes a relationship between refractive index fluctuations and fractal dimensions in weakly scattering tissue-like optical disordered media. Based on the box-counting approach, an analytical model is developed, showing that the fractal dimension has a functional dependency on the degree of structural disorder or refractive index fluctuation for short-range correlation and approximately depends linearly on these media. The weak multifractality of tissue's optical scattering is explored using the box-counting method. It is shown that with a functional transformation of the fractal dimension, the transformed distribution follows an easy-to-quantify Gaussian form. Peak values across different cancer stages show a systematic increase in most cases.

G-3M22 Could Phenolic Bioherbicide Become a New Tool Against Resistant Palmer Amaranth?

Trisa Das

Mississippi State University, Mississippi, USA

Soybean (*Glycine max*) is a major cultivated crop in the southern United States, with nearly half U.S production being exported globally. Its productivity, however, is severely threatened by Palmer amaranth (Amaranthus palmeri), an aggressive weed that can reduce soybean yields by up to 80% and also causes substantial losses in other row crops. Its prolific seed production and resistance to as many as ten herbicide modes of action leave few effective chemical options. To address this problem, this study evaluated the potential of allelochemicals, caffeic acid, coumarin, and chlorogenic acid, as natural bioherbicides for suppressing Palmer amaranth while ensuring soybean safety. A greenhouse experiment was conducted using a split-plot randomized complete block design with pre-emergence and post-emergence applications at seven rates (0-250 ppm). Plant height, visual injury, photosynthesis, fresh and dry biomass were recorded and analysed through JMP software. It is hypothesized that allelochemicals will induce stress in Palmer amaranth by generating reactive oxygen species (ROS), thereby reducing photosynthesis, inhibiting cell division and elongation, and significantly decreasing biomass. Finding suggests that Caffeic acid produced the strongest response, suppressing Palmer amaranth most effectively at 150 to 200 ppm. There was significant reduction in shoot and root biomass by roughly 60%, accompanied by visible chlorosis, stunting, and plant death. Coumarin was moderately phytotoxic and chlorogenic acid offered only limited suppression, while soybean showed minimal injury across treatments. This study highlights the promise of allelochemical-based bioherbicides as eco-friendly alternatives to synthetic herbicides, offering a sustainable weed management tool to reduce economic losses and support long-term agricultural profitability.

G-3M23 Optical Design Optimization of an In-Situ Laser Monitoring System for the ePIC pfRICH Detector

Zakia Sultana Tithi[1], Wenliang Li[1], Bob Azmoun[2]

[1]Mississippi State University, [2]Brookhaven National Laboratory

This work presents the design optimization of an in-situ laser monitoring system for the ePIC pfRICH detector. Reliable pfRICH performance requires stable HRPPD timing and sensor response during long-term operation, since changes in alignment, optical components, or detector response can affect the quality of particle-identification measurements. A laser monitoring system provides controlled optical pulses as an independent reference to track these variations over time. In this study, an ideal optical monitoring geometry was simulated using TracePro to evaluate light delivery to the HRPPD sensor plane. The main design criteria include broad sensor-plane coverage, controlled light distribution, compatibility with mechanical integration, and practical diffuser fabrication. Three diffuser opening-angle cases were studied to represent the expected variation around the nominal 47° design. The 47° nominal diffuser was selected as the baseline configuration because it provides 81.22% HRPPD-plane coverage while maintaining a practical balance between optical performance and fabrication feasibility.

POSTER (P)

High School Poster (H-P)

H-P1 Cosmic Watch

Abigail McTaggart

Cosmic rays' high-energy particles originating from space travel through Earth's atmosphere and produce showers of secondary particles when they collide with atmospheric atoms. We adapted and constructed a compact detector based on the well-known CosmicWatch project. This system can detect cosmic-ray events and will be used to calibrate particle-detector modules being developed for the Electron-Ion Collider at Brookhaven National Laboratory.

H-P3 Radioactivity in Soils Collected in the Vicinity of a Nuclear Plant

Armond Trevillion[1], Steve Adzanu[2], Jermiah Billa[3], Manoj Bolugallu Padmayya[3], Sonia Eley[3], Martha Ravola[3], John Adjaye[3]

[1]Vicksburg High School, MS; [2]Hinds Community College, Vicksburg, MS Department of Advanced Technologies, Alcorn State University, Lorman, MS 3909

Earth's crust is filled with many naturally occurring elements (isotopes), and among them, the Naturally Occurring Radioactive Materials (NORM) are of great importance from a radiological health perspective, as they can pose health hazards to living organisms. The concentrations of NORM isotopes vary widely across geographical locations, soil (rock) types, and other human activities in the vicinity. However, it is well known that NORM activity in soils is limited, regardless of geographical location. Industries such as nuclear power plants may release trace quantities of man-made isotopes into the environment during their routine operations. Specifically, man-made isotopes such as Cs-137 have longer half-lives and may remain in the environment for extended periods. In this context, a pilot study was performed on soils collected in the vicinity of a Nuclear Power Plant located within a few miles of the Alcorn State University campus. The soils were analyzed using a solid-state detector (germanium detector) of 35% relative efficiency via gamma spectroscopic techniques. While the NORM isotopes of Ra-226, Th-232, and K-40 were identified, trace quantities of Cs-137 and Mn-54 (both man-made) were identified in the soils. Based on this study, it is strongly recommended that routine monitoring of radioisotopes within 5-, 10-, 20-, and 25-mile radii around the nuclear power plant be conducted continuously. Also, it is suggested that a clear database be created and made available to residents living within a 25-mile radius of the plant, detailing activity and radiation dose levels.

H-P4 Radioactive Potassium (K-40) in Water Softeners

Antoniah Erves, Jermiah Billa, John Adjaye, Manoj Bolugallu Padmayya, Sonia Eley, Martha Ravola

[1]Warren Central High School, Vicksburg, MS, [2]Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

Water is an essential resource for human life. In the United States, residents in urban areas primarily rely on municipal water supplies, whereas a significant proportion of the rural population depends on groundwater. Depending on the geographical location, groundwater may contain elevated concentrations of dissolved salts. To reduce water hardness caused by minerals such as calcium and magnesium, many consumers use water softeners before using the water for domestic and industrial purposes. The state of Mississippi, where approximately 52% of the population resides in rural areas, relies extensively on groundwater systems. Consequently, the use of water softeners is common in many rural communities. One of the most widely used water-softening agents is potassium chloride (KCl), which naturally contains the naturally occurring radioactive isotope potassium-40 (K-40). The concentration of K-40 in KCl products varies depending on the source and purity of the potassium. In this context, a pilot study was conducted to theoretically estimate and experimentally measure the concentration of K-40 in commercially available potassium chloride water softeners using gamma spectroscopic analysis. The experimentally determined K-40 concentrations were then compared with the theoretical estimates to assess the accuracy of the measurements and evaluate the consistency between the two approaches. The results demonstrated good agreement between the theoretical and experimental K-40 concentrations, indicating that gamma spectrometry is an effective method for quantifying naturally occurring radioactivity in potassium chloride-based water softeners.

H-P5 Radioactive Radon Concentrations in Underground Water Samples Collected from the Alcorn State University Campus

Maghan Rankin[1], Jermiah Billa[2], John Adjaye[2], Manoj Bolugallu Padmayya[2], Sonia Eley[2], Martha Ravola[2]

[1]Jefferson County High School, Fayette, MS, [2]Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

Located in rural Mississippi in the counties of Claiborne and Jefferson, Alcorn State University serves approximately 5,000 students and 500 staff members. Water supply for ASU is provided by wells (Ground Water) located on the campus. Ground water primarily consists of Radon (Rn-222), a colorless and odorless radioactive gas that is naturally present in soils and is one of the daughters of U-238. Depending on the geography, types of soil, and types of rocky materials in the earth's crust, the levels of radon significantly varies. According to the EPA, community water suppliers should provide drinking water to citizens with Radon levels no higher than 4,000 pCi/L. Per EPA, Claiborne and Jefferson counties are sunder radon zone 3 (Counties with predicted average indoor radon screening levels less than 2 pCi/L). However, there is limited data on Radon levels in groundwater within the region of interest. A pilot study is executed to measure Radon concentration levels in water collected from wells that supply water to ASU community using an Alpha Guard

Professional Radon Meter. Multiple samples were collected (at least 10 samples for week and for up to 3 months) and analyzed for Radon concentration so that statistically justifiable and reliable results are obtained. The presented data consists of a comparison of measured radon concentration values in drinking water evaluated in this study to the EPA's recommendations on radon concentration in drinking water.

H-P6 Obstacle Detection and Safe Navigation with the Boston Dynamics Spot Robot

Divya Sai[1], Jane Moorhead[2], Lalitha Dabbiru[1]

[1]The Mississippi School for Mathematics and Science, [2]Mississippi State University

As robots become more common in public spaces and workplaces, it is crucial that they can detect people and obstacles to navigate safely without causing harm. We have developed a Boston Dynamics Spot robot, a four-legged quadruped platform, designed to recognize and avoid obstacles while maneuvering effectively. Equipped with an array of sensors, cameras, and an onboard computing system, Spot can operate in complex environments. When the robot encounters an obstacle, it estimates the obstacle's position and calculates a safer route to continue moving toward its destination. This capability for real-time obstacle avoidance allows Spot to respond swiftly to unexpected situations, greatly reducing the likelihood of collisions. Research has shown that Spot can safely avoid both stationary and moving objects while maintaining a safe distance from them. This functionality is particularly valuable for various applications, including construction site inspections, industrial monitoring, defense operations, and search-and-rescue missions. Moreover, enhanced object detection improves the safety and efficiency of autonomous robots working alongside humans in dynamic real-world scenarios.

H-P7 Linear-Attenuation Coefficients of Selected (Copper, Aluminum, and Lead) Shielding Materials

Yeshua Agyepong, John Adjaye, Jermiah Billa, Sonia Eley, Manoj Bolugallu Padmayya, Martha Ravola

Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

Shielding against radioactive sources, such as X-rays and gamma rays, is an important aspect of external dosimetry. The shielding process becomes more challenging because radiation sources often emit photons over a broad range of energies. One of the key physical properties considered when selecting a shielding material is its Linear Attenuation Coefficient (LAC), which describes the material's ability to attenuate radiation. In this study, a simple experiment was conducted to determine the LACs of three different shielding materials: lead, copper, and aluminum. Gamma spectrometric analyses were performed using a 35% relative-efficiency high-purity germanium (HPGe) detector and a cesium-137 (Cs-137) point source. The experimental results showed that the measured LAC values for the three materials were in good agreement with their corresponding standard values. However, slight deviations from the standard values were observed, suggesting that the materials were not completely pure and were likely present as alloys or contained impurities. These compositional differences influenced the measured attenuation coefficients. As expected, lead exhibited the highest attenuation coefficient and proved to be the most effective shielding material among the three materials investigated.

H-P88 Impact of combined heat and drought stress on seed weight and number in soybean

Willie McGee[1], Lekshmy V Sankarapillai[1], Seth Givens[2], Sachin Cooray[2], Mary Love Tagert[2], Donna Peterson[3], Nuwan Wijewardane[2], Raju Bheemanahalli[1]

[1]Department of Plant and Soil Sciences, Mississippi State University, MS, USA
[2]Department of Agricultural & Biological Engineering, Mississippi State University, MS, USA
[3]School of Human Sciences, Mississippi State University, MS, USA

Changes in the frequency of heat and drought threaten global food security. While the independent effects of drought and extreme heat on crops are well-documented, their combined occurrence creates a distinct, more damaging impact. However, their combined effects on seed yield components and quality remain poorly understood. We hypothesized that combined heat and drought stress would impose greater damage than either stress alone. To test this hypothesis, Soybean genotypes DS25-1, DT97-4290, and Williams 82 were exposed from full bloom (R2) through seed development to control conditions (CNT; 32°C, full irrigation), heat stress (HS; 38°C, full irrigation), drought stress (DS; 32°C, 40% irrigation), or combined stress (HS+DS; 38°C, 40% irrigation) in a split-plot design. Plants were harvested at physiological maturity to assess yield components and seed traits. Total pod number decreased by only 4.1% under HS but by 25.9% under DS and 36.7% under HS+DS. Under DS, the numbers of filled and unfilled pods declined by 25% and 37%, respectively. Total pod weight decreased progressively by 9.9% under HS, 32.6% under DS, and 57.2% under HS+DS. Stress-induced changes in seed size distribution are being quantified. Overall, combined heat and drought caused substantially greater reproductive losses than either stress alone.

Undergraduate Poster (U-P)

U-P8 Viscosity of Mars-Relevant Ternary Brines

Timothy J. Ward[1], Ardith Bravenec[2]

[1]Millsaps College, MS, USA, [2]NASA Johnson Space Center, USA

We report experimental viscosity measurements for the NaClO,,-NaCl-H,,O, Na,,SO,,-NaCl-H,,O, and NaNO,ƒ-NaCl-H,,O systems at 294.15 K over a broad range of ionic strengths and evaluate several calibrated fit models for mixed electrolyte solutions. Models based solely on binary contributions tend to underestimate viscosity at elevated concentrations, whereas incorporation of an explicit ion-ion interaction coefficient within a modified extended Jones-Dole framework reduces typical deviations to below 1.0%. A reduced log-viscosity surface model provides comparably accurate fits with fewer, well-constrained parameters. Application of the calibrated ternary models to Mars-relevant salt ratios derived from the Phoenix Wet Chemistry Laboratory shows that mixed NaCl-NaClO,,, brines can attain viscosities substantially higher than either single-salt endmember at the same total molality, indicating that binary-based models may systematically underestimate fluid resistance in chemically complex Martian systems. These results demonstrate the necessity of experimentally calibrated ternary viscosity models that explicitly account for non-ideal mixing effects when extending into multiple-anion systems.

U-P9 Photochemical Cyclization Reactions involving the Saccharin Chromophores

Alex A. Bremond, Wolfgang Kramer

Millsaps College, Mississippi, USA

In this project, we investigate the use of saccharin as a chromophore in photochemical cyclization reactions. Saccharin has an absorption maximum that is comparable to phthalimide, but due to its asymmetry provides regiospecificity for any type of photoreaction. Cyclization of substituted chromophores with the goal of targeted synthesis requires control of the regiochemistry of the photochemical reaction. Further modification of the photochemical product depends on the substituent on the phenyl group. Substitution on the 6 or 7 position would lead to modification on the opposite side of the cyclization direction, while 4 and 5 substituents could produce structures that show activity as kinase inhibitors towards glycogen synthase kinase and cyclin dependent kinases. Acknowledgement: This work was supported by the Mississippi INBRE, funded by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM103476.

U-P10 Synthesis of Isoindolone Piperidines As Kinase Inhibitors: Preparation of Photochemical Starting Materials and Photoreactions

Caleb Solangi, Wolfgang Kramer

Millsaps College, *MS, USA*

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, and which substituents are tolerated during the photocyclization. The target structures, valmerins, are inhibitors of two key phosphorylating enzymes, glycogen synthase kinase-3 (GSK3) and cyclin-dependent kinases (CDKs). Inhibition of these 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. 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-P11 Innovative Hydrogel Composite Increases Bone Healing, Improves Neurobehavior Performance, And Decreases Chronic Inflammation Following Craniofacial Defects In Adolescent Rats

Clara Lee , Jonathan W Lee, Kelly E Cantrell, Almia S Valentine, Tyra Z Lockett, Chloe J Batiste, Amol V Janorkar, Chipo A. Chapusha, William R. Farmer, Charles L Matheny, Shuying Lin, Madison Klim, Susana M. Salazar Marocho, Alexandre A da Silva, Bernadette E Grayson, Michelle A Tucci, Lir-Wan Fan

University of Mississippi Medical Center, Mississippi, USA

Pediatric head trauma can cause significant morbidity and mortality, as well as cranial bone defects that require craniectomy to reduce brain swelling. Cranioplasty following craniectomy may increase the risk of bone resorption in developing children and often results in the need for additional surgical intervention, as leaving the skull without bone can result in sunken skull syndrome. In addition, pediatric head trauma and inflammation are linked to long-term inflammation and memory deficits. Therefore, there is a need for a biomaterial that can both assist in bone regeneration and improve cranial defect healing. The objective of the current study was to assess the healing and resorption rates of cranial defects using resorbable hydrogel-based composite materials as a scaffold, and to evaluate the potential for inflammation-mediated changes in neurobehavior and healing in adolescent rats. A 5-mm central critical-sized cranial defect was created in postnatal 49-day-old (P49) male and female Sprague-Dawley adolescent rats, which were then randomly assigned to one of five experimental groups: (1) sham-operated, (2) empty defect, (3) placement of autologous bone, (4) composite with hydrogel, (5) placement of autologous bone and composite with hydrogel (n = 6/sex/groups). Neurobehavioral assessment, including a Y-maze test, was performed biweekly, and characterization of bone remodeling and brain inflammation was conducted at the 8-week endpoint. Our results showed that the empty defect group exhibited decreased short-term memory in both male and female rats at 2, 4, and 6 weeks after surgery, with a greater effect in males. The autograft (bone placement) group exhibited decreased short-term memory at two and four weeks, followed

by recovery at six weeks post-surgery, whereas the hydrogel composite group and the autograft plus hydrogel composite group did not show such deficits. In addition, bone remodeling results, as determined by micro-CT scans, showed that the bone placement plus composite with hydrogel group achieved the most enhanced bone growth compared with composites lacking hydrogel eight weeks after surgery in both male and female rats. The empty defect also caused a chronic increase in the number of activated microglia (Iba1+) in the cortex at the bregma and dorsal hippocampus levels. The number of cortical microglia (Iba1+) was decreased in the treatment groups at the bregma level. Our results suggest that the hydrogel composite, which enhanced bone repair and neurobehavioral performance and decreased chronic brain inflammation, is superior to the autograft in our rat defect model.

U-P12 Functional Analysis of Human Retroviral-Like Protease Domains in Yeast Protein Quality Control And Secretion

Dilber Annageldiyeva, Galen Collins

Mississippi State University

Protein homeostasis requires cellular pathways that recognize, traffic, and remove misfolded or damaged proteins. Ddi1 is a conserved ubiquitin-associated protein with a retroviral-like protease domain that has been linked to protein quality control and secretion, but it is not fully understood whether human retroviral-like protease domains can replace Ddi1 function in yeast. This project uses Saccharomyces cerevisiae as a model system to test whether human RVP-containing or RVP-like proteins can rescue secretion defects in a yeast ddi1 background. Candidate human sequences, including DDI2-related regions and proteins such as ASPRV1, NRIP3, NRIP2, PEG10, and RTL1, are being cloned into MTV yeast expression vectors. Inserts are amplified by PCR, digested with restriction enzymes, gel-purified, ligated into plasmids, transformed into Escherichia coli, selected on ampicillin, purified by miniprep, and confirmed by restriction digestion and Sanger sequencing before transformation into Îddi1 yeast. Functional rescue will be tested by measuring Kap2p secretion using a Bradford assay. Preliminary work has established the cloning workflow, including PCR amplification, digestion, ligation, bacterial transformation, plasmid purification, and sequencing analysis. Initial sequencing results indicate that some constructs require further validation or re-cloning because reads matched vector or non-target sequences rather than the expected insert. These results highlight the importance of sequence confirmation before functional assays. It is expected that some human RVP-domain constructs may partially or fully rescue the Îddi1 secretion phenotype, while others may not. This work may help identify conserved functions of RVP-like proteins in protein quality control and secretion and support the use of yeast as a model for studying human proteostasis factors.

