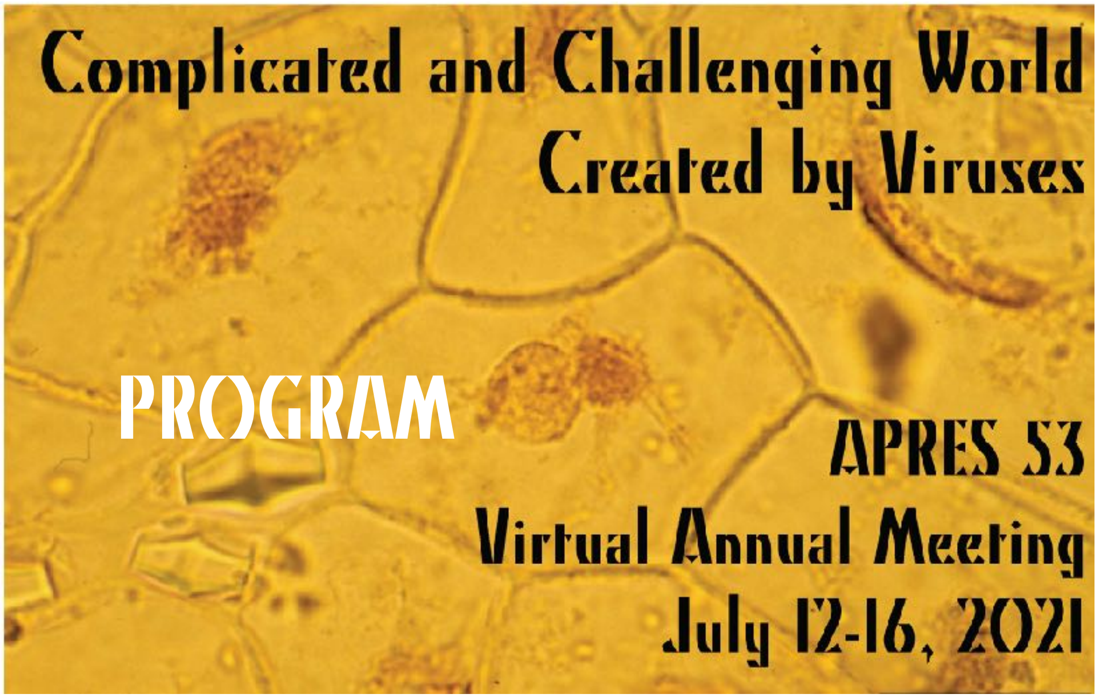
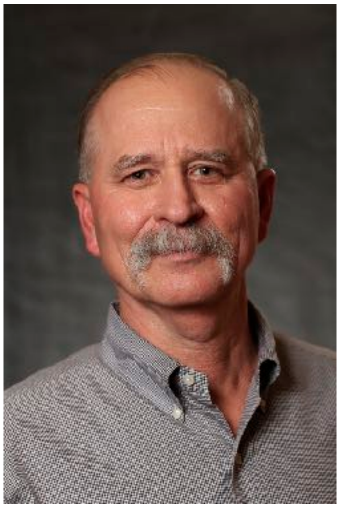
Proceedings
WELCOME TO APRES 53





Gary Schwarzlose
President
APRES

David Jordan
2021 Program Chair
APRES

Jeff Dunne
2021 Technical Program Chair
APRES

APRES 53

Schedule at a Glance
July 12-16, 2021

			USA-EST
Monday	7/12/21	Joe Sugg Competition (M.S.)	8:00-2:30
Monday	7/12/21	Graduate Student Seminar	12:00-1:00
Tuesday	7/13/21	General Session	8:00-9:00
Tuesday	7/13/21	Virus Symposium	10:00-12:30
Tuesday	7/13/21	Lunch	12:30-1:30
Tuesday	7/13/21	Breeding, Genetics, Biotechnology I	1:30-5:30
Wednesday	7/14/21	Joe Sugg Competition (Ph.D.)	8:00-3:15
Wednesday	7/14/21	Economics	3:30-4:15
Wednesday	7/14/21	Food Science	4:15-5:00
Thursday	7/15/21	Breeding, Genetics, Biotechnology II	8:00-11:30
Thursday	7/15/21	Harvesting	11:30-12:00
Thursday	7/15/21	Lunch	12:00-1:00
Thursday	7/15/21	Extension	1:00-2:00
Thursday	7/15/21	Weed Science	2:00-2:15
	7/15/21	Entomology	2:15-2:30
Thursday	7/15/21	Plant Pathology	2:30-4:30
Friday	7/16/21	Physiology, Seed	8:00-9:30
Friday	7/16/21	Production	9:30-10:30
Friday	7/16/21	Business Meeting/Awards	11:00-12:00
Online Content		General Posters	PDFs & Videos
		NPB Graduate Student Competiton Posters	Beginning
		www.apresinc.com	12-Jul-21

July 12, 2021
Schedule of Events

Joe Sugg Award Competition
M.S. Student Division

Moderator: Bob Kemerait
7:00AM - 1:30PM CST
8:00AM - 2:30PM EST

Sponsored by:
North Carolina Peanut Growers Association and National Peanut Board