U-P13 Using Yeast to Study How Human Proteases Control Vesicle Trafficking

Emily Snodgrass, Galen Collins

Mississippi State University, MS, USA

Protein trafficking within cells is essential for maintaining cellular function. For example, proteins that need to be transported to the plasma membrane to function as surface receptors or to be secreted as signals require an organized and effective pathway. This is done through intracellular vesicles whose fusion with the cell membrane is mediated by SNARE proteins, such as Sso1 within S. cerevisiae. The job of Sso1 is to pull transport vesicles to the membrane through a zipper-like motion. Studies show that Ddi1, a ubiquitin-dependent protease, negatively regulates exocytosis by binding to SNARE proteins like Sso1. Our aim is to investigate the relationship between Ddi1 and Sso1 and identify specific binding regions involved in this interaction. These regions can serve as representatives of the behind-the-scenes action of protein control and degradation. We are using the model organism S. cerevisiae, baker's yeast, to investigate how Ddi1 binds the SNARE protein Sso1. Mapping the interactions between these proteins will provide insight into the protein quality-control processes associated with protein secretion pathways. These findings should also apply to higher eukaryotes, such as humans; much remains to be discovered about Ddi2, the human ortholog of Ddi1. Acquiring more knowledge of its role within the body through examining Ddi1 can contribute to the study of a variety of diseases involving protein degradation. The process of identifying these conserved regions in Ddi1 and Sso1 focuses on amino acids that participate in hydrogen bonding and salt-bridge formation between the two. Modeling protein structures in AlphaFold3 and using PDBePISA programs has enabled an interface analysis of these sites in Ddi1, Sso1, their phosphorylated forms, and other related proteins within the Ddi1 and SNARE protein families. Preliminary information on binding sites in specific areas of focus has revealed highly conserved amino acids that mediate binding (particularly within phosphorylated Sso1), opening the door to testing these regions through experimental validation. Various domain mutations will be created to test the effect of altering structural connections on protein secretion. Both wild-type and mutant Ddi1 proteins will be expressed in yeast strains; this mutagenesis will allow evaluation of effects on vesicle trafficking. This will be done using invertase secretion assays. Invertase is an enzyme that catalyzes the hydrolysis of sucrose into glucose and fructose and is present in yeast. We will test the invertase secretion rate in DDI1 and SSO1 mutants using both an enzymatic assay (functional, folded invertase) and antibodies against Suc1 (total invertase). We expect that, although functional protein secretion does not increase significantly, misfolded protein (and thus total protein) will. Hopefully, previously unknown interactions between Ddi1 and Sso1 can be identified, indicating a specific role for them in the SNARE- mediated trafficking of invertase. These studies will help us gain further insight into how Ddi1 proteins fit into the processes of visible trafficking and protein regulation in cells, contributing to our understanding of essential processes for the cellular health of many organisms.

U-P14 Human-horse cardiac coupling on student perceived stress levels during a collegiate-based equine-assisted interaction program

Emma Morgan[1],Molly Nicodemus[2], Emma Farnlacher[2], Emily Curran[2]

[1]East Mississippi Community College, [2]Mississippi State University

Following the COVID-19 pandemic, college campuses experienced a substantial increase in student mental health concerns, prompting the adoption of alternative therapeutic approaches, including equine-assisted interaction (EAI). Although survey-based studies have examined collegiate EAI programs, research evaluating physiological biomarkers during these activities remains limited. This study investigated relationships among physiological responses in both humans

and horses, participant-perceived stress, and potential human-horse physiological coupling during EAI. Twenty-six full-time college students participated in a one-hour EAI session involving horse grooming and leading. Heart rate monitors recorded physiological responses in both students and horses, while perceived stress was assessed before and after the session using a 4-point Likert scale (4 = high stress). Heart rates increased significantly following the session in both students (mean change: 13.8 ± 16.7 bpm) and horses (6.4 ± 6.6 bpm; $P < 0.001$). A moderate negative correlation was observed between human and horse heart rates ($r = -0.46$), suggesting physiological coupling during the interaction. Participants also reported significantly lower stress after the session (mean change: -0.7 ± 1.1; $P < 0.001$). Human heart rate showed a moderate negative correlation with perceived stress ($r = -0.30$), whereas horse heart rate was not associated with participant stress ($r = -0.07$). These findings suggest that EAI may reduce perceived stress while eliciting coordinated physiological responses between humans and horses, highlighting its potential as an exercise-based therapeutic strategy for supporting college student mental health.

U-P15 Impact of Seed Size and Composition on Soybean Seedling Development

Fernando Ereno, Bala Subramanyam Sivarathri, Chami Rampati Dewage, Raju Bheemanahalli

Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Soybean (*Glycine max* L.) is one of the world's leading agricultural commodities, valued for its protein and oil content. Our earlier research indicated that resources allocated during grain filling influence seed weight and quality, including protein and oil. Notably, intra-generational variation in seed quality can establish a memory effect, either advantageous or detrimental, that affects subsequent generations' performance. We hypothesize that, under stress, high-protein seeds may act as molecular chaperones, thereby enhancing seedling vigor. In this study, we employed near-infrared spectroscopy (NIRS) to assess protein variability across 220 soybean genotypes. Protein content varied substantially, ranging from 39% to 51% on a dry weight basis, with a mean of 51%. Approximately 44% of the genotypes recorded protein levels below 44%, specifically within the 39.1% to 43.8% range. Oil concentrations ranged from 14% to 24%, with an average of 19%. Protein content was significantly and negatively correlated with oil content ($r = ˆ'0.53$, P < 0.01). Seeds with known quality (protein and oil) were germinated under low and high temperatures to assess the impact of seed protein content on seedling vigor traits, including root and shoot biomass. Individual seed weight positively correlated with shoot growth under high ($r=0.33$, $p<0.01$) and low temperatures ($r=0.40$, $p<0.01$). Oil content showed weak positive correlations with shoot weight under high and low temperatures, but no significant correlation with root weight. Protein content was not significantly associated with shoot or root weight under either condition, indicating that variation in seed protein did not affect seedling growth.

U-P16 Identification of Pulque Biomarkers Comparison of Extraction Techniques

Jasmine Brewer, Timothy J Ward

Millsaps College, Mississippi, USA

Pottery produced in Mesoamerica could have been used for storage and distribution of economic products. It is thought that a specific vessel called Blanco Levantado was used to store and transport a fermented drink called pulque. If these vessels were used for pulque, it would give insight into the economy of the time that could help archeologists further map these Mesoamerican civilizations. To confirm the presence of pulque a lipid extraction method has been prepared and tested on pulque to identify the biomarkers of the drink after being analyzed on GC/MS. To confirm that the developed method is effective in identifying biomarkers, the Folch extraction method will also be used to compare the data gathered versus the previous total lipid extraction technique used in our lab. Once biomarkers are identified from the extraction techniques, pottery sherds from archeological sites in the Yucatan can be analyzed for the presence of pulque.

U-P17 Application of Function-on-Scalar Regression to Chronic Motor Effects Following LPS Exposure in Neonatal Rats

Jonathan W Lee[1,2], Md Mushfiqur Rahman[1], Md Rokibul Hasan[1], Lu-Tai Tien[3], Yu-Ching Tu[4], Michelle A Tucci[5], Norma B Ojeda[6], Yi Pang[2], Lir-Wan Fan[1,2,], Pratim Guha Niyogi[1,*]*

[1]Department of Data Science, University of Mississippi Medical Center, Jackson, MS 39216, USA, [2]Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA, [3]School of Medicine, Fu Jen Catholic University, Xinzhuang Dist, New Taipei City 24205, Taiwan, [4]Department of Long-Term Care Management, Chung Hwa University of Medical Technology, Rende Dist, Tainan City, 71703, Taiwan, [5]Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA, [6]Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA

Preterm birth remains a major public health concern in the United States, with infection- and inflammation-related mechanisms contributing significantly to early-life neurological vulnerability. Previous studies have shown that intracerebral lipopolysaccharide (LPS) exposure in postnatal day 5 (P5) rats disrupts dopaminergic developmental pathways and induces motor dysfunction in male adult. To determine if neonatal systemic LPS exposure has the same effects and sex-specific differences, the present study used a function-on-scalar regression approach to evaluate systemic LPS exposure-induced long-lasting motor dysfunction in both male and female rats. 48 Sprague–Dawley rats (balanced by sex) received LPS or saline intraperitoneally on P5 and were assessed across ten locomotor, sensorimotor, and growth outcomes from P5 to P70. Longitudinal trajectories were analyzed using naïve linear regression, generalized least squares with compound-symmetry correlation, and function-on-scalar regression (FOSR). Across outcomes, systemic LPS exposure produced long-lasting motor impairments followed by spontaneous recovery by P63–P70, with the period of maximum divergence localized to approximately P14–P49, corresponding to a critical window of dopaminergic and sensorimotor maturation. LPS-exposed groups exhibited concurrent locomotor hyperactivity and sensorimotor deficits, consistent with dopaminergic sensitization alongside fine-motor disruption. FOSR substantially outperformed conventional models, with adjusted R^2 gains up to 0.59, revealing nonlinear, age-specific treatment effects not captured by linear interaction terms. Sex differences were modest but detectable in age-varying trajectories. These findings demonstrate that

systemic LPS administration effectively recapitulates the neurobehavioral effects of systemic exposure, with sex-specific differences, and validate systemic LPS as a biologically and clinically relevant model of neonatal inflammatory injury.

U-P18 A Preliminary Investigation of Grooming-Based Equine-Assisted Experiences for Supporting College Student Emotional Well-Being

Julius Culwell[1], Molly Nicodemus[1], Kaitlyn Butze[1].Emma Morgan[2]

[1]Mississippi State University, [2] East Mississippi Community College, MS, USA

Mental health concerns among college students have increased since the COVID-19 pandemic, prompting universities to expand wellness initiatives, including animal-assisted interventions. Although equine-assisted experiences (EAE) have shown promise for promoting emotional well-being, evidence-based curricula for campus-based equine programs remain limited. This study developed and evaluated a grooming-based EAE curriculum designed to support college student emotional well-being. The curriculum was developed in collaboration with the Mississippi State University Extension Equine Assisted Services Program and emphasized stress reduction, mindfulness, cognitive engagement, emotional regulation, and social connection. The program was offered during a student wellness event at the university equine facilities during spring semester finals week. Nine students participated after being recruited through social media and class announcements. Heart rate was continuously monitored throughout the session, and participants completed a post-session verbal interview. All participants reported an improved mental state following the session. Mean heart rate did not differ significantly from pre- to post-session (83.2 ± 8.4 vs. 89.4 ± 11.1 bpm; P = 0.08) and remained within normal resting values. However, maximum heart rate during the session (105.4 ± 12.1 bpm) was significantly greater than minimum heart rate (73.1 ± 8.1 bpm; P < 0.05), with peak values occurring midway through the activity. One participant exhibited their lowest heart rate after the session. These findings suggest that a grooming-based EAE curriculum may support emotional well-being while maintaining low physiological stress, supporting its potential as a campus wellness intervention, although further investigation is warranted.

U-P19 Research Intelligence Center: Mapping Critical and Emerging Technology Research

Kavya Gautam, Narcisa Pricope

Mississippi State University, Mississippi State, MS, USA

Research security has become a growing priority for federal agencies and universities, yet few tools exist that give institutions a clear, data-driven picture of their research landscape in relation to research security concerns. The Research Intelligence Center (RIC) is a web application developed as part of the NSF SECURE Center under NSF Cooperative Agreement No. 2403771 that maps the research output and federal funding landscape of all 187 R1 doctoral universities in the United States, with a focus on Critical and Emerging Technology areas designated by federal policy. The platform integrates data from multiple authoritative sources including OpenAlex, NSF NCSES, the Research Organization Registry, USASpending, and Carnegie Classifications to generate institution-level research profiles. A key output of the platform is the Research Compliance Complexity Score, a composite metric that characterizes the breadth and intensity of a university's engagement with federally designated critical technology areas. RIC also maps the funding relationships among universities, federal laboratories, nonprofits, and industry partners to provide a broader picture of the research ecosystem.This poster presents work on the data infrastructure underlying RIC, including a subfield-weighted publication sampling approach that draws proportionally from 254 OpenAlex subfields to better represent each institution's research profile. This approach addresses limitations of citation-based sampling by ensuring each institution's publication data reflects its actual research distribution across fields. Ongoing work focuses on improving data update pipelines, expanding entity coverage, and ensuring the accuracy of cross-institutional comparisons.

U-P20 Chromosomal Aberrations Caused by Echinochloa crus-galli ON Lolium multiflorum

Kayla Bolden, Jennifer Laifa, Hattie Spencer

Mississippi Valley State University, MS, USA

Mitosis is the division of cells for the growth of plants. Plants can impact the growth of each other, causing disturbances in the cell division. The study hypothesized that chromosomal aberrations would occur in Lolium multiflorum when growing with Echinochloa crus-galli. In the present study, seeds of the L. multiflorum and Echinochloa crus-galli were grown for 7 days. After 7 days, two mm of freshly grown L. multiflorum root was cut with a razor blade. The root was prepared to observe the phases of mitosis and chromosomal aberrations. A microscope was used to observe phases of mitosis. The mitotic index was 33%. After 14 days, the mitotic index decreased to 20%. When L. multiflorum was growing with E. crus-galli, chromosome stickiness, bridges, c mitosis, lagging and fragments were observed. In conclusion, when L. multiflorum is growing alone, there is a high activity of cell division which decreases with time and when growing with other plants, cell division is disturbed as observed from chromosomal aberrations.

U-P21 Azithromycin reduces hypoxia-ischemia-induced sensorimotor impairments, brain injury, inflammation, and oxidative stress in neonatal rats

Kelly E Cantrell1, Jonathan W Lee1, Madison Klim1, Clara Lee1, Shuying Lin2, Sumana Ramarao1, Michelle A Tucci3, Norma B Ojeda4, Mary A Kosek1, Lir-Wan Fan1

1Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA, 2Department of Physical Therapy, University of Mississippi Medical Center, Jackson, MS 39216, USA, 3Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA, 4Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA

Hypoxic-ischemic (HI) brain injury is a major cause of neonatal morbidity and mortality and can result in long-term neurological impairments, including motor, cognitive, and developmental deficits. Following HI injury, activated microglia release pro-inflammatory cytokines that amplify the inflammatory response and contribute to neuronal damage. While azithromycin possesses immunomodulatory and anti-inflammatory properties and is considered safe for use in pregnant women and neonates, its neuroprotective effects following HI brain

injury remain unclear. The objective of the current study was to determine whether azithromycin, a putative suppressor of microglial activation, reduces microglial activation, decreases neuroinflammation, and improves neurological performance following hypoxic-ischemic injury in neonatal rats. Researchers hypothesized that suppressing the inflammatory response would lessen brain injury and improve early neurobehavioral outcomes. Male and female Sprague-Dawley rats were subjected to HI at postnatal day 5 (P5) and randomized to Sham+Vehicle, Sham+Azithromycin, HI+Vehicle, or HI+Azithromycin groups (n=18/sex/group). The rats underwent bilateral common carotid artery ligation or sham surgery, followed one hour later by 15 minutes of hypoxia (8% oxygen) or room air exposure, respectively. Immediately after, rats received either intraperitoneal azithromycin (20 mg/kg) or vehicle (phosphate-buffered saline) as a control. Twenty-four hours later, sensorimotor neurobehavioral performance was assessed, and brain inflammation and injury were examined in P6 rats. Brain tissue was also analyzed for interleukin-1β (IL-1β) levels, a key pro-inflammatory cytokine released by activated microglia, and TBARS contents, an index of lipid peroxidation indicating the oxidative stress. The results demonstrated that HI injury significantly increased IL-1β expression and TBARS levels, indicating enhanced neuroinflammation and lipid peroxidation, and produced sensorimotor neurobehavioral deficits. Azithromycin treatment significantly reduced IL-1β expression and TBARS levels while improving performance across all neurobehavioral assessments, including righting reflex, negative geotaxis, wire-hanging, and hind-limb suspension tests, which evaluate motor coordination, strength, balance, and neurological development. These findings suggest that azithromycin may provide neuroprotective benefits by suppressing microglial-mediated inflammation and oxidative stress after neonatal HI injury. Given its established clinical safety profile, azithromycin represents a promising therapeutic candidate for reducing inflammation and oxidative stress and improving neurological outcomes following neonatal hypoxic-ischemic brain injury.

U-P22 Longitudinal Analysis of Neonatal Inflammation-Induced Sex-Specific Effects on Sleep in Adolescent Rats

Lir-Wan Fan[1,2] Md Rokibul Hasan[1], Jonathan W Lee[1,2], Md Mushfiqur Rahman[1], Silu Lu[2], Joseph C Crosby[2], Charles L Matheny[2], James P Shaffery[3], Norma B Ojeda[4], Haifeng Wang[5], Lu-Tai Tien[6], Michelle A Tucci[7], Pratim Guha Niyogi[1],**

[1]Department of Data Science, University of Mississippi Medical Center, Jackson, MS 39216, USA, [2]Department of Pediatrics, Division of Newborn Medicine, University of Mississippi Medical Center, Jackson, MS 39216, USA, [3]Department of Psychiatry and Human Behavior, Animal Behavior Core, University of Mississippi Medical Center, Jackson, MS 39216, USA, [4]Department of Advanced Biomedical Education, University of Mississippi Medical Center, Jackson, MS 39216, USA, [5]Department of Industrial & Systems Engineering, Auburn University, Auburn, AL 36849, USA, [6]School of Medicine, Fu Jen Catholic University, Xinzhuang Dist, New Taipei City 24205, Taiwan, [7]Department of Anesthesiology, University of Mississippi Medical Center, Jackson, MS 39216, USA*

Perinatal exposure to inflammation may play an important role in the association between sleep disturbances and the development of neurodevelopmental disorders, such as attention-deficit/hyperactivity disorder. This study aims to longitudinally examine the detailed changes in sleep patterns in adolescent 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 and female rat. Sleep recording electrodes were implanted on P39, and sleep-disruption exposure began on P47 for 24 hours. Baseline sleep and recovery sleep were recorded for 24 hours on P46 and P48, respectively. A hierarchical sequence of six models, including ordinary least squares regression to fit baseline or recovery data and longitudinal models to fit simultaneously across both light and dark phases, was fitted for each sleep stage, including wake, REM, non-REM, and total sleep. Our results showed that neonatal LPS treatment interfered with spontaneous REM sleep duration and episode duration (baseline sleep), with a greater effect in males. Neonatal LPS treatment also interfered with sleep homeostatic responses in both non-REM and REM sleep to sleep disruptions, including sleep duration, episode duration, and episode number (recovery sleep), with a greater effect in males. Our study provided a comprehensive view of chronic inflammation and sleep disruptions affecting sleep patterns and sex-specific homeostatic responses, and could serve as a strong tool for identifying neurodevelopmental disorders using sleep data in subjects exposed to perinatal inflammation and sleep disruptions.

U-P23 Natural Antioxidants, Unnatural Outcomes: Thymoquinone and Epigallocatechin Gallate Suppress SKOV3 Ovarian Cancer Cell Viability

Luke I. Carpenter[1], Gary L. Hamil, Jr.[2], Michelle A. Tucci[3], Hamed A. Benghuzzi[4], and Kenneth R. Butler, Jr.[1]

[1]University of Mississippi Medical Center, Department of Pharmacology and Toxicology, [2]University of Mississippi Medical Center, School of Nursing, [3]University of Mississippi Medical Center, Department of Anesthesia, [4]Jackson State University, Department of Biology and the JSU College of Science, Engineering and Technology, Jackson, MSUSA

Ovarian cancer remains difficult to treat because most cases are diagnosed in the later stages of the disease. Malignant cells spread rapidly throughout the abdomen and often develop resistance to chemotherapy. These challenges make it important to explore ways ovarian cancer cells can be suppressed through different treatments and combinations of treatments. In this project, SKOV3 ovarian cancer cells were examined microscopically at 24, 48, and 72 hours incubation following bolus administration of thymoquinone (TQ), epigallocatechin gallate (EGCG), and combination TQ+EGCG and compared to untreated control cultures using nuclear, cytoplasmic, and other cytomorphologic characteristics and bioassay results including BCA protein (total protein), nitric oxide (inflammatory and stress-related signaling), and glutathione (antioxidant capacity) levels. Across these conditions, the SKOV3 cells showed substantial variation in viability and structural integrity ($p<0.05$). Several treated groups contained very few viable cells, with most dead or in later stages of viability, especially in the 48- and 72-hour phases of the experiment. The control slides at each phase showed thriving groups of ovarian cancer cells. Morphological features such as increased nuclear-to-cytoplasmic ratios, hyperchromasia, irregular nuclear borders, multinucleation, cytoplasmic vacuoles, and pyknosis were common, especially in treated groups and later time points. The quantitative measurements supported these observations, showing differences in cell size, nuclear area, and cell density that aligned with the levels of cell death and debris (pyknosis, karyorrhexis, and karyolysis) seen microscopically and from bioassay findings ($p<0.05$). Together,

the cytomorphometry and bioassay results provide a clearer picture of how ovarian cancer cells respond to the powerful, naturally occurring antioxidants TQ, EGCG, and their combination over time. In the future, these antioxidants may provide promise as adjunctive therapy to traditional treatments for ovarian cancer by inducing apoptosis or necrosis or successfully suppressing their growth and division.

U-P24 LFHCAL Scintillator Tile Wrapping and Assembly Procedure At Mississippi State University

Megan Searcy

Department of Physics, Mississippi State University, Mississippi State, MS

From August 2025 to March 2026, the nuclear physics group in the Department of Physics and Astronomy at Mississippi State University prepared scintillator tiles for Oak Ridge National Laboratory's contribution to the Electron-Ion Collider (EIC) project. This work supported the Electron-Proton/Ion Collider (ePIC) detector and its Longitudinally Segmented Forward Hadronic Calorimeter (LFHCal). Each scintillator tile was precision-injection molded and wrapped in enhanced specular reflector (ESR) foil to preserve the light signal inside the module. The reflected light signal is later collected by a silicon photomultiplier (SiPM) detector. During Phases I and II, the group wrapped individual tiles, arranged them in 2 Ã— 4 formations, and wrapped each eight-tile assembly as a rectangular chocolate bar.Tiles with visible flaws, such as bubbles, bumps, or scratches, were separated from the production stream and classified as rejected tiles. For individual tile wrapping, ESR foil was folded around each tile. The wrapped tiles were then placed into molds and sealed using small polyimide stickers. For chocolate-bar assembly, eight individually wrapped tiles were placed into a mold and sealed together using large polyimide stickers to form one complete wrapped unit. Phase I concluded with 1,088 wrapped tiles assembled into 136 wrapped chocolate bars and shipped to Oak Ridge National Laboratory. Phase II concluded with 1,432 wrapped tiles assembled into 179 wrapped chocolate bars, which were also shipped to Oak Ridge National Laboratory. A longer-term objective of this work is to develop an automated tile-wrapping system that can increase production efficiency and help meet the large-scale EIC project requirement of approximately 600,000 scintillator tiles.

U-P25 Restoration of a Mirror Reflectivity Test Stand with Modern Motion-Control Integration

Mohnish Sao

Mississippi State University

The Dark Box project aims to restore and modernize the motion-control system of an existing mirror reflectivity test stand used to precisely position and rotate spherical mirrors under a monochromatic light beam. Because much of the original documentation and wiring information was incomplete or lost when the system was previously housed at Jefferson Lab, the project began by identifying the stepper motors, motion assemblies, connectors, cables, and supporting electronics. Continuity testing and cable tracing were performed to determine and verify the motor wiring configurations. A benchtop test system was developed using a Raspberry Pi, a digital stepper-motor driver, and a 36 V DC power supply. The Raspberry Pi generates the step and direction signals, while the driver provides the voltage and current required to operate each motor independently. Current work focuses on validating motor operation, confirming wiring configurations, and establishing reliable motion control. Future work will integrate the system into the Dark Box, implement precise position-control software, evaluate positioning accuracy and repeatability, and document the complete hardware and software architecture for future maintenance and upgrades.

U-P26 Do Yeast Throw Out Their Trash? Testing if loss of Ddi1 increases protein secretion by reducing protein degradation.

Morgan Grace Sheffield, Galen Andrew Collins

Mississippi State University

Ddi1 is a ubiquitin-dependent protease found in the budding yeast Saccharomyces cerevisiae. It is a homolog of the mammalian Ddi2, which mediates Endoplasmic Reticulum-Associated Degradation (ERAD). However, Ddi1 has not been implicated as a contributor to ERAD in yeast. We hypothesize that the loss of Ddi1 leads to increased protein secretion, as previously observed, because this is an adaptive response of yeast that is unable to remove misfolded proteins from the ER. Our work determines whether Ddi1 plays a role in ERAD by measuring the effects of deleting Ddi1 in yeast on protein secretion, degradation, ER stress, and cell viability. Folding of secreted or membrane proteins occurs in the ER, so it is important to study the factors that influence ER protein degradation, as cancer cells are often undetected due to the clearance of misfolded proteins. If Ddi1 can be inhibited to halt protein degradation or to increase ER protein secretion to signal apoptosis, it may have therapeutic relevance. Yeast is easier to study than humans. Regardless of its medical significance, a better understanding of how Ddi1 affects ERAD in yeast will allow us to more fully comprehend how Ddi2 plays a similar but more complex role in the human ubiquitin-proteasome pathway. To determine the effects of Ddi1 in ERAD, protein secretion levels in the ER will be measured by comparing the effects of deleting dsk2 and rad23, which are known proteases in ERAD, with that of Ddi1. To test the effect of Ddi1 on degradation, I will add cycloheximide to inhibit protein synthesis and measure the levels of CPY*, a misfolded protein found in the ER lumen, in the presence and absence of Ddi1. Tunicamycin is known to increase CPY* secretion, thereby increasing cellular stress. To determine whether Ddi1 is important for stress tolerance, I will inoculate strains with and without Ddi1 onto Tunicamycin plates and compare growth. These experiments will be replicated to increase the reliability of the results. So far, deleting Ddi1 has increased protein secretion, as expected. Furthermore, I expect Ddi1 to help yeast tolerate ER stress and possibly increase cell viability under such conditions. However, there may be nuances in the function of Ddi1 that could lead to results that differ from expectations; even so, these results will increase our understanding of Ddi1's role in ERAD.

U-P27 Pyridine-based HIV Integrase Inhibitors: Pyridine-Core Development

Tyler D. Twedt, Wolfgang Kramer

Millsaps College, Mississippi, USA

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.

U-P28 Ring-Expansion of Substituted Indoles

Vivian Jordan, Wolfgang Kramer

Millsaps College, *MS, USA*

Substituted quinolines show activity against HIV integrase. Challenging aspects of many quinoline syntheses are the variation of aryl substituents and the introduction of the C3 side chain. To bypass these problems, we decided to use a skeletal-editing strategy to leverage commercially available indoles. Using a diazoester for ring expansion, substituted indoles can be converted into the corresponding quinolines. While commercially available indoles contain substituents on the phenyl ring, the eventual quinoline 4-substituent is introduced at the indole stage before ring expansion. In this project we report the synthetic steps towards substituted quinolines via a ring expansion pathway from indole.

U-P89 Palmer Amaranth or Waterhemp? Phenotypic and Genotypic Identification of a Misidentified Pigweed Population from Florida

Ana C. Carneiro Leao, Celso M. Franca, Ranieri Borsari, Ednaldo A. Borgato

West Florida Research and Education Center, University of Florida, FL, USA

Weed identification is essential for selecting effective management strategies, particularly among closely related weed species. A farmer in Santa Rosa County, Florida, reported plants presumed to be Palmer amaranth (*Amaranthus palmeri*) that exhibited unusual morphology and were suspected to be mutated after herbicide applications. This study aimed to identitify this species using phenotypic and genotypic analyses. We hypothesized that the plants belonged to a closely related *Amaranthus* species rather than representing a morphological variant of Palmer amaranth. Seeds collected from the suspected plants were grown in a greenhouse maintained at 30/20°C day/night temperatures under a 15-h photoperiod. A known Palmer amaranth population was grown under the same conditions for comparisons. Morphological characteristics were evaluated throughout plant development. For genotypic identification, five individuals from the Santa Rosa County collection were sequenced, and nucleotide position 678 of the acetolactate synthase gene was examined. This position is known to contain thymine in Palmer amaranth used for comparison in both phenotypic and genotypic comparisons, and cytosine in waterhemp (*A. tuberculatus*), which was later included in genotypic assays. Morphological differences between the two groups were evident during plant development. At maturity, plants from Santa Rosa County exhibited shorter petioles, longer and narrower leaves, and less conspicuous lateral veins than the confirmed Palmer amaranth plants. These traits were consistent with waterhemp (*A. tuberculatus*) morphology. Genotypic results supported the phenotypic identification: all five Santa Rosa County individuals contained cytosine rather than thymine at nucleotide position 678, a genetic characteristic associated with waterhemp. The combined phenotypic and genotypic evidence identified the plants as waterhemp rather than Palmer amaranth. Suspected waterhemp individuals will be sent to a taxonomist for species confirmation, and further research is needed to characterize their sensitivity to herbicides.

U-P90 Factors influencing understory plant species diversity in recently burned upland pine forests

Felix Afiat

University of Florida

Prescribed fire is important for the maintenance of upland pine forest ecosystems in the southeastern United States. Many plant species native to these forests are dependent on fire. Prescribed fire may increase plant species diversity in the understory of upland pine forests by increasing soil nutrient availability, clearing the midstory and subcanopy of vegetation, and preventing light-demanding species from being shaded out. Understory plant diversity is fundamental to a healthy upland pine ecosystem, by providing food for a diversity of wildlife and for pollinators. Frequent burning has been shown to increase species richness in pine ecosystems however, the relationship between years since burned and species diversity is less certain. Increased fire severity may also positively impact species richness. In addition to fire, many other factors may influence plant biodiversity, including canopy structure, stand basal area, soil type, and weather-related disturbances. This project aims to measure several fire-related and fire-unrelated factors, specifically, years since burned, burn intensity, canopy structure, and soil type, and determine whether they have a positive or negative impact on understory plant species diversity in upland pine forests in Mississippi. We measured loblolly pine forest stands in the John Starr Memorial Forest and Noxubee National Wildlife Refuge in northeastern Mississippi that have been burned this past spring and up to three years ago. Species diversity was measured by randomly sampling quadrats of the forest floor and identifying every understory species inside each quadrat. Burn intensity was estimated by measuring the height of the burn marks on the pines. Light detection and ranging (LiDAR) was used to estimate leaf area index (LAI), canopy cover, and gap fraction of the forest. Data will be analyzed using multiple linear regression and principal component analysis to determine the effect of each explanatory variable on understory plant species diversity metrics. These findings will help forest land managers to identify the optimum burn frequency to maintain understory plant diversity in forest systems based on soil conditions, forest productivity and stocking levels.

Graduate Poster (G-P)

G-P29 Tabular Foundation Models for Digital Soil Mapping: Sample Efficient Mapping Across Spectral and Environmental Covariate Frameworks

Abhishek Panchadi, Prakash Kumar Jha

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Digital soil mapping (DSM) aims to predict soil properties continuously across landscapes using remotely sensed and terrain-derived data. Most DSM workflows depend on carefully tuned machine learning models and sufficient labeled samples constraints that limit scalability in data-scarce agricultural settings. This study evaluates emerging tabular foundation models (TFMs) transformer-based models that perform in-context learning without conventional training as a unified alternative across two contrasting DSM frameworks. A classic DSM framework is applied using terrain-derived covariates and multispectral satellite indices. These datasets represent fundamentally different input modalities, testing TFMs' ability to generalize without model redesign or retuning. Beyond benchmarking TFMs against established baselines under cross-validation, we investigate practical significance by looking into sample efficiency : how prediction accuracy scales with the number of soil samples, informing minimum sampling requirements for reliable mapping. Results across both frameworks will be presented. This work aims to establish TFMs as a low-overhead, sample-efficient approach to DSM, with broad implications for scalable soil monitoring in precision agriculture.

G-P30 Whole-Plant Digital Phenotyping: Identifying Heat-Tolerant Rice Genotypes

Alekhya Chakravaram[1], Manoj Kumar Reddy Allam[1], Sujan Poudel[1], Nuwan Wijewardane[2], Raju Bheemanahalli[1]

[1]Department of Plant and Soil Sciences, Mississippi State University, MS, USA, [2]Department of Agricultural and Biological Engineering, Mississippi State University, MS, USA

Rice-growing regions are often exposed to above-optimum temperatures during the reproductive stages, thereby impairing plant health and reducing yield. Thus, identifying and developing high-yielding, heat-stress-tolerant genotypes is critical to sustaining productivity. However, achieving this goal requires phenotyping germplasm and breeding populations quickly and accurately. Recently, several sensing-based approaches have been applied to address this challenge. Thus, this study aimed to assess whether high-throughput scanning with the Phenospex system improves the efficiency and accuracy of plant health or pigment-based screening compared with handheld methods. To establish an efficient phenotyping method, eight rice genotypes were subjected to control (32/24°C) and heat-stress (38/24°C) conditions from flowering to physiological maturity. During the stress treatment, temporal pigment measurements were collected at 7, 14, 21, and 28 days after stress (DAS) imposition using both the handheld method and the Phenospex. In addition, biomass and yield components were measured to correlate with digitally measured spectral characteristics and manually measured leaf pigment. Using a combination of visible (Red, Green, Blue) and Near-Infrared wavelengths, key spectral indices were extracted and compared between Phenospex digital indices (Normalized Difference Vegetation Index - NDVI, Normalized Pigment Chlorophyll Index - NPCI, and Plant Senescence Reflectance Index - PSRI) and manual readings. Manually measured chlorophyll showed a significant positive correlation with NDVI at 14 DAS, but this correlation weakened at 21 DAS. In contrast, manually measured chlorophyll showed strong negative correlations with NPCI (-0.68) and PSRI (-0.58) under heat stress. This study advances rice phenotyping from single-leaf to whole-plant digital methods, providing an effective way to monitor and identify stress-tolerant genotypes in rice breeding.

G-P31 Listeria Monocytogenes Persistence In High and Low Concentrations of Second Generation QAC, Ster-Bac In Water And Recovery Of Small Colony Morphotypes

Stephen Schade, Ramakrishna Nannapaneni, Andrew Williams

Mississippi State University

As most outbreaks of listeriosis are traced back to food processing plants despite sanitization with quaternary ammonium compounds (QACs), the possibility of Listeria monocytogenes developing increased tolerance to QACs following exposure to low concentrations must be evaluated as a potential risk factor. This study therefore aimed to determine whether two L. monocytogenes strains, Bug600 (serotype 1/2a) and ScottA (serotype 4b), could persist in lethal and sublethal concentrations of the second-generation QAC, Ster-BAC, and whether they would resume growth once conditions became favorable again. **Methods**: A high and low concentrations of Ster-BAC in a 96 well plate were exposed to L. monocytogenes strains for 1 h kill step in water and then the real-time growth rate (by OD600 nm) of surviving L. monocytogenes cells were examined by mimicking the high and low conditions that it may encounter in some food processing environments. In another experiment using Eppendorf tubes, L. monocytogenes cells were exposed to a lethal Ster-BAC for 1 h kill step and then after diluting Ster-BAC QUAT, the persisting cells were allowed to grow in high and low nutrient conditions to recover if any colony morphotypes are formed. The Ster-BAC MIC values were 1 µg/ml for Bug600 and 2 µg/ml for ScottA. After a rapid reduction of 5-7 logs CFU/ml when exposed to 6 µg/ml Ster-BAC in water for 1 h, a few cells of L. monocytogenes were still recoverable for one of the two strains (ScottA) in water. When such persisting cells were incubated under high- or low-nutrition conditions, they gave rise to 1-2 CFU/mL of L. monocytogenes progeny after 24 h ($P < 0.05$). Some survivors of both strains displayed a unique phenotype in which colony size varied widely irrespective of any concentration or any nutrition level tested. Low concentrations of stagnated QAC if found in food processing plants, could exert a selective pressure on L. monocytogenes. Our results show that L. monocytogenes strains can persist in some concentrations of second generation QACs. Small colony morphotype variants have been isolated which might be an adaptative mechanism.

G-P32 Detecting Phishing in the Era of Generative AI: A Machine Learning Analysis of Human-Written vs. AI-Generated Emails

Anna Essel, Kwabena Agyepong, Erol Sarigul, Jermiah Billa, John Adjaye, Manoj Bolugallu Padmayya, Sonia Eley

Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

The widespread adoption of generative artificial intelligence has enabled the creation of highly convincing emails, presenting new challenges for traditional phishing detection systems. This study investigates how AI-generated email content affects the performance of a machine-learning-based phishing-detection model. A Logistic Regression classifier with Term Frequency-Inverse Document Frequency (TF-IDF) feature extraction was trained using a dataset of human-written phishing and legitimate emails. The model was initially evaluated on human-authored emails to establish a baseline and subsequently tested on a separate dataset containing AI-generated phishing and legitimate emails. While the classifier maintained strong performance on human-written data, its effectiveness declined when evaluated on AI-generated emails, primarily due to an increase in false-positive predictions for legitimate messages. An analysis of text features indicates that AI-generated legitimate emails exhibit vocabulary characteristics commonly associated with phishing emails in the training data, leading the classifier to misclassify them. These findings demonstrate that generative AI introduces a distribution shift that can reduce the reliability of conventional phishing detection models. The results highlight the importance of validating cybersecurity systems against AI-generated content and developing more resilient machine learning approaches capable of adapting to evolving phishing techniques.

G-P33 Development and Field Evaluation of RTK GNSS-Guided Waypoint Navigation For an Autonomous Soil Sampling UGV

Asifur Rahman[1], Nuwan K. Wijewardane[1], Xin Zhang[2], Vitor S. Martins[1], Yehani Ekanayake[1]

[1]Department of Agricultural and Biological Engineering, Mississippi State University, [2]School of Environmental, Civil, Agricultural and Mechanical Engineering, University of Georgia

Autonomous soil sensing systems require reliable field navigation to reach predefined sampling locations with minimal human operation. This study developed and evaluated a real-time kinematic global navigation satellite system (RTK GNSS) guided waypoint navigation framework for a Clearpath Husky A300 unmanned ground vehicle intended to support an integrated spectroscopic soil sensing system for in situ soil health assessment. The navigation framework used RTK GNSS position feedback to compute cross-track error and an inertial navigation system (INS) based yaw estimate to align the robot before each path segment. Pure Pursuit and Stanley controllers, which are commonly used path-tracking methods in mobile robot navigation, were first evaluated in field trials, and a proportional-derivative (PD) cross-track error controller was then implemented to improve waypoint following. The final framework included waypoint stopping, distance-based speed reduction, and heading realignment after each waypoint. Field testing was conducted using predefined waypoint layouts with straight paths, sharp turns, and large heading changes. In a three-waypoint random layout test, the rover stopped at all waypoints and achieved a median absolute cross-track error of 6.4 cm, a 95th percentile error of 11.9 cm, a maximum error of 16.6 cm, and a standard deviation of 3.2 cm. The average waypoint stopping error was 9.5 cm. These preliminary results show that RTK GNSS-based cross-track control with INS-based heading alignment can provide a practical navigation foundation for autonomous agricultural UGVs and future in situ soil health sensing.

G-P34 Heat Stress and Soybean: The Battle for Reproductive Success and Yield Potential

Bala Subramanyam Sivarathri, Renganathan Vellaichamy Gandhimeyyan, Raju Bheemanahalli, Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Heat stress during reproductive phases severely compromises photosynthetic function, plant health, and reproductive success. Although soybean yield losses due to heat have been documented, the genetic variability of soybeans in response to heat stress has been studied less than that of cereals under field conditions. Here, 240 soybean genotypes from Maturity IV were exposed to heat stress (~38 °C) and optimal temperature (~33 °C, control) to assess variability in pigments, physiology, yield, and quality under field conditions. Heat stress was imposed by using custom-designed heat tunnels from R2 to maturity. Heat stress reduced the chlorophyll index by 15.5%, while anthocyanins increased by 16.6% compared with the control temperature. In addition, stomatal conductance increased by 48.7% under heat, and the electron transport rate declined significantly (-22.5%), confirming non-stomatal limitation as the dominant constraint on photosynthetic capacity. Furthermore, heat stress induced a cascade of yield-component losses: pod number declined by 21.5%, seed number by 25.6%, pod weight by 17.4%, and seed weight by 21.8%. Genotypic variation observed in photosynthetic and agronomic traits is being used to map genetic loci associated with heat tolerance. Discovered traits, loci, and thermotolerant genotypes can accelerate soybean breeding for a hotter future.

G-P35 AI Prediction of the Impact of Traditional and Virtual Reality-Based STEAM Outreach Activities on Student Learning

Bhavya Kaanadka Purushothama, Ping Zhang, Kwabena Agyepong, Erol Sarigul, Manoj Bolugallu Padmayya, Jermiah Billa, John Adjaye, Sonia Eley

Department of Computer and Information Science, Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

The rapid advancement of Artificial Intelligence (AI) and Virtual Reality (VR) is transforming educational practices by providing innovative approaches to teaching and learning in Science, Technology, Engineering, Arts, and Mathematics (STEAM). This study examines the potential of AI to analyze and predict student learning outcomes by comparing assessment data from two STEAM outreach programs conducted by the Department of Advanced Technologies at Alcorn State University. The first dataset was collected during three four day traditional STEAM Summer Camps conducted in 2025 at Alcorn State University in Lorman, Mississippi, and Hinds Community College in Vicksburg, Mississippi. Students in Grades 4 through 11 participated in experiential learning activities that included robotics, electronics, networking, Sphero programming, biology, physics, HP radiation, and automation. Student achievement was evaluated through assessments administered at the conclusion of each camp. The second dataset was obtained from the 2024-2025 Southern University Reaching Across the Digital Divide (SURADD) project, in which middle school students participated in immersive VR-based STEAM learning experiences aligned with the Mississippi State Science Curriculum. This study utilizes only the assessment results of students who received VR-based instruction. A Random Forest machine learning algorithm was implemented using Google Colab to analyze assessment data, identify learning patterns, and predict student performance across the two instructional approaches. The comparative analysis provides

insights into the eAectiveness of traditional and VR-supported learning environments. The findings are expected to demonstrate the value of AI-driven educational analytics and highlight the potential of immersive VR technologies to enhance student engagement, conceptual understanding, and academic achievement, thereby supporting the adoption of innovative instructional practices in STEAM education, particularly in underserved rural communities.

G-P37 Integrated Remote Sensing and Physical Modeling for Aboveground Biomass Mapping Across Forests and Agricultural Systems

Bipin Bastakoti, Prakash Kumar Jha

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Accurate estimation of aboveground biomass (AGB) is essential for monitoring ecosystem productivity, carbon sequestration, sustainable land management, and climate change mitigation. However, biomass retrieval across heterogeneous forest and agricultural landscapes remains challenging due to differences in vegetation structure, canopy architecture, and sensor-specific limitations. This research proposes a physics-guided, multi-model framework for estimating AGB by integrating the Water Cloud Model (WCM) with complementary radiative transfer models and machine learning approaches using multi-source remote sensing data. Synthetic Aperture Radar (SAR), optical, hyperspectral, and spaceborne LiDAR observations will be combined to characterize vegetation structural and biophysical properties across diverse land-cover types. The proposed framework aims to improve the accuracy, robustness, and transferability of biomass estimation while providing scalable methods for regional biomass mapping and carbon monitoring. The outcomes will support ecosystem management, precision agriculture, forest monitoring, and climate-informed decision-making.

G-P38 From Vegetative to Reproductive: Salinity Tolerance of Soybean across Growth Stages

Chami Rampati Dewage, Bala Subramanyam Sivarathri, Dingiswayo Mwanza, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Soil salinity is a significant abiotic stressor that reduces soybean productivity by hindering germination and growth, thereby lowering yield potential. However, it remains unclear whether salinity tolerance observed during early seedling or vegetative stages persists into later developmental stages. To address these knowledge gaps, multiple experiments were conducted to investigate tolerance to sodium chloride (NaCl) across germination and reproductive growth using a diverse set of soybean genotypes. A threshold salt concentration was identified by testing the response of a high-yielding genotype to NaCl concentrations from 0 to 10 dS/m during emergence or seedling development. The most substantial declines occurred at 6 dS/m during both the emergence and seedling stages, with higher salinity levels (8 dS/m and 10 dS/m) causing seedling death. Using the identified threshold, a diverse set of 24 soybean genotypes was screened for salt tolerance at the germination and seedling stages. From this repeated screening, four genotypes contrasting in salt tolerance were selected, exposed to salt stress (6 dS/m) during the vegetative stage (V2) for 14 days, and assessed for physiological and other growth metric responses. In addition, a subset of stressed and unstressed plants was allowed to recover to assess their yield potential. In an independent experiment, the same genotypes were exposed to salt stress at the reproductive stage (R1) to determine whether tolerance observed during the vegetative stage translated to the reproductive stage. In all experiments, a common set of parameters, including pigments, gas exchange, biomass accumulation, and root traits, was assessed. Results from the vegetative stage indicated significant genotypic differences in salt tolerance for the vigor traits. Among the evaluated genotypes, LS5009XS showed a relatively smaller reduction in the efficiency of photosystem II (30%), electron transport rate (32%), and shoot dry weight (3%) during the vegetative stage. Biophysical and rhizosphere data are being collected to identify the key differences between salt-sensitive and salt-tolerant genotypes across growth stages.

G-P39 Cafestol Attenuates the Proliferation, Migration and Clonogenic Survival of Breast Cancer Cells through Modulating mTOR Signaling

Christian Capers, Taylor Raff, Rose Pwint , Hana Khalifa, Alessandra Martinez, Kasia Michalak, Zakaria Abd Elmageed, Hassan Ebrahim

Department of Biomedical Sciences, Edward Via College of Osteopathic Medicine, Monroe, LA, 71203

Breast cancer (BC) is the most diagnosed cancer in women and the second leading cause of cancer death, just behind lung cancer. BC is a heterogenous group of diseases, characterized by a wide range of subtypes that vary in their biological features, clinical presentation, and response to treatment. mTOR (mechanistic target of rapamycin) is a key regulator of cellular processes, including growth, proliferation, metabolism, and survival. It is a part of the complex mTOR signaling pathway, which integrates signals from growth factors, nutrients, energy status, and cellular stress. mTOR plays a crucial role for the growth of breast cancer cells, and its dysregulation can contribute to progression, metastasis, and resistance to therapies. Green coffee has been studied for its potential health benefits, particularly its possible role in cancer prevention and therapeutic intervention. It harbors a diverse range of bioactive ingredients including fatty acids, terpenes and phenolics. Cafestol is a diterpene (C20) found in unroasted coffee beans that has attracted considerable attention due to its diverse biological activities, including anti-inflammatory and antioxidant properties. As a part of an ongoing efforts to discover anticancer molecules of natural origin, we explored anticancer effect of cafestol against breast cancer cells and decoded its underlying molecular target. MTT-based assay was conducted to evaluate the effect of cafestol on the growth of BC cells, while wound-healing assay was used to monitor its effect on cell migration. Western blot analysis and molecular modeling were used to uncover the potential molecular target mediating the anticancer effects of cafestol. Bioassay-guided fractionation of coffee beans alcoholic extract led to the identification of cafestol as potential anticancer furanoditerpene against multiple BC cells. Cafestol effectively attenuated the growth, migration, and colonization of BC cells at low Î¼M levels. Furthermore, cafestol inhibited mTOR kinase and its downstream signaling as demonstrated by immunoblotting studies. Furthermore, molecular docking experiments suggested that cafestol adopts a favorable low-energy binding conformation within the mTOR kinase pocket, stabilized by interactions with key amino acid residues in the C-terminal lobe of the kinase domain. Cafestol is a novel mTOR modulator amenable for further development as a lead compound for the control of breast malignancies.

G-P40 Obesity in Mississippi: Contributing Socioeconomic and Health Factors

Clever Nyengera, Ham Benghuzzi

Department of Biology, Jackson State University, Jackson, MS, USA

Obesity is a major public health concern in the United States, with Mississippi consistently ranking among the states with the highest prevalence. Defined as a body mass index (BMI) of 30 or greater, obesity is strongly associated with chronic conditions such as type 2 diabetes, cardiovascular disease, stroke, hypertension, and certain cancers. This study examines obesity trends, contributing factors, and health impacts in Mississippi, with a focused case study on the city of Jackson. Recent data indicate that obesity rates in Mississippi have increased dramatically, rising from approximately 15% in the 1990s to over 40% in 2023, with many counties exceeding 30–35%. Jackson is identified as a significant hotspot, with an estimated obesity prevalence of approximately 37%, placing it among the most affected cities in the United States. Key contributing factors include limited access to healthy foods, high poverty rates, low levels of physical activity, and reliance on calorie-dense diets. Rural communities face additional challenges such as limited healthcare access, transportation barriers, and economic hardship. From a physiological perspective, obesity is influenced by complex endocrine mechanisms including insulin resistance, leptin resistance, and chronic stress-related hormonal imbalances. These factors contribute to metabolic dysfunction and increased disease risk. Current treatment approaches emphasize lifestyle and behavioral interventions, including improved diet, increased physical activity, and counseling, with pharmacologic therapies such as GLP-1 receptor agonists used in certain cases. Addressing obesity in Mississippi requires a multifaceted approach that includes improving access to healthy foods, expanding physical activity infrastructure, strengthening education programs, and implementing supportive health policies. Community engagement and targeted interventions are essential to reduce disparities and improve long-term health outcomes across both urban and rural populations.

G-P41 Racial Disparities and Socioeconomic Factors in Compounded Air Pollution and Asthma Risk in U.S. Metropolitan Areas

Clifford Boateng, Shrinidhi Ambinakudige

Department of Geosciences, Mississippi State University, Mississippi State, MS

Asthma and air pollution are major public health concerns that exhibit spatial variation across U.S. urban centers; however, their spatial co-occurrence remains underexplored. This study examined the geographic overlap of asthma prevalence and air pollutants (NO2, SO2, and aerosol optical depth [AOD]) across the eight most populous U.S. metropolitan areas. Zip code tabulation area (ZCTA)-level asthma prevalence estimates from the 2024-release Centers for Disease Control and Prevention PLACES dataset were combined with satellite-derived pollutant data from Sentinel-5P and the Moderate Resolution Imaging Spectroradiometer (MODIS). Hotspot comparison analysis was used to identify areas of compounded risk, defined as overlapping asthma and pollutant hotspots significant at the 95% and 99% confidence levels. Multivariable logistic regression models were then applied to examine associations between sociodemographic characteristics and the likelihood of compounded risk. Compounded risk areas were concentrated within urban cores, with overlap ranging from 0.23% to 71.53% across pollutants and metropolitan areas. Across adjusted models, every 10-percentage point increase in the proportion of Black residents was associated with 37%-54% higher odds of compounded risk after accounting for neighborhood poverty, while corresponding increases in Asian populations were associated with about 28% higher odds. Lower educational attainment was consistently associated with increased odds across pollutants, whereas higher renter occupancy was associated with increased NO2- and AOD-related risk. These findings highlight areas where asthma burden and pollution coincide spatially, although the cross-sectional design and focus on spatial co-occurrence limit causal inference. They underscore the role of urban infrastructure and historical segregation in shaping environmental health inequities. Without targeted efforts to address socioeconomic and environmental inequalities in the U.S., disadvantaged populations will continue to bear a disproportionate burden of asthma and other pollution-related respiratory diseases.

G-P42 Genome-Wide Association Analysis of Agronomic Traits in Finger Millet

Deekshitha Nimmagudem[1], Mohan Bista[1], Alekhya Chakravaram[1], Renganathn Vellaichamy Gandhimeyyan[1], Nisarga Kodadinne Narayana[1], Ajay Prasanth Ramalingam[2], Ramasamy Perumal[2], Raju Bheemanahalli[1]

[1]Department of Plant and Soil Sciences, Mississippi State University, Mississippi, USA, [2]Department of Agronomy, Kansas State University, Manhattan, KS

Millets are known to have a richer nutritional profile than other major staple cereals. Finger millet (*Eleusine coracana* (L.) Gaertn), commonly known as Ragi, is a stress-resilient, nutrient-rich cereal valued for its well-known health-promoting properties. However, the genomic regions linked to yield-related agronomic traits in finger millet remain elusive. A diversity panel of 259 finger millet accessions was extensively phenotyped over three years. Major agronomic traits such as days to flowering (DTF), days to heading (DTH), days to maturity (DTM), and grain yield (GY) showed significant variation across years. Furthermore, this panel was genotyped by sequencing, and 15,405 high-quality SNPs were used in the genetic analysis. A multi-locus genome-wide association analysis was conducted on these traits using 15.4K SNPs to identify marker-trait associations (MTAs) associated with flowering and yield traits. A total of 10 significant MTAs were identified, explaining 5-31% of the phenotypic variation. Among these, one MTA or genomic region on chromosome 5 showed a significant association with DTF, DTH, and DTM across both BLINK and FarmCPU models, explaining 19-31% of the phenotypic variation. Another genomic region on chromosome 3 is significantly linked to grain yield. Furthermore, post-GWAS gene mining revealed a DREB (dehydration-responsive element-binding factor) within the genomic region. This transcription factor is known to regulate flowering traits in crops. This study is the first attempt to identify genetic loci associated with phenological and yield traits. These identified regions could potentially be targeted for marker-assisted breeding and downstream molecular analysis.

G-P43 Effects of Echinochloa crus-galli, Lolium multiflorum, and Nicandra physalodes on the Germination of The Maize Innvictis 1857 Double Pro

Denetrise S. Johnson, Jennifer Laifa, Hattie Spencer

Mississippi Valley State University, MS, USA

Maize is an important crop that when affected by weeds, its productivity decreases. The study hypothesized that germination and growth of maize Innvictis 1857 Double Pro would decrease in the presence of the Lolium multiflorum, Echinochloa crus-galli, and Nicandra physalodes. In the present study, seeds of maize Innvictis 1857 Double were grown with the L. multiflorum, E. crus-galli, and N. physalodes. The results showed that the maize started germinating on day 3. The germination percentage for the maize growing with L. multiflorum, and E. crus-galli, was 100% and 50% for the one growing with N. physalodes. On day 7, the germination percentage of the maize growing with N. physalodes was 100%. After 10 days, the lengths of the maize seedlings were recorded. There were significant differences of lengths between the maize growing with L. multiflorum, E. crus-galli, and N. physalodes. In conclusion, the germination of the maize Innvictis 1857 Double Pro is affected by L. multiflorum, E. crus-galli, and N. physalodes.

G-P44 Oropouche Virus Infection Interrupts Fetal Neurodevelopment

Denyoh Prince Mark Dela

University of Southern Mississippi

Oropouche virus (OROV) is an emerging orthobunyavirus responsible for periodic outbreaks of febrile illness in South and Central America. Although the virus is primarily transmitted by arthropod vectors such as biting midges and mosquitoes, recent clinical reports suggest the possibility of maternal to fetal transmission; however, experimental evidence supporting vertical transmission remains limited. In this study, we investigated the susceptibility of neural and embryonic-derived cells to OROV infection and assessed its potential impact on fetal development. Murine neuroblastoma cells (N2a), mouse embryonic stem cells (ESCs), and ESC-derived neural progenitor-like cells were infected with OROV. Viral replication was evaluated using RT-qPCR and plaque-forming assays. Additionally, in vivo experiments were conducted to detect OROV RNA in fetuses at embryonic day 10.5. Our results demonstrate that all tested cell types are susceptible to OROV infection and support productive viral replication. In vivo analysis revealed the presence of OROV RNA in both the head and body of fetuses, indicating the likelihood of vertical transmission. Furthermore, gene expression analysis showed that OROV infection significantly downregulates key neurodevelopmental regulators, including Sox-1 and Tbr2, in both N2a cells and fetal tissues. Taken together, these findings provide evidence that OROV can infect and replicate in neural and embryonic-derived cells, disrupt neurodevelopmental gene expression, and potentially undergo vertical transmission. This study highlights the neurotropic potential of OROV and its possible role in impaired fetal neurodevelopment

G-P45 Quantifying Morpho-Physiological Responses in Corn Hybrids to Waterlogging

Dingiswayo Mwanza, Chami Rampati Dewage, Renganathan Vellaichamy Gandhimeyyan, Mohan K Bista Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, USA

Early-season waterlogging (WL) is a major constraint in corn-producing regions, particularly where heavy rainfall coincides with poorly drained soils. During vegetative growth, WL reduces root oxygen, weakening crop establishment and yield. Despite mounting evidence of WL-induced changes in stand and yield, comprehensive studies on WL tolerance in corn remain limited. Identifying resilient genotypes that perform well and remain adaptive in saturated soils is key to reducing WL losses. Multiple experiments were conducted using 2-24 corn hybrids to investigate the impact of WL stress during the vegetative stage and on yield potential. In experiment 1, progressive WL treatments were applied for different durations (0-7 days) at the V3 seedling stage. Nearly all shoot and root parameters were inversely related to WL duration. In experiment 2, twenty-four corn hybrids were exposed to 7 WL, and a range of morpho-physiological and pigment data were collected. The results showed that trait responses to WL varied by hybrid. On average, exposure to WL resulted in substantial reductions in plant height (29%), leaf area (50%), shoot biomass (44%), and root biomass (50%) compared with the control. Based on these results, B73 and HT-7500 were identified as tolerant, while DKC117-27 was sensitive to WL stress. Furthermore, these selected genotypes are being validated and evaluated for yield potential in response to WL at the vegetative stage. The findings suggest that choosing hybrids with early tolerance to WL is crucial for maintaining high yield potential.

G-P47 Allelopathic activity of sweet potato (*Ipomoea batatas*) Morado: allelochemical profiling and phytotoxicity against three weed species

Fabiana HernÃndez Mazzini[1], Ester Goenaga[2], Te-Ming Paul Tseng[2]

[1]National Institute of Agricultural Research, Las Brujas Research Station, Canelones, Uruguay, [2]Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, USA

Sustainable weed management requires alternatives to synthetic herbicides. Allelopathy has emerged as a promising biological strategy due to the ability of certain crops to release phytotoxic allelochemicals. Sweet potato (Ipomoea batatas L.) has been identified as a crop with allelopathic potential for weed suppression. The objective of this study was to evaluate the effects of root exudates from the sweet potato cultivar 'Morado' on the germination and early seedling growth of three agronomically important weed species (Amaranthus palmeri, Cyperus esculentus, and Echinochloa crus-galli), and to characterize their allelochemical profile. Root exudates were collected weekly over a six-week period and characterized using High-Performance Liquid Chromatography. The phytotoxic activity of the sixth-week exudates was evaluated using Petri dish germination bioassays arranged in a completely randomized design with ten replicates per treatment, using distilled water as the control. Germination percentage and seedling growth parameters were recorded. Data were analyzed using analysis of variance (ANOVA) and binomial generalized linear models (GLMs) (Î± =0.05). Weed responses to the root exudates were species-dependent. In E. crus-galli, no significant effects were detected on germination or early seedling growth. In A. palmeri, germination and root growth were not affected, whereas shoot length was significantly reduced ($p < 0.001$). In contrast, root exudates significantly increased germination ($p = 0.018$), shoot length ($p = 0.006$), root length ($p < 0.001$), and biomass ($p = 0.013$) of C. esculentus. These findings provide new evidence that sweet potato root exudates differentially affect weed species and support further identification of the allelochemicals involved.

G-P48 Optical Spectroscopic Analysis of Biochemical Changes Using Infrared Spectral Discrimination of Transgenic Mice Serum to Study the Potential Correlation of the Nano-Structural Disorder Alterations for Neurological Diseases.

FNU Sweety[1], Ishmael Apachigawo[1], Santanu Maity[1], Prabhakar Pradhan[1], Sazzd Khan[2], Moshaid Khan[2]

[1]Mississippi State University, Mississippi State, MS, [2]University of Tennessee Health Science Center, Memphis, TN

We investigated biochemical changes in the serum of Alzheimer's and Parkinson's disease (AD/PD) mouse models relative to their control using FTIR spectroscopy. This study corroborates the structural modifications and nanoscale structural disorder, with techniques like Inverse Participation (IPR) within macromolecules such as DNA and RNA, in AD/PD conditions. Serum samples (1Î¼L) were analyzed using a Jasco ATR Pro 4x FTIR spectrometer in the mid-infrared range. Secondary protein analyses were performed on the spectra using identified AD/PD biomarkers from a previous study. Quantification of these identified biomarkers was performed using curve-fitting analysis, which indicated statistically significant changes in the Î²-sheet/Tyrosine ratio. The experimental results show an accumulation of intermolecular Î²-sheets associated with amyloid Î²/tau changes. Additionally, marked changes in lipid-protein balance were observed, demonstrating the role of lipids in modulating the structure/function of the subcellular membrane, which served as a distinctive parameter for distinguishing disease from control states. This serum-based spectroscopic analysis complements our previously conducted nanoscale disorder studies in mouse brain tissues. By combining brain and serum biomarkers, we aim to provide a translational framework that bridges central pathology to systemic signatures and underscores the potential of FTIR-based biomarkers for early diagnosis of AD/PD.

G-P50 Simultaneous Prediction of Plant Macro and Micronutrients from Mid-Infrared Reflectance Spectra Using Multi-Output Regression Models

Ishini Sangarasekara[1], Chamika Silva[1], Nuwan K Wijewardane[1], Raju Bheemanahalli[2]

[1]Department of Agricultural and Biological Engineering, Mississippi State University, MS, USA. [2]Department of Plant and Soil Sciences, Mississippi State University, MS, USA,

Rapid estimation of plant nutrients is essential for precision agriculture. This study evaluated mid-infrared (MIR) reflectance spectroscopy (2000-6000 nm) for simultaneous prediction of eleven nutrients: nitrogen, calcium, potassium, magnesium, phosphorus, sulfur, boron, iron, manganese, zinc, and copper across leaf and stem tissues of corn, soybean, cotton, and sorghum. A dataset of 1,747 dried plant tissue samples (975 leaf, 772 stem) was used to develop and compare four prediction frameworks: single-output and multi-output partial least squares regression (SO/MO-PLSR) and single-output and multi-output Gaussian process regression (SO/MO-GPR). Spectra were preprocessed using standard normal variate transformation to correct for scatter and baseline variation. Models were trained on 60% of the data, tuned on a 20% validation set, and evaluated on a held-out 20% test set with stratified random splits to preserve crop-tissue group balance. Multi-Output models jointly predicted all eleven nutrients simultaneously, while Single-Output models treated each nutrient independently. GPR models incorporated PCA-based dimensionality reduction to handle the high-dimensional spectral feature space (1,667 bands). Performance was assessed using R^2, RMSE, and the ratio of performance to deviation (RPD). MO-GPR consistently achieved the highest accuracy, exceeding R^2 = 0.80 for nitrogen, calcium, potassium, phosphorus, and boron. GPR-based models markedly outperformed PLSR across all nutrients, and multi-output models outperformed their single-output models, with the greatest gains observed for nutrients with stronger inter-correlations. This work demonstrates that MIR spectroscopy, combined with multi-output Gaussian process regression, is an effective tool for comprehensive, simultaneous profiling of plant nutrients from a single spectral measurement.

G-P51 Systematic Review of CRC in Mississippi: Perspective of Etiology, Clinical Presentation, Diagnosis, and Treatment Strategies.

Jakira Luckett, Ham Benghuzzi

Biology Department, Jackson State University, Jackson, MS

Colorectal cancer (CRC) remains a significant public health concern and is the second leading cause of cancer-related mortality in the United States. Mississippi bears a disproportionate burden, reporting the highest incidence and mortality rates nationwide, largely driven by low screening uptake, late-stage diagnosis, and persistent socioeconomic and healthcare access disparities. This study presents a systematic review of CRC in Mississippi, focusing on its etiology, clinical presentation, diagnosis, and treatment strategies. Data were obtained from the Mississippi Department of Health and recent peer-reviewed literature to evaluate regional trends and compare them with national statistics. CRC is often asymptomatic in early stages, with symptomatic patients commonly presenting with changes in bowel habits, rectal bleeding, abdominal pain, fatigue, and unexplained weight loss. Advanced disease may manifest as bowel obstruction or jaundice. Current prevention strategies emphasize lifestyle modifications, including increased dietary fiber intake, reduced consumption of red and processed meats, regular physical activity, and avoidance of tobacco and excessive alcohol use. Treatment approaches include surgery, chemotherapy (e.g., 5-fluorouracil, oxaliplatin, irinotecan), and targeted therapies, often used in combination. Despite advancements, drug resistance and limited access to care continue to hinder long-term survival outcomes. In conclusion, reducing the burden of CRC in Mississippi will require expanded screening programs, improved access to care, and targeted interventions addressing racial and rural disparities. Future research should focus on genetic susceptibility, precision medicine approaches, and the effectiveness of behavioral interventions to improve prevention and outcomes.

G-P53 Systematic Review: Incidence of Hypertension Leading to Chronic Kidney Disease and Management Strategies

Kenya Watson, Ham Benghuzzi

Biology Department, Jackson State University, Jackson, MS

Hypertension, or high blood pressure, is a prevalent and often asymptomatic condition that poses a significant risk to long-term health outcomes. It is a leading contributor to chronic kidney disease (CKD), a progressive condition characterized by the gradual loss of kidney function. This study explores the relationship between hypertension and CKD, focusing on underlying pathophysiological mechanisms, clinical manifestations, and current management strategies. Sustained elevated blood pressure damages the small blood vessels in the kidneys, resulting in vascular thickening, reduced blood flow, and impaired filtration capacity. Over time, this damage leads to

kidney scarring and functional decline. Clinical presentation is often delayed, with symptoms such as fatigue, nausea, edema, and proteinuria emerging in advanced stages. A review of literature, including over 6,000 PubMed articles and national health data, highlights the widespread prevalence and serious outcomes associated with hypertension-related CKD, including high mortality rates. Current treatment approaches primarily focus on blood pressure control through pharmacologic interventions such as diuretics, ACE inhibitors, angiotensin receptor blockers, calcium channel blockers, and beta-blockers. Effective management of hypertension is critical in preventing the onset and progression of CKD. Maintaining blood pressure below 130/80 mmHg remains a key clinical goal. Future research should prioritize early detection in younger populations, investigate long-term blood pressure trends, and explore molecular pathways, including hypoxia-inducible factor (HIF) stabilization and inflammatory mechanisms. Overall, hypertension represents a major public health challenge, and improved prevention and management strategies are essential to reduce the burden of chronic kidney disease.

G-P54 Using Artificial Intelligence to Detect Plagiarism in AI-Generated Student Assignments

Kiranmai Kondeti, Kwabena Agyepong, Jermiah Billa, Erol Sarigul, John Adjaye, Manoj Bolugallu Padmayya, Sonia Eley

Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

Artificial Intelligence (AI) coding tools, such as ChatGPT and Claude.ai, have made it easier for students to engage in plagiarism in their class assignments. Documented literature indicates that students may rely on AI systems to obtain quick answers, often by simply copying and pasting assignment questions into these platforms. While this practice violates academic integrity policies, it also deprives students of opportunities to develop essential problem-solving and critical-thinking skills during their education. At the same time, AI technologies can also be leveraged to detect plagiarized content. Numerous studies have explored methods for identifying plagiarism, including text-based, token-based, and syntax tree-based approaches. Plagiarism detection has evolved beyond simple comparisons between student submissions and known solutions, incorporating more advanced techniques such as structural code analysis combined with decision-support modeling. A recent study found that AI platforms capable of generating solutions can also be used to detect plagiarism. This study examines and compares the solutions generated by several AI-based systems to a solution on the GI tract model problem provided by the instructor. Assignment questions are submitted to selected AI platforms to generate responses, while faculty also produce authentic solutions. Both AI-generated and authentic answers are then used as inputs for plagiarism detection across these platforms. Additionally, AI-generated responses are slightly modified to evaluate the robustness of detection mechanisms. The performance of these AI-supported systems is assessed using recall and precision as evaluation metrics.

G-P55 A Systematic Overview of Type 2 Diabetes in Mississippi

KymMiyiah Vernado and Ham Benghuzzi

Jackson State University, Jackson, MS

Type 2 diabetes mellitus (T2DM) is a chronic metabolic disorder characterized by persistent hyperglycemia resulting from insulin resistance, impaired insulin secretion, or both. It represents a growing public health burden in the United States, with Mississippi consistently ranking among the states with the highest prevalence. Currently, over 38 million Americans are affected, with Mississippi reporting a prevalence rate of approximately 15.3%, the second highest in the nation, and continuing to rise. This study provides a systematic overview of T2DM in Mississippi, examining its pathophysiology, clinical presentation, risk factors, and treatment strategies using data from the Centers for Disease Control and Prevention (CDC), Mississippi State Department of Health (MSDH), and other peer-reviewed sources. T2DM and prediabetes often develop gradually and may remain asymptomatic in early stages. When present, symptoms include polyuria, polydipsia, fatigue, blurred vision, slow wound healing, and neuropathic manifestations. Key risk factors identified include obesity, physical inactivity, poor dietary habits, genetic predisposition, age, race, hypertension, and duration of disease. Epidemiological findings show that prevalence increases with age and disproportionately affects Black Mississippians compared to other racial groups, as illustrated in the poster figures. Management strategies emphasize a comprehensive approach, including lifestyle modifications (healthy diet, physical activity, and weight management), glucose monitoring, and pharmacologic interventions such as metformin, insulin therapy, GLP-1 receptor agonists, and SGLT2 inhibitors. In conclusion, T2DM is not only a metabolic condition but also a critical public health issue in Mississippi. Addressing its growing burden will require sustained prevention efforts, improved access to healthcare, expanded community education, and targeted interventions to reduce disparities across populations.

G-P56 National-Scale Solar Radiation Estimation For Brazil Via Remote Sensing And Artificial Intelligence

Lucas Maltoni Andrade[1,2], Lucas Borges Ferreira[2], Fernando FranÃ§a da Cunha[1]

[1]North Mississippi Research and Extension Center, Mississippi State University, Verona, MS, 38879, USA and [2]Department of Agricultural Engineering, Federal University of ViÃ§osa, ViÃ§osa, MG, 36570-000, Brazil

Global solar radiation (GSR) is an essential variable for understanding hydrological and agricultural processes. However, its measurement remains limited by the sparse spatial availability of weather stations (WSs) equipped with solar radiation sensors. Developing remote sensing-based approaches to estimate GSR opens new opportunities to monitor this variable across space and time without relying on point measurements and depending on WS availability and sensor maintenance. This study evaluated the potential of GOES-16 satellite data to estimate daily GSR by combining sub-hourly (30-minute) time series from reflective and emissive bands, extraterrestrial solar radiation, and artificial intelligence. To develop the study, a dataset was compiled by extracting GOES-16 pixels corresponding to the locations of 501 WSs in Brazil and pairing them with GSR measured at the WSs. The training set consisted of 365 WSs (2018-2021), and the testing set consisted of 136 WSs (2022-2024). Two models were trained to estimate daily GSR: one-dimensional convolutional neural networks (1D-CNN) and Light Gradient Boosting Machine (LightGBM). Both models performed very well across the test stations, with the 1D-CNN model yielding a mean absolute error of 1.04 MJ m^{-2} (5.83%) and the LightGBM yielding 1.02 MJ m^{-2} (5.74%). Given the equivalent performance, the LightGBM model stands out for its lower computational and deployment cost relative to the 1D-CNN. Our findings are promising and could help develop an operational product for national-scale GSR

monitoring. Future work will extend the analysis to spatial patches around the stations, rather than point-wise modeling.

G-P57 Yield and Nutritional Responses of Rice Genotypes Under Salt Stress

Manoj Kumar Reddy Allam, Alekhya Chakravaram, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Rice(Oryza sativa L.) is classified as a salt-sensitive crop; however, its sensitivity varies with growth stages. The effects of salinity during the seedling and early vegetative phases were well established. Studies indicate that rice seedlings are vulnerable to salt but can recover from moderate levels of salinity. Conversely, the impact of salinity during reproductive stages is less documented, and the damage it causes is often irreversible. Thus, screening and identifying salt-tolerant plants during the reproductive stages are crucial for breeding and managing productivity. In this study, 15 rice genotypes were exposed to a control (0 NaCl) and a salt stress (7 dS/m NaCl) during the reproductive stage to quantify pigment- and yield-related parameters. Under salt stress, the chlorophyll index dropped from 30.9 µg/cm^2 at 7 days after treatment (DAT) to 17.61 µg/cm^2 at 21 DAT (a decrease of 43.2%). Salt stress decreased spikelet fertility by 24.1% (ranging from 38.6% to 90.0%). Six genotypes recorded more than a 40% yield reduction under stress. In addition to yield potential, grain nutrient accumulation varied significantly among genotypes and salinity treatments. Nitrogen ranged from 0.81% to 1.90%, zinc from 23.7 to 47.0 ppm, iron from 11.7 to 56.7 ppm, and grain sodium from 0.013% to 0.083%, reflecting genotypic differences in sodium accumulation and micronutrient uptake. Among all genotypes, 20NTPID270 exhibited the highest-quality grain and the lowest Na accumulation during the reproductive stage. This could serve as a potential donor for decoding molecular regulation or as a trait donor for breeding after Rice (Oryza sativa L.) is classified as a salt-sensitive crop; however, its sensitivity varies with growth stages. The effects of salinity during the seedling and early vegetative phases are well established. Studies indicate that rice seedlings are vulnerable to salt but can recover from moderate levels of salinity. Conversely, the impact of salinity during reproductive stages is less documented, and the damage it causes is often irreversible. Thus, screening and identifying salt-tolerant plants during the reproductive stages are crucial for breeding and managing productivity. In this study, 15 rice genotypes were exposed to a control (0 NaCl) and a salt stress (7 dS/m NaCl) during the reproductive stage to quantify pigment- and yield-related parameters. Under salt stress, the chlorophyll index dropped from 30.9 µg/cm^2 at 7 days after treatment (DAT) to 17.61 µg/cm^2 at 21 DAT (a decrease of 43.2%). Salt stress decreased spikelet fertility by 24.1% (ranging from 38.6% to 90.0%). Six genotypes recorded more than a 40% yield reduction under stress. In addition to yield potential, grain nutrient accumulation varied significantly among genotypes and salinity treatments. Nitrogen ranged from 0.81% to 1.90%, zinc from 23.7 to 47.0 ppm, iron from 11.7 to 56.7 ppm, and grain sodium from 0.013% to 0.083%, reflecting genotypic differences in sodium accumulation and micronutrient uptake. Among all genotypes, 20NTPID-270 exhibited the highest nutritional quality grain and the lowest Na□º accumulation during the reproductive stage. This could serve as a potential donor for decoding molecular regulation or as a trait donor for breeding.

G-P58 Integrated SWAT+ Machine Learning Framework for Continuous Nutrient Concentration Estimation

Marionei Fomaca de Sousa, Jr, Prem Parajuli, Sayantan Samanta

Mississippi State University

Nutrient concentration data are generally obtained through discrete sampling at irregular intervals, limiting the feasibility of continuous monitoring. Moreover, the complex interactions among hydrological processes controlling nutrient transport limit the accuracy of conventional extrapolation methods such as LOADEST and WRTDS. The present study introduces a framework that integrates uncalibrated SWAT+ simulations with machine learning models, such as Support Vector Machine (SVM) and Random Forest (RF), to learn from discrete water quality observations and estimate continuous daily time series of total nitrogen (TN) and total phosphorus (TP) concentrations. The default SWAT+ configuration was used to simulate daily hydrologic variables, including streamflow, sediment load, surface runoff, percolation, evapotranspiration, curve number, and water yield. Machine learning models were then trained on discrete TN and TP concentration data from USGS water quality monitoring stations across six Ohio River subbasins, using SWAT+ simulated daily hydrological variables as input features. Additional engineered features capturing watershed memory through lagged values and rolling-window averages of sediment and precipitation over three, seven, fourteen, and thirty-day periods were also considered during the model training process. Model performance was assessed using the Kling-Gupta Efficiency (KGE) on both training and test datasets, and variable importance was evaluated via permutation-based Nash-Sutcliffe Efficiency (NSE) drop analysis. Both models produced reasonable concentration estimates. For total N, RF achieved KGE values of 0.92 and 0.50 on the training and test sets, respectively, while SVM achieved 0.65 and 0.46. For total P, RF attained KGE values of 0.73 and 0.53, compared to 0.57 and 0.47 for SVM. RF demonstrated stronger training performance but exhibited greater overfitting, whereas SVM yielded more consistent results across datasets. Sediment load was identified as the most influential predictor for TN, while precipitation was most important for TP prediction, indicating distinct hydrological pathways for each nutrient. Load estimates derived from predicted concentrations reflected the general temporal patterns of observed TN and TP loads. These findings indicate that coupling uncalibrated SWAT+ with machine learning provides a viable approach for generating continuous nutrient concentration time series from sparse observations in data-limited watersheds.

G-P59 Neighborhood Disadvantage as a Social Determinant of Adult Asthma Emergency Department Utilization in South Carolina, 2010-2019

Minhazul Abedin, Joshua R. Mann, Benjamin H. Walker, Ph.D., Fazlay S. Faruque

School of Population Health, University of Mississippi Medical Center

Background: Neighborhood disadvantage, as measured by the Social Vulnerability Index (SVI), may be an important social determinant of asthma morbidity, but its association with adult asthma emergency department (ED) utilization across diverse subgroups remains underexamined using small-area data. Methods: We analyzed 131,696 adult asthma ED visits (2010-2019; ICD-9-CM 493.xx/ICD-10-CM J45.x, primary diagnosis) from the South Carolina Revenue and Fiscal Affairs Office (SCRFA).

Geocoded 2010 census tract identifiers were linked to the 2016 CDC/ATSDR Social Vulnerability Index (SVI), yielding 10,176 tract-year observations across 1,085 census tracts. Poisson regression with robust standard errors estimated incidence rate ratios (IRRs) for asthma ED visits by overall SVI tertile, age group, sex, race/ethnicity, and SVI themes (socioeconomic status, household composition, minority/language status, housing/transportation), using unadjusted, mutually adjusted, and year-adjusted models. Compared with low-disadvantage tracts, high-disadvantage tracts had nearly three times the rate of asthma ED visits (IRR 3.10, 95% CI 2.99-3.22). This gradient was evident across all subgroups, with the strongest effects among adults aged 45-64 and women. Disparities by minority status were pronounced within the lowest-disadvantage tertile (IRR 3.84, 95% CI 3.65-4.04) and attenuated but persisted in higher-disadvantage tertiles, indicating significant effect modification (ï‡2=77.68, df=2, p <0.001). Among SVI themes, the socioeconomic domain showed the strongest independent association with ED utilization in mutually adjusted models (IRR 1.90, 95% CI 1.82-1.99). Neighborhood-level social vulnerability, particularly socioeconomic disadvantage, is strongly and independently associated with adult asthma ED utilization in South Carolina, with disparities most pronounced among racial/ethnic minorities in lower-disadvantage areas.

G-P61 Beyond Leaves: Cotton Bract Physiology Under Drought Stress

Mohan K. Bista, Bala Subramanyam Sivarathri, Nisarga Kodadinne Narayana, Brian Pieralisi, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Maintaining balanced physiological interactions between source and sink organs is essential for enhancing cotton yield potential during drought stress. Extensive research has examined drought-induced changes in leaf physiology, but bract (a non-leaf green organ) physiology remains poorly understood. We hypothesized that variability in cotton bract traits would be more strongly associated with yield than leaves under drought. To test this, ten genetically diverse cotton genotypes were subjected to two soil moisture regimes: (i) control (CNT), and (ii) drought stress (DS) during the reproductive stage. Pigments and physiological traits, including stomatal density and gas exchange, along with thermal load, were assessed in leaves and bracts. Although bract stomatal conductance was low, the drought-induced decline was 34% lower in bracts than in leaves. Bract stomatal density remained constant, whereas leaf stomatal density decreased by 16% under DS. Furthermore, stressed plants exhibited greater temperature differences between leaves and bolls than their corresponding controls. Under DS, the reduction in leaf expansion (30%) was significantly greater than that in bract expansion (16%) relative to the control. On average across cultivars, DS had a greater impact on yield components (50% reduction in seed cotton yield) than on fiber quality traits (<15% decline). Principal component analysis revealed positive associations among seed cotton yield, bract stomatal density, and bract stomatal conductance under DS. In addition, yield-related traits were grouped with bract pigments and physiological traits into a single factor and loaded in a similar direction under DS. Collectively, these findings emphasized that tapping into bract physiological variability could be a potential avenue for improving drought tolerance in cotton.

G-P62 Comparing GHG Emissions from Corn and Soybean Cropping Systems to a Bare Soil Control in the Blackbelt Soils of Mississippi

Oluwafemi Oyedele1, Reis Andre[2], Vaughn Reed[1], Prakash Kumah Jha[1], Calhoun Justin. S.[1], Wallace John[1], Olomitutu Emmanuel O[1]., Mulvaney Michael J.[1]

[1]Mississippi State University, [2]University of Missouri

Previous field research has compared greenhouse gas (GHG) emissions from corn (Zea mays L.) and soybean (Glycine max L.) production systems, but comparisons to a bare soil control are rare. We reason that if emissions during crop production do not differ from those of bare soil, one cannot attribute those emissions to the crop itself. Therefore, our objective is to compare GHG (CO2, N2O, and CH4) emissions during corn and soybean production to a soil-only control. We hypothesize that emissions during soybean production will not differ from the soil-only control, while those during corn production will be greater, likely due to nitrogen (N) fertilization. The inclusion of a control treatment is fundamental to well-designed research, yet it is generally overlooked in this critically important area. This novel approach has the potential to redefine how GHG emissions are attributed to crops, with broad implications for commodity sustainability initiatives, national and international commodity marketing, and the calculation of global warming potential associated with agronomic crop production.

G-P63 Development of Kartogenin-Loaded Electrospun PCL-PLGA Scaffolds for enhanced Microfracture Repair

Prachi Pannu and Steve H. Elder

Department of Agricultural and Biological Engineering, Mississippi State University, Mississippi State, MS

Articular cartilage defects remain a significant clinical challenge because cartilage possesses limited intrinsic regenerative capacity. Microfracture is a commonly performed cartilage repair procedure that recruits bone marrow-derived mesenchymal stem cells (MSCs) to the defect site; however, the resulting repair tissue is predominantly fibrocartilage, which lacks the composition and mechanical properties of native hyaline cartilage. Thus, there is a need for strategies that improve the quality and durability of cartilage repair. Kartogenin (KGN) has emerged as a promising candidate for cartilage regeneration as it selectively stimulates chondrogenic differentiation of MSCs. Our long-term objective is to develop a bioactive electrospun scaffold capable of delivering chondrogenic and chemotactic signals within a cartilage defect while supporting endogenous cell recruitment. Electrospun PCL/PLGA scaffolds have previously demonstrated sustained delivery of KGN; however, scaffold architecture and surface characteristics remain important considerations because they influence accessibility to the scaffold interior and opportunities for bioactive functionalization. The purpose of this study was to investigate techniques to increase scaffold pore size and enhance its surface properties. Pore size was addressed through polymer concentration, solvent mixture, and solution flow rate during electrospinning. Polydopamine (pDA) coating was incorporated as a surface modification strategy to enhance scaffold hydrophilicity and provide reactive functional groups for future growth factor immobilization. Scaffolds were characterized in terms of fiber size (indirect indicator of pore size), tensile modulus and strength, wettability, and kinetics of KGN release. Ongoing studies are focused on PDGF-BB functionalization and incorporation of sacrificial PEO fibers to generate macroporous scaffolds with enhanced cellular infiltration capacity.

G-P64 Integrated Remote sensing analysis of irrigation dynamics and Evapotranspiration for agricultural water resource assessment

Prathiksha Raghava, Prakash Kumar Jha, Drew Gholson, Prachi Singh

Mississippi State University, Mississippi State, MS

Sustaining agricultural productivity while reducing the strain on increasingly scarce water resources requires effective irrigation management. Improving water-use efficiency and promoting sustainable water resource management requires an understanding of long-term trends in crop water usage and irrigated agriculture. This study integrates geospatial information, ground observations, and water balance principles to provide a remote sensing-based framework for assessing irrigation dynamics and evapotranspiration (ET) variability across important agricultural regions in the United States. The research identifies regional patterns of irrigation expansion and contraction across the nation by combining satellite-derived land-use records with historical analyses of irrigated acreage. To facilitate the assessment and validation of remotely sensed evapotranspiration products, AmeriFlux cropland and pasture sites (2020-2024) were selected as representative field locations. To provide a thorough understanding of agricultural water availability, a grid-scale water balance framework was used to evaluate the relationships between precipitation, evapotranspiration, runoff, soil moisture, and groundwater storage. To investigate regional variations in crop water use and demonstrate how remote sensing products can be used for large-scale agricultural water assessment, the study also assesses ET at coarser spatial resolutions. The findings show that irrigation dynamics vary geographically throughout the United States. A few agricultural hotspots, mostly in the Lower Mississippi Delta and the Central Plains, which include Nebraska, have seen significant irrigation expansion. This suggests that irrigated agriculture is still expanding in these extremely productive areas. These divergent patterns show that irrigated agriculture is shifting from historically water-stressed western areas to parts of the central and southeast United States. The spatial distribution of AmeriFlux monitoring stations further demonstrates how well-suited they are for verifying remotely sensed evapotranspiration estimates across a variety of agricultural settings. Overall, the suggested approach demonstrates how irrigation dynamics and agricultural water use can be characterized across wide spatial scales by combining remote sensing, geospatial analysis, field observations, and water balance principles. In addition to offering important insights into shifting agricultural water demands, the identified irrigation hotspots, declining irrigation regions, and evapotranspiration variability lay a solid basis for future evaluations of irrigation efficiency, water resource sustainability, and climate-resilient agricultural management throughout the United States.

G-P65 Antimicrobial Efficacy of Potassium Ferrate Against Listeria Monocytogenes Survival In Water

Ajay Kumar Yenduri, Ramakrishna Nannapaneni

Agriculture and Plant Sciences, Mississippi State University, Mississippi State University, Mississippi State, MS

Listeria monocytogenes is a significant foodborne pathogen, and its persistence poses an ongoing challenge for the food industry, highlighting the continuous need for effective, broad-spectrum disinfectants that can target *L. monocytogenes* on various surfaces and in water systems. Ferrate (FeO4) a high-oxidizing compound primarily used in synthetic organic transformations, water oxidation catalysis, and wastewater remediation, has gained attention for its antimicrobial potential. However, its efficacy against foodborne pathogens, particularly *L. monocytogenes*, remains largely unexplored.This study evaluated the antimicrobial effectiveness of potassium ferrate at concentrations ranging from 1 to 16 mg/ml in water when exposed for 5 or 10 min against two strains of L. monocytogenes, Bug600 (serotype 1/2a) and ScottA (serotype 4b). Potassium ferrate exhibited a concentration-dependent reduction against both strains of L. monocytogenes by decreasing the counts by 2-3 log CFU/ml at 2 mg/ml or by 4-5 log CFU/ml at 4 mg/ml within 5 to 10 min of exposure in water. At potassium ferrate concentrations of 8 mg/ml for 5 or 10 min, almost no colonies were recovered, confirming near-complete inactivation of both Bug600 and ScottA strains in water. This study provides preliminary data for a potential investigation into the use of potassium ferrate as an effective disinfectant to reduce *L. monocytogenes* contamination in certain food processing environments. Further research is recommended to optimize disinfection protocols and maximize the complete elimination of persistent *L. monocytogenes* in wastewater, on food-contact and non-food-contact surfaces, and in facility floors and drains.

G-P66 AI-Assisted Suspicious Incident Classification for Emergency Dispatch and Security Operations

Raylon Reynolds, Kwabena Agyepong, Erol Sarigul, Victor Njiti, Manoj Bolugallu Padmayya, Jermiah Billa

Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

This study looked at whether artificial intelligence and machine learning can help with classifying suspicious incidents in emergency dispatch and security operations. The project used a public safety dataset with 5,000 simulated incident records. This dataset was designed to be realistic dispatch and security operation scenarios, without using real law enforcement or emergency dispatch records that could cause privacy or legal issues. Each incident had information and text fields like what kind of incident it was, where it happened how important it was and what the dispatcher thought. The study used machine learning to see how well the classification worked. The text from the incidents and dispatcher notes was processed using TF-IDF extraction, and the information was prepared for the machine learning models. Five different machine learning models were tried: Logistic Regression, NaÃ¯ve Bayes, Decision Tree, Random Forest and Gradient Boosting. Another technique called Isolation Forest was also used to find anomalies. The results showed that Logistic Regression was the best at classifying incidents with an accuracy of 92.7 percent. Gradient Boosting was second best at 90.2 percent. Random Forest was third at 87.2 percent. Isolation Forest identified suspicious incidents more often than routine incidents. The study suggests that artificial intelligence can help classify incidents, and support decision-making in public safety, but humans still need to be involved to make sure everything is done correctly.

G-P67 Nutrition Environment of SNAP Stores in Jackson, Mississippi, using NEMS

Rebecca Butz[1], Tasnim Tabassum[1], Mickel Sandifer[1], Kaylen Taylor[2], Khadeejah Franklin[2], Taylor Lampkin[2], Salit Chakma[1], Victoria Gholar[1], Fazlay Faruque[1]

[1]School of Population Health at the University of Mississippi Medical Center. [2]School of Medicine at the University of Mississippi Medical Center

Heart disease, obesity, diabetes, and diet-related cancers remain leading contributors to morbidity and mortality in the United States. Although individual lifestyle behaviors influence chronic disease risk, many environmental factors, including food access, affordability, and availability, substantially shape dietary behaviors, particularly among populations experiencing food insecurity and relying on Supplemental Nutrition Assistance Program (SNAP) benefits. Understanding the consumer nutrition environment of SNAP-authorized retailers is critical for informing food policy, community interventions, and efforts to improve equitable access to healthier foods. The objective of this study was to assess the nutrition environment of SNAP-authorized food retailers in Jackson, Mississippi using the Nutrition Environment Measures Survey (NEMS) tool. Specifically, this study evaluated differences in the availability, quality, and affordability of healthier food options across store types to better understand barriers to healthy food access in an urban area in a state with the second-highest obesity rate (40.4%). A cross-sectional assessment of 171 SNAP-authorized food retailers was conducted between June 2025 and June 2026 using the validated NEMS tool. Stores were categorized as grocery, convenience, or other retail types, and total NEMS scores were calculated to evaluate the availability, quality, and affordability of healthier food options. Differences in NEMS scores across store types were assessed using the Kruskal-Wallis test. Total NEMS scores were categorized into sample-derived quartiles representing progressively higher nutrition environment quality (Q1 being the lowest NEMS scores; Q4 being the highest NEMS scores). The distribution of store types across quartiles was evaluated using Pearson's chi-square test. A total of 171 SNAP-authorized food retailers were assessed, including 111 convenience stores (64.9%), 44 other store types (25.7%), and 16 grocery stores (9.4%). Overall nutrition environment quality was low, with a mean NEMS score of 6.7 and a median score of 4. Grocery stores demonstrated substantially higher NEMS scores (mean = 20.1; median = 28) than convenience stores (mean = 3.0; median = 2) and other store types (mean = 10.9; median = 10), with statistically significant differences observed across store types (Kruskal-Wallis test, p < 0.001). Store-type distribution also differed significantly across NEMS quartiles (Pearson chi-square test, $p < 0.001$). Nearly 82% of convenience stores were in the two lowest-scored NEMS quartiles, while only 3.6% were in the highest-scored quartile. Of all stores in the healthiest nutrition environments, only 10.5% were convenience stores. Nearly two-thirds (62.5%) of grocery stores were classified into the highest nutrition-environment quartile. The nutrition environment of SNAP-authorized retailers in Jackson, Mississippi differed substantially by store type, with convenience stores consistently demonstrating the poorest nutrition environments. Because convenience stores represented nearly two-thirds of all SNAP-authorized retailers and predominated in the lowest NEMS quartiles, many SNAP participants may encounter barriers to accessing healthier food options. These findings provide evidence to inform food policy, community-based interventions, and future research aimed at improving equitable access to nutritious foods in underserved communities.

G-P68 Analysis of Redox-Mediated Transcriptional Dynamics in Arabidopsis During Systemic Acquired Resistance

Rezwana Rahman Setu[1], Sargis Karapetyan[2], Mohammad A. Ghanbari[3], George V. Popescu[4], Sorina C. Popescu[5]

[1]Department of Biochemistry, Nutrition and Health Promotion, Mississippi State University, Mississippi State, MS 39762, [2]Department of Biology, Duke University, PO Box 90338, Durham, NC., [3]Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University, Mississippi State, MS 39762, [4]Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University, Mississippi State, MS 39762, [5]Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology (BCH-EPP)

In plants, systemic acquired resistance (SAR) provides long-lasting, broad-spectrum protection against pathogens through priming mechanisms involving redox and phytohormonal signaling. Despite its importance, transcriptional dynamics during SAR onset and the role of redox signaling in SAR maintenance remain poorly understood. Here, we investigated these dynamics by analyzing GRXS13 (Glutaredoxin 13, At1g03850), a CC-type glutaredoxin strongly inducible by salicylic acid; NUDT6 (Nudix hydrolase 6, At2g04450), a gene implicated in SAR-associated nucleotide/redox signaling; and PAD4 (Phytoalexin-deficient 4, At3g52430), a third-cluster SAR-upregulated gene that works with EDS1 and is essential for full SAR establishment. To track in vivo transcriptional dynamics, promoter regions of GRXS13, NUDT6, and PAD4 were fused to luciferase reporters using Gateway cloning and transformed into Arabidopsis thaliana wild type and the SAR-defective top2 mutant via Agrobacterium-mediated floral dip. T2 plants were infiltrated with Pseudomonas syringae pv. tomato DC3000 expressing avrRPT2 to induce SAR, and promoter activity was monitored by bioluminescence at two-hour intervals over four days under 12 h light and 12 h dark cycles. In parallel, in vitro qPCR time-course analyses of additional SAR marker genes like PR1 (Pathogenesis-Related 1, At2g14610), ICS1 (Isochorismate Synthase 1, At1g74710), including GRXS13 and NUDT6, were conducted to obtain precise, quantitative measurements of transcriptional responses. Oscillatory expression patterns of GRXS13 and NUDT6 were observed, and comparisons with known SAR driver genes revealed distinct differences between WT and top2 mutants, reflecting the impact of dysregulated redox and nucleotide signaling on SAR onset. Together, these in vivo and in vitro analyses define key temporal control points of SAR-associated transcription, revealing how redox signaling coordinates systemic immunity and establishing a framework to improve disease resistance strategies in plants.

G-P70 A Multimodal 3D Point Cloud Fusion Pipeline for RGB-D, Thermal, and Hyperspectral Phenotyping of Soybean Under Drought and Heat Stress Conditions

Sachin Cooray

Department of Agricultural & Biological Engineering, Mississippi State University, MS, USA.

Drought and heat stress are major constraints on soybean productivity, creating a need for high-throughput phenotyping methods that capture both three-dimensional canopy structure and physiological responses. This study presents a multimodal 3D point cloud fusion pipeline integrating RGB-D geometry with thermal and hyperspectral imaging for per-point analysis of canopy temperature and spectral reflectance. Top-down RGB and depth images were used to reconstruct 3D point clouds of individual plants and multi-plant canopies, with vegetation segmented using an Excess Green (ExG) index combined with hue-based filtering. Thermal and hyperspectral images, which had different fields of view from the RGB-D sensor, were registered to the reconstructed geometry using a cluster-shape-matching transformation. Registration accuracy was evaluated using Intersection-over-Union (IoU) and Dice similarity coefficients between segmented canopy masks from each modality and the corresponding RGB-derived reference masks. Across two capture sessions with different canopy densities, IoU values ranged from

0.39 to 0.74 and were further validated through direct image-overlay comparisons. The resulting fused point clouds preserve true RGB color while assigning temperature and hyperspectral reflectance values to each 3D point, enabling multimodal visualization and analysis in CloudCompare. This pipeline establishes a validated framework for constructing modality-fused 3D plant models and provides a foundation for future per-point trait extraction, multimodal data fusion, and early detection of drought and heat stress in soybean.

G-P71 Providing Universal School Meals Can Reduce Food Insecurity: A Policy Review of The Community Eligibility Provision in Mississippi

Sadie Studdard, Rahel Mathews

Department of Biochemistry, Nutrition, & Health Promotion at Mississippi State University, MS, USA

Food insecurity is a significant public health, economic, and social issue that affects communities across all US counties. The national prevalence of child food insecurity is 19%, while in Mississippi it is 25%. Federal school meal programs, which provide free and reduced-cost meals, play an important role in reducing food insecurity and supporting child health and well-being; however, participation is influenced by factors such as perceived social stigma. The Healthy, Hunger-Free Kids Act authorizes the Community Eligibility Provision (CEP) to expand access to school meals for all students in eligible schools or districts, through free school meals- essentially universal free meals. CEP aims to reduce barriers to school meal participation in order to reduce food insecurity. Another feature of offering universal free meals is eliminating family meal applications, thus reducing the administrative burden. The aim of this policy review is to document the current evidence on CEP implementation in Mississippi by broadly examining the positive outcomes and challenges for participating in schools and districts. Government reports, policy documents, and published scholarly articles were examined and reviewed between March and June 2026. While the purpose of this review was to examine Mississippi in particular, the available evidence on this policy was much broader. Participation characteristics of eligible school districts across the US showed that 56% of eligible schools in the southern US participated in CEP, which was higher than in every other region. Evidence supported that increased access to school breakfast and lunch programs improved diet quality, academic performance, and administrative burden across the US. Families from schools that implemented CEP were less likely to report food insecurity across the US (5%). In some cases, districts and schools reported a reduction in obesity prevalence. Rural CEP schools reported larger improvements in participation, academic, and health-related outcomes than schools in urban and metropolitan areas. In the 2024-2025 school year, 52 school districts in Mississippi adopted CEP. An additional 98 districts had schools eligible to participate but did not participate. There was a gap in the research that would have explained this trend. Future Implications: Evidence from this review suggests that rural schools may experience greater positive impacts from CEP implementation than other areas. While Mississippi has high rates of child food insecurity and a large rural population, many eligible schools still do not participate. There is a nationwide gap in research on how CEP affects school operations. Further research on the financial and operational implications of CEP in Mississippi schools is needed to inform policies and programs that maximize CEP's benefits for children's health statewide. The significant potential impact of CEP in Mississippi schools/districts raises important questions regarding its role in addressing childhood food insecurity and implementation barriers.

G-P72 HOTSPOT ANALYSIS OF HUMID HEATWAVES, THE SILENT KILLER, IN MISSISSIPPI

Salit Chakma[1], Mohammad Al-Hamdan[2], Lauren S. Pongetti[1], Benjamin Walker[1], Fazlay Faruque[1]

[1]University of Mississippi Medical Center, [2]University of Mississippi

Heatwaves are often referred to as the "silent killer" in public health. Heatwaves accompanied by high humidity are known as humid heatwaves (HHW), which are more detrimental as they amplify the apparent temperature (compared to dry-bulb air temperature). HHWs affect the human body's thermoregulation and worsen underlying illnesses. Therefore, it is imperative to understand the spatial distribution of HHWs to enable spatially targeted preventive measures. We used the heat index (HI), an established measure of apparent temperature, as a measure of apparent temperature. We used downscaled (1-kilometer) North American Land Data Assimilation System (NLDAS) daily HI data covering 1,848 days of warm seasons (May-September) between 2011 and 2022. HHWs were defined as periods of ‰¥3 consecutive days with an HI exceeding 90 „‰ and 100 „‰, and were characterized by frequency, intensity, and duration. Emerging hotspots of these three aspects were determined using ArcGIS Pro. The nonparametric Mann-Kendall test was used for trend analysis. The hotspots of intense and long HHWs were predominantly persistent in the Mississippi Delta with no change in frequencies at the 95 „‰ threshold. A mix of persistent and sporadic intense hotspots in the Mississippi Delta, with emerging hotspots of varying duration and oscillating frequencies, was found at the 100 „‰ threshold. Trend analysis revealed that, over time, a few other parts of Mississippi were experiencing increasing trends in frequency and duration. In Mississippi, the predominant emerging hotspot types are oscillating (a mix of significant hot and cold spots across time), persistent (significant hotspots for 90% of the time), and sporadic (historically on- and off-again hotspots with no historically significant cold spots). The persistent hotspots delineate areas with recurrent exposure to elevated humid heat conditions, where heat-related health risks are not only potentially harmful but also sustained over time. Such repeated exposure could increase cumulative health risks for residents with limited adaptive capacity, such as those in the Mississippi Delta. Variations in HHW hotspots indicate the need for different preparedness strategies. For example, regions with persistent hotspots may require long-term structural interventions, whereas early-warning and seasonal interventions might be sufficient for regions experiencing sporadic or oscillating hotspots. This study improves past research by utilizing high-resolution gridded temperature data. These improvements enable the delineation of zones requiring preventive measures to minimize the adverse impacts of extreme humid heat on human health.

G-P73 Evaluation of Soil-to-Plant Radioisotopic Transfer in Sweet Potatoes from Mississippi

Samuel Ratan Bunga, Jermiah Billa, John Adjaye, Kwabena Agyepong, Erol Sarigul, Manoj Bolugallu Padmayya, Sonia Eley

Department of Advanced Technologies, Alcorn State University, Lorman, MS 39096

Plants absorb various nutrients present in soils and groundwater via the root system during their growth period. To improve crop

yields, farmers add fertilizers to soils and plants tend to uptake nutrients in fertilizers during their growth process. Presence of radioisotopes in soils may result in uptake of radioisotopes into plants which will eventually accumulate in the edible parts of the plants. Root plants such as sweet potatoes would be an excellent source for providing information on uptake rates of nutrients from the soils. Being one of the prominent producers of sweet potatoes in the country, in 2025 the state of Mississippi harvested 29,000 acres of sweet potatoes with a production value of $123 million. Soils and sweet potatoes produced from Claiborne County of Mississippi were analyzed for the key isotopes of Ra-226, Th-232, and K-40 using a high purity germanium detector of 35% relative efficiency. Using the measured radioactivity values, the isotopic transfer factors (TF) from soils to edible parts of sweet potato plants were computed. As there is limited or no information on the levels of isotopic concentrations in sweet potatoes produced in the region of interest, results from this study serve as a template for researchers and agriculturalists on the levels and uptake rate of nutrients (radioisotopes) in sweet potatoes.

G-P74 AEGIS: A Real-Time Geospatial Early-Warning System for Threats to United States Agriculture

Sk Nafiz Rahaman[1], Narcisa G. Pricope[2]

[1]Department of Geosciences, Mississippi State University, [2]Professor and Associate Vice President for Research, Office of Research and Economic Development, Mississippi State University

Threats to United States agriculture, including pathogen outbreaks, emerging crop diseases, climate stress, trade disruptions, and food-supply shocks, frequently originate abroad and appear in operational data before they reach mainstream reporting. Geospatial and remote-sensing systems monitor the physical environment well, but ground-level signals such as trade-barrier filings, outbreak bulletins, hunger metrics, and maritime traffic are rarely fused into one operational view. We present AEGIS (Agriculture Early-warning Geospatial Intelligence System), an open-source real-time dashboard that combines five public data streams into a single picture of agricultural risk reaching the United States. AEGIS ingests ERA5 climate anomalies, World Trade Organization sanitary and phytosanitary (SPS) notifications, multi-source food-security and outbreak news, the World Food Programme HungerMap, and live vessel positions from an Automatic Identification System (AIS) feed. From the active layers it computes a composite Agricultural Risk Index (0-100), refreshes it every 30 seconds, and flags cargo and tanker traffic inbound to U.S. ports from regions carrying elevated risk. The system is built entirely on free public APIs, is released under the MIT license, and runs locally or as a hosted instance with responsive support for desktop, tablet, and phone. AEGIS is a working prototype; vessel coverage is partial because the AIS layer depends on a rate-limited public stream. Planned stages are: a satellite-derived vegetation-vigor layer for crop-condition monitoring; validation of the risk index against historical agricultural incidents to calibrate its weights; port- and commodity-level resolution of inbound-vessel risk; extension from nowcasting to short-horizon forecasting; and evaluation with agency stakeholders.

G-P75 Can Lignocellulolytic Fungi Improve the Sustainable Reuse Of Paddy Straw?

Smruthi Sagarika Mahapatra

Mississippi State University, Mississippi State, MS. USA

Paddy straw, an abundant agricultural residue, poses significant environmental challenges due to its improper management and disposal practices, including the prevalent practice of residue burning. To address this issue, there is a growing need to explore sustainable alternatives for paddy straw decomposition. This study aims to unravel the crucial role of lignocellulolytic microbes in facilitating rapid paddy straw decomposition. In this study, fungal cultures were isolated and screened for lignocellulolytic enzyme activities such as CMSase, FPase, Xylanase, Laccase, and LPMO. Fungal isolates exhibiting superior enzymatic activities were subsequently identified using targeted sequencing of the ITS region. Based on the compatibility test, microbial isolates processing higher lignocellulolytic activity were selected, and isolates with different combinations were evaluated under ex-situ conditions to find out their effects on reducing the C/N ratio. This study highlights the important role of fungi in utilizing cellulose and emphasizes the need to further explore their potential for facilitating paddy straw decomposition.

G-P76 Discovering Genomic Regions Associated with Yield Traits in Cowpea

Sujan Poudel, Lekshmy V Sankarapillai, Dingiswayo Mwanza, Gaurav Joshi, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, USA

Cowpea (Vigna unguiculata L. Walp.) is a climate-resilient grain legume valued for its nutritional quality and adaptability to marginal environments. Despite a large and diverse germplasm collection, commercial cultivars exhibit limited genetic variability. Improving seed yield remains a major breeding goal due to the complex genetics and environmental interactions throughout the growing season. Discovering genomic regions associated with yield-related traits accelerates the development of high-yielding genotypes for rainfed conditions. In this study, a diverse panel of cowpeas (n=200) was phenotyped for phenological traits and agronomic traits, including seed yield and yield components. Substantial phenotypic variation was observed among genotypes across measured traits. Seed yield per plant ranged from 3.0 to 84.0 g plant⍰»[1], while days to flowering and maturity ranged from 33 to 83 days after sowing (DAS) and 53 to 97 DAS, respectively. Considerable variation was also observed in yield components, with pod length ranging from 10 to 23 cm, pod weight from 3.6 to 121.7 g, and pod number from 2 to 56 per plant. A significant negative correlation (r = -0.48, p < 0.001) was observed between days to flowering and nitrogen balance index (NBI). Seed weight was highly correlated with pod weight (r = 0.96) and pod number (r=0.7) and moderately correlated with pod length (r = 0.37) and days to maturity (r = 0.37). Further, genome-wide association studies (GWAS) revealed significant marker-trait associations for various traits on different chromosomes. Six genomic regions were consistently identified by both FarmCPU and BLINK, including one locus each for NBI and pod length, and two loci each for days to maturity and pod number. These QTLs showed high phenotypic variance (~10%). These identified QTLs provide useful genetic resources for improving yield in cowpeas.

G-P77 Screening Commercial and Breeding Tomato Varieties for Tolerance to Heat and Herbicide Stress

Trisa Das

Mississippi State University, Mississippi, USA

Tomato (*Solanum lycopersicum* L.) production in the Mississippi Delta is frequently constrained by high summer temperatures and increased risk of herbicide exposure due to the proximity of row crop agriculture, making stress resilience an important trait for

varietal selection. This study screened 31 commercially available and breeding tomato varieties representing genetics from Bayer, BHN, Heinz, and BASF to identify genotypes with improved tolerance to combined heat and herbicide stress. Plants were exposed to a heat stress of 35 °C for 7 days, followed by a two-week recovery period, after which 2,4-D was applied to evaluate subsequent herbicide injury. Following heat stress, 20 of the 31 varieties maintained equal or greater plant height compared to unstressed controls and exhibited visibly lower injury, characterized by reduced chlorosis, wilting, and leaf scorching, with approximately 80% to full recovery. These same varieties also maintained higher or unchanged levels of chlorophyll, flavonoids, and anthocyanins after stress, suggesting stronger antioxidant and protective responses. The combination of reduced visual injury, sustained growth, and higher pigment levels indicates a greater potential for physiological tolerance not only to heat stress but also to subsequent herbicide exposure. Overall, this screening approach identified a subset of tomato varieties with improved resilience to heat stress and a greater capacity to tolerate herbicide injury, providing a useful framework for selecting genotypes better suited for stress-prone production environments in the Mississippi Delta.

G-P78 Depth-Wise Distribution of Easily Extractable Glomalin-Related Soil Protein In Mississippi Benchmark Soils

Yehani Ekanayake, Praveen Amarasinghe, Nuwan K. Wijewardane

Mississippi State University, Mississippi State, MS, USA

Glomalin-related soil protein (GRSP), produced by arbuscular mycorrhizal fungi (AMF), plays an important role in soil aggregation, carbon sequestration, water retention, and overall soil health. Understanding its vertical distribution within soil profiles is essential for evaluating belowground biological activity and ecosystem functioning. This study investigated the depth-wise distribution of easily extractable glomalin-related soil protein (EE-GRSP) across benchmark soil series in Mississippi. Approximately 200 soil samples were collected from five depth intervals (0-5, 5-15, 15-30, 30-60, and 60-121 cm), with about 40 samples per depth. EE-GRSP concentrations were determined using citrate extraction, autoclaving, and the Bradford protein assay. Descriptive statistics and inferential analyses were conducted to evaluate depth-related variations in EE-GRSP. The overall dataset exhibited a positively skewed and non-normal distribution. Mean EE-GRSP concentrations generally decreased with depth, ranging from 9.62 mg/g in the 0-5 cm layer to 1.95 mg/g at 60-121 cm. Significant differences in EE-GRSP were observed among soil depths, indicating strong vertical variation in glomalin distribution within benchmark soil profiles. The results indicated that EE-GRSP is concentrated near the soil surface, reflecting greater root abundance and arbuscular mycorrhizal activity in upper soil horizons. Preliminary analyses further suggested that both visible-near infrared (Vis-NIR) and mid-infrared (MIR) spectroscopy show potential for estimating glomalin-related soil protein from fresh, 2mm, and fine ground soils, providing a rapid and non-destructive alternative to conventional laboratory methods.

G-P79 Optimizing Harvest Time of Microgreens Through Metabolomic Profiling: A Species-Specific Approach to Enhancing Nutritional Value

Zonia Elizabeth Caro Carvajal, Tibor Pechan, Olga Pechanova

Mississippi State University - Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University, Mississippi State, MS

Microgreens, young shoots of vegetables, grains, and herbs harvested early in growth, emerged in high-end cuisine in the 1980s and are increasingly recognized for their nutritional potential. Despite their popularity, the influence of harvest timing on final nutrient content remains barely understood. It represents a knowledge gap for producers and consumers seeking to maximize microgreens' nutritional health benefits. This study employs both untargeted and targeted liquid chromatography-mass spectrometry (LC-MSn)-based metabolomics to characterize species-specific variations in nutrient composition across different growth stages. Preliminary experiments were conducted on shiso (Perilla frutescens) and chives (Allium schoenoprasum) to establish reproducible growth, sampling, and extraction protocols. Metabolomic profiling identified 17,424 features, including 1,063 compounds with assigned molecular formulas, and 222 confidently annotated metabolites using the mzCloud database. Principal Component Analysis revealed clear, statistically significant separation between the metabolomes of two species. Differential abundance analysis detected 445 compounds that varied between species, highlighting pathways associated with flavonoid biosynthesis (e.g., flavanones), fatty acid metabolism (e.g., Î±-linolenic acid), phenylpropanoids biosynthesis (e.g., catechin), phytosterol synthesis (e.g., beta-sitosterol), and others that are linked to several health-promoting effects. These results demonstrate the feasibility of LC-MS-based metabolomics for evaluating nutrient variability in microgreens, and they provide insight into species-specific biochemical differences. The data also establishes methodological foundations for larger studies comparing different species across multiple harvest time points. This research will potentially generate data-driven recommendations for producers to optimize harvest timing and enhance nutritional quality of microgreens, contributing to broader efforts to improve population health via offering specialty crops as a functional, health-promoting food.

G-P96 Self-Amplifying Mrna Vaccine Against Chikungunya Virus (CHIKV)

Sabin Shrestha, Shazeed-Ul Karim, Denyoh Prince Mark Dela, Faqing Huang, Fengwei Bai

University of Southern Mississippi

Chikungunya virus (CHIKV) is a mosquito-borne alphavirus that has emerged as a significant global public health concern due to its ability to cause large-scale outbreaks in tropical and temperate regions. CHIKV infection leads to acute fever, severe joint pain, and myalgia, which can persist for weeks or months. The rare cases involve severe or atypical manifestations such as persistent arthralgia, neurological complications, and occasionally death. According to the WHO, 502,264 CHIKV cases with 186 deaths have been reported worldwide in 2025. As of Feb 28, 2026, 32,758 cases with 9 deaths have been reported worldwide. Currently, only one vaccine is approved for use in the USA: the virus-like particle vaccine (VIMKUNYA). Another live attenuated vaccine, IXCHIQ, was also available, but the FDA suspended its US license on August 22, 2025, due to safety concerns. Therefore, safer and more effective CHIKV vaccines are still needed. We have generated a flavivirus-based self-amplifying mRNA replicon (FV SAM) with a novel live-attenuated Zika virus strain. Our results showed that the FV SAM exhibited higher efficiency of antigen expression than an alphavirus-based SAM replicon (AV SAM), which is widely used to generate SAM vaccines. This has been confirmed by using confocal imaging, qPCR, flow cytometry, and western blotting. In addition, we also showed that FV SAM reduced type I interferon activity compared to AV SAM. Type I interferons have been suggested to play a detrimental role in the

induction of antibody production. Our preliminary data suggest that FV SAM can be a novel and powerful platform for self-amplifying mRNA-based vaccines against CHIKV, other viral infections, and even cancers.

G-P91 Addressing Behavioral Health Disparities in Mississippi

Annyasha Mukherjee[1], Debarshi Roy[2]

[1]College of Health Sciences, Department of Behavioral and Environmental Health, Jackson State University, Jackson, MS, [2]Department of Biological Sciences, Alcorn State University, Lorman, MS

Mississippi experiences significant behavioral health challenges, largely driven by historical and ongoing gaps in the state's healthcare infrastructure. Our project seeks to analyze the interrelation between the SDOH and increasing rates of anxiety, major depression, and suicidal ideation in the rural and impoverished environment of Mississippi. The main objective will be to examine the effect of economic and structural barriers on mental health outcomes and come up with an intervention strategy. Initial analysis based on national health surveillance data points to clear disparity in terms of prevalence and usage of health care services in the state. The poverty levels and shortage of mental health professionals in Mississippi correspond to higher rates of unaddressed mental problems. The data suggests that there is a compounded crisis in the rural areas characterized by geographic distance, transport difficulties, and stigma. Such inequity is largely experienced by racial minorities, especially African American/Black people, who utilize the treatment less even though the demand for services is high. Moreover, information collected after the pandemic reveals that one of the biggest problems in the state is the emergence of anxiety disorders among low-income families and adolescents, a tendency which is intensified due to poor housing conditions and lack of broadband access. In order to combat growing inequities, future research will include development of an AI-powered machine learning algorithm aimed at detection and prediction of behavioral health hot spots, for example, the Mississippi Delta. This would be achieved through the use of multiple layers of socio-environmental factors, including median income, rural index, density of providers, and level of education. In other words, this research would provide public health policymakers with crisis prevention tools through prediction of hot spots before the crises become an issue.

G-P92 Identification of Antifungal Metabolites in Maize Silk Using Liquid Chromatography-Mass Spectrometry

Lillian Butler, Tibor Pechan

Mississippi State University, Mississippi State, MS, USA

Annual worldwide maize production exceeds 1.3 billion metric tons, with the United States producing nearly a third of the crop. However, *Aspergillus flavus*, a pathogenic fungus which can lead to ear rot and Aflatoxin B1 production, commonly infects this widely valued crop. Since Aflatoxin B1 is the most potent carcinogenic mycotoxin and can lead to hepatocellular carcinoma and immunosuppression, the FDA limits the amount that can be present in crops intended for human consumption to 20 ppb. This limitation results in large economic losses for farmers. Previous studies have determined that the fungus can infect corn silk and then spread to the surface of developing kernels. This study aims to identify corn silk metabolites involved in fungal resistance. Using liquid chromatography-mass spectrometry and the discovery/untargeted metabolic methodology, metabolites were identified with the Compound Discoverer software. Several metabolic pathways were identified involved in natural pathogenic resistance showing that corn silk contains anti-fungal properties. Future studies can use this knowledge to develop anti-fungal and commercially successful corn species through targeted breeding or genetic manipulation.

Investigator Poster (I-P)

I-P80 Transferability Of Stable Quadrant Between Soybean And Corn

Amrit Shrestha[1], Tulsi P. Kharel2, Madhav Dhakal[1], Ammar B. Bhandari[2], Krishna N. Reddy[2]

[1]Mississippi Water Resources Research Institute, Mississippi State University, Mississippi State, Mississippi, USA, [2]Crop Production Systems Research Unit, USDA-ARS, 141 Experiment Station Road, Stoneville, Mississippi, USA,

One approach for delineating management zones is the stability quadrant method, which classifies each pixel into four categories based on multi-year yield data: high yield low variability (high), low yield low variability (low), high yield high variability, and low yield high variability. The first two quadrants are considered stable because they exhibit low temporal variability. This study evaluates underlying hypothesis that whether the high-low stable quadrant identified in soybean (Glycine max (L.) Merr.) would remain stable when applied to corn (Zea mays). This was examined by delineating stability quadrants for four fields (Field 1-4) based on 3-years of soybean yield data collected between 2015-2020. Then, Kruskal-Wallis test, a non-parametric analysis of variance, was performed on corn yield data from the stable high and stable low quadrant based on soybean yield. In addition, quadrant pixels that fall within ± 0.135 Mg ha-1 (2 bu ac-1) of field average yield and SD were reclassified as one of the stability quadrants based on their nearest neighboring pixels. The result indicated that significant difference (p<0.05) in corn yield exists between stable high and low quadrant. However, the direction of response varied across fields and year i.e. average value of corn yield in soybean stable high-low quadrants were either reversed or remain unchanged. These findings suggest that stability quadrants identified for soybeans have limited applicability for the corn management highlighting the need for crop specific stability quadrant. Moreover, reclassification of pixels generated a smoother map, improving its practical utility for precision management.

I-P81 Deploying Advanced On-Site Technologies for Vegetable Disease Detection and Extension Education

Emran Ali Sumyya Waliullah

Alcorn State University, Lorman, MS

Rapid and accurate diagnosis of vegetable diseases is essential for timely management and reducing crop losses. This presentation highlights the deployment of advanced, field-ready

diagnostic technologies, including lateral flow immunoassays (ImmunoStrip), loop-mediated isothermal amplification (LAMP), recombinase polymerase amplification (RPA), portable real-time PCR, and nanopore sequencing, for rapid, on-site detection of major vegetable pathogens. Through contemporary Extension programming, these technologies are integrated into hands-on workshops, field demonstrations, and grower training to improve disease identification, biosecurity, and integrated disease management. The program emphasizes practical applications for small-scale and underserved producers by providing accessible diagnostic tools that support informed management decisions and sustainable vegetable production. This approach strengthens Extension outreach while enhancing producer capacity to respond quickly to emerging disease threats.

I-P82 Unlocking the Genetic Secrets of Stay-Green Trait in Rice under Heat Stress

Gaurav Joshi, Alekhya Chakravaram, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS, USA

Rice (Oryza sativa L.) is a major cereal crop and a staple food for more than half of the world's population. Heat stress severely impairs plant health by altering photosynthetic pigments, posing a major threat to the sustainability of yield and quality. Heat-induced degradation of chlorophyll (greenness) accelerates senescence, thereby impairing photosynthetic efficiency, shortening grain filling, and ultimately reducing yield. In response, plants activate protective mechanisms, including the accumulation of secondary metabolites such as flavonoids, to mitigate stress damage. Understanding the genetic regulation of pigments under heat stress is crucial for breeding heat-tolerant rice. To map genetic loci linked to pigments, 271 rice genotypes were evaluated for pigments at the milk (14 days) and dough (28 days) stages under control (32 °C) and heat stress (38 °C). All traits showed significant genotype Ã— treatment interaction at both stages. A highly significant positive correlation was observed between chlorophyll content and nitrogen balance index, whereas flavonoids showed a significant negative correlation with chlorophyll. A genome-wide association study (GWAS) revealed multiple loci for different traits, including several co-localized candidate genes, such as OsDET1 for chlorophyll or stay greenness. The detection of unique loci across distinct stress time periods indicates that distinct stress-tolerance mechanisms operate at different developmental stages. These identified genetic loci, once functionally validated, can be used in breeding programs to improve heat tolerance. We identified genotypes with high chlorophyll levels or stay-greenness during grain development and high yield under heat stress. Such donors can serve as potential donors for breeding resilient rice in warmer environments.

I-P83 Olibanum as a Novel Source of Bioactive Metabolites for the Control of Triple-Negative Breast Cancer

Taylor Raff , Rose Pwint , Roya Noorbakhsh, Kayla Griffith, Hannah Khairandish, Francheska Brzazgon, Kasia Michalak, Zakaria Abd Elmageed, Hassan Ebrahim

Department of Biomedical Sciences, Edward Via College of Osteopathic Medicine, Monroe, LA, 71203

Breast cancer (BC) is the most diagnosed cancer in women and the second leading cause of cancer death, after lung cancer. Recent statistics estimate that 316,950 women will be diagnosed with invasive BC and 42,170 women will die in 2025. BC is a highly heterogenous disease, characterized by a wide range of subtypes that vary in their biological features, clinical presentation, and response to treatment. Subtypes like hormone receptor-positive, HER2-positive, and triple-negative breast cancer (TNBC) exhibit distinct patterns of growth, metastasis, and resistance to therapies. TNBC is the most aggressive subtype with highest potential for metastasis and recurrence. Chemotherapy remains the mainstay therapeutic modality for TNBC, as hormone and HER-2 targeted therapies are ineffective. c-Met is a receptor tyrosine kinase that is overexpressed in TNBC and is associated with tumor aggressiveness, invasion and metastasis, chemotherapy resistance. Frankincense, also known as olibanum, is an aromatic resin used in incense and perfume for spiritual, religious, and meditative purposes. Recent research has shown its utility for the management of inflammation, pain, arthritis and cancer. Incensole acetate (IA) is the main diterpene found in olibanum and can be purified using chromatographic techniques. As a part of an ongoing project to discover novel c-Met modulators, we explored the anti-breast cancer potential IA against BC cells. The tetrazolium-based cell viability assay was used to evaluate the effect of IA on the proliferation of BC cells. The scratch and transwell assays were utilized to monitor the antimigratory effect of IA. Western blot was used to uncover the potential molecular target mediating the anticancer effect of IA. IA effectively suppressed the proliferation, migration, invasion, and colonization of TNBC cells at low Î¼M concentrations. Furthermore, IA effectively suppressed the phosphorylation (activation) of c-Met in a dose-dependent manner. Furthermore, molecular modeling studies suggested in-pocket binding conformation of IA which is energetically stabilized by interactions with amino acids at the hinge region of the kinase domain. Our ongoing research focuses on exploring the effect of IA on the downstream signaling pathways of c-Met. IA is a novel c-Met modulator diterpene amenable for further development as a lead compound for the control of aggressive c-Met-addicted TNBC.

I-P84 Natural variation and genetic regulation of leaf architecture and leaf physiology in soybean

Lekshmy V Sankarapillai, Bala Subramanyam Sivarathri, Sujan Poudel, Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, MS, USA

Leaf thickness is a key structural trait shaped by mesophyll development, tissue density, leaf water content, and intercellular air-space volume, making direct assessment complex. Specific leaf weight (SLW), defined as leaf dry mass per unit area, is therefore widely used as a proxy for leaf thickness and structural investment. However, the extent of variation in leaf structural and physiological traits, and the genomic regions underlying this variation, remain poorly resolved in soybean (*Glycine max* L.). We hypothesized that natural variation in SLW is associated with variation in leaf physiological traits and is regulated by distinct genomic regions. Accordingly, this study phenotyped leaf morphological and physiological traits and mapped associated genomic regions using pot and field experiments. Substantial genotypic variation was observed in leaf traits. Leaf area (LA) ranged from 17.03 to 218.46 cm^2 and 15.53 to 336.95 cm^2 in the pot and field conditions. Leaf dry weight (LDW) ranged from 0.07 to 1.96 g in potted plants and from 0.05 to 1.47 g in field-grown plants. These differences resulted in wide variation in SLW, ranging from 0.003 to 0.040 g cm-2 in pots and from 0.003 to 0.008 g cm^2 under field conditions. Variation in SLW was accompanied by differences in stomatal conductance (gs; 0.015-1.05 µmol m^2 s^1) and photosynthetic pigment index (0.30-0.93) in the pot

experiment. Field-grown germplasm also exhibited substantial variation in gs, ranging from 0.27 to 2.10 µmol m⁻² s⁻¹. Although phenotypic correlations were generally weak, genome-wide association analysis using 36,535 SNP markers identified significant marker-trait associations for SLW, gs, and pod weight, primarily under pot conditions. SLW-associated markers were mainly located on chromosomes 2, 8, and 17, whereas gs-associated markers were detected on chromosomes 3, 12, and 17. Chromosome 17 also showed a strong association with SLW under field conditions, with SNP ss715625833 showing the strongest association. These genomic regions represent promising targets for further candidate-gene discovery and may support breeding efforts to improve canopy function and yield potential.

I-P85 Association of Nurses' Hand Hygiene Knowledge, Attitudes, Practices, And Hand Hygiene Methods On Bacterial Hand Contamination

Lir-Wan Fan, Yu-Ching Tu

Department of Long-Term Care and Management, Chung Hwa University of Medical Technology, Rende District, Tainan City, 71703, Taiwan

I-P86 Upland and Pima Cotton Responses to Drought and Salinity Stress under Ambient and Elevated CO2 Levels

Naflath Thenveettil[1], Navneet Kaur[1], K.N. Reddy[2] and K. Raja Reddy[1]

[1]Mississippi State University, Mississippi State, MS, [2]USDA-ARS, Stoneville, MS

Drought and soil salinity pose significant challenges to agriculture, hindering its ability to meet the growing population's increased demand for food and fiber by adversely affecting plant growth, crop yields, and ecosystem stability. A pot study was conducted on two cotton species, Gossypium barbadense (Pima) and G. hirsutum (Upland). The experiment was conducted under sunlit, controlled-environment conditions. The experiment combined drought (DS; 0.08 m3 m-3 soil) and salinity (SS; 6 dSm-1), with two atmospheric CO2 concentrations: ambient (aCO2; 425 ppm) and elevated (eCO2; 725 ppm). The control (CNT) treatment received a volumetric water content of 0.14 m3 m-3 and standard Hoagland's nutrient solution. Treatments were applied from the third-leaf stage until flowering, and physiological and growth measurements were recorded throughout the study. In Pima, photosynthetic rate (PN) and stomatal conductance (gsw) decreased by 61% and 81%, respectively, under DS relative to CNT, whereas in Upland, the reductions were 25% and 62%, respectively. Under SS, by contrast, Pima showed 10% higher PN and gsw than CNT, whereas Upland showed reductions of 29 and 55%, respectively. Both species benefited from eCO2 fertilization under CNT, DS, and SS conditions. Fewer nodes were recorded under DS (Pima: 11 and Upland: 12 vs 17 under CNT), but they partly recovered under DS+eCO2 (13 and 14). Under SS and SS+eCO2, Upland produced 16 and 17 nodes, respectively, and Pima produced 14 and 15 nodes. Mainstem leaf length also decreased under DS, with greater reductions beginning at the 6th node in Pima and 7th node in Upland, while leaf length increased under eCO_2 across all treatments. DS and SS reduced the stem elongation rate and node addition rate, with DS causing 41% reductions in Pima and 39% and 34% reductions in Upland, respectively. The reductions were smaller under SS (12% for each rate in Pima, and 17 and 6% in Upland, respectively). Under DS and SS, plants allocated more biomass to roots and reproductive organs, with Pima partitioning more to roots than Upland. This study shows that both cotton species can tolerate salinity levels of up to 6 dS m-1 with minimal adverse effects. However, drought stress negatively impacts the growth and development of both species. Additionally, CO2 fertilization helps ameliorate the negative impacts of drought and salinity stress on both cotton species.

I-P87 Physiological and Agronomic Responses of Finger Millet to Heat and Drought Stress

Renganathan Vellaichamy Gandhimeyyan, Chami Rampati Dewage, Mohan K Bista, Dingiswayo Mwanza Raju Bheemanahalli

Department of Plant and Soil Sciences, Mississippi State University, Mississippi State, MS

Finger millet (Eleusine coracana L. Gaertn.) is emerging as a potential game-changer for healthy diets and future resilience, especially given challenges such as adverse crop conditions and reduced arable land resulting from unsustainable practices. Despite being relatively new in the US, finger millet's resilience and health benefits highlight its significance as a climate-resilient, nutritious crop. Studies have shown that finger millet can adapt to stress at the cellular and whole-plant levels, thereby surviving and maximizing production. However, the interactive effects of these stressors on physiology, growth, and grain yield parameters of finger millet have not been studied to date. The present study examined 12 finger millet genotypes exposed to four treatments: control (CNT; 100% irrigation), heat (HS; 38°C daytime), drought (DS; 30% irrigation), and a combination (HS+DS; 38°C+30% irrigation) during the reproductive stage. HS or DS alone reduced stomatal conductance by 65%, leading to a 1-2 °C rise in leaf temperature. When combined as HS+DS, stomatal conductance decreased by 75%, and leaf temperature rose by 4 °C relative to CNT. DS decreased chlorophyll content by 23%, and HS increased flavonol by 24%; the most significant effects were observed under HS+DS, with flavonol increasing by 36% and chlorophyll content decreasing by 40%. DS had a greater impact on reducing grain yield, with a 72% decrease with HS and a 51% decrease without HS. Combined-stressed plants decreased the thousand-grain weight by 29%, while HS plants showed a 22% reduction compared to CNT. These results show that the combined stress had a stronger impact on physiological and agronomic traits than either individual stress.