Time - USA	Speaker	Title
7:00AM CST 8:00AM EST	Ivan Chapu	High-Throughput Phenotyping Enables Indirect Selection for Leaf Spot and Groundnut Rosette Disease Resistance In Peanut Breeding Program in Uganda
7:15AM CST 8:15AM EST	Danielle Essandoh	Identification and Genetic Mapping of Novel Sources of Resistance to Groundnut Rosette and Late Leaf Spot Diseases in a Collection of *Arachis* Wild Derivatives
7:30AM CST 8:30AM EST	Ellah Liwonde	Estimating Aflatoxin in Farmers' In-Shell Groundnuts by Testing Various Groundnuts-Grade Components in Malawi
7:45AM CST 8:45AM EST	Michael Meya	Evaluating the Effectiveness of Aflasafe and Agronomic Practices in Reducing Aflatoxin Contamination and Yield of Groundnuts in Malawi
8:00AM CST 9:00AM EST	Brian Mkanda	Effect Of Boron and Calcium Fertilizer Application and Harvesting Dates on Seed Quality and Yield Components of Groundnuts
8:15AM CST 9:15AM EST	Precious Mtengezo	Response of Groundnuts To Rhizobia Seed Inoculation, Inorganic Fertilizer Application and Plant Density
8:30AM CST 9:30AM EST	Jennifer Abogoom	Assessment of Genetic Purity of Commercially Cultivated Peanut Varieties in Ghana
8:45AM CST 9:45AM EST	Dominic Ndela	Evaluation of Selected F6 Peanut Progenies of Bc3-Derived Introgression Lines and Spanish Parents for Resistance to *Aspergillus flavus* Infection
9:00AM CST 10:00AM EST	Emmanuel Sie	Photogrammetry Enables Indirect Selection and Increase Genetic Gains for Leaf Spot Tolerance in Peanut Breeding Program in Ghana
10:15AM EST	**[BREAK]**	**[BREAK]**

Joe Sugg Award Competition-M.S. Student Division, Continued

Time - USA	Speaker	Title
9:30AM CST 10:30AM EST	Jessica Bell	Sensitivity of *Athelia rolfsii* from Commercial Peanut Fields in Georgia to Tebuconazole and Flutolanil
9:45AM CST 10:45AM EST	Kathleen Costello	A Potential New Source Of Rust (*Puccinia Arachidis)* Resistance From Wild Peanut Relatives *Arachis stenosperma* And *Arachis batizocoi*
10:00AM CST 11:00AM EST	Anushi Deraniyagala	Development of A Taqman Assay for The Detection of Groundnut Bud Necrosis Orthotospovirus on Peanut: A Quarantine Pathogen in the USA
10:15AM CST 11:15AM EST	Ethan Foote	Interactions of Foliar Applied Herbicides with Residual Herbicides and Fungicides
10:30AM CST 11:30AM EST	Katelyn Fritz	Development of Genomic Resources for Increased Folate Content in Peanut *(Arachis hypogaea)*
10:45AM CST 11:45AM EST	Anna Gaudin	Effects of Prohexadione Calcium Application Timing on Peanut (*Arachis hypogaea* L.) Growth and Yield in Mississippi
11:00AM CST 12:00PM EST	**[LUNCH]**	**[LUNCH]**
11:00AM CST 12:00PM EST	**Graduate Student Seminar 12 Noon - 1:00PM**	**Mind, Brain & Education APRES Graduate Student Organization Webinar See Invitation from President Nick Hurdle for Details**
12:00PM CST 1:00PM EST	Hayden Godwin	Tractor Planting Speed and Downforce Effect on Peanut Seed Spacing, NDVI, Plant Stand, and Yield
12:15PM CST 1:15PM EST	Raegan Holton	Screening Various Peanut (*Arachis hypogaea* L.) Genotypes for Aflatoxin Contamination using in vitro Seed Colonization of *Aspergillus flavus*
12:30PM CST 1:30PM EST	Kenyanna Taylor	Effect of Mixing Elemental Sulfur with Demethylation Inhibitors (DMI) And Quinone Outside Inhibitors (Qoi) On the Management Of Late Leaf Spot (*Nothopassalora Personta*) and Rust *(Puccinia Arachidis*) Of Peanut (*Arachis hypogaea*)
12:45PM CST 1:45PM EST	Macie Wheeler	Effects of In-Furrow Fertilizer on Peanut Germination
1:00PM CST 2:00PM EST	Qiong Zhang	Physiological Responses of Peanut Varieties to Mid Season Drought Stress

CST = USA Central Time
EST = USA East Coast Time

July 13, 2021
Schedule of Events

General Session

Presiding: Gary Schwarzlose
7:00AM - 8:30AM CST
8:00AM - 9:30AM EST

Time - USA	Speaker	Title
7:00AM CST 8:00AM EST	**Gary Schwarzlose** **President, APRES**	**APRES 53 - President's Report**
7:20AM CST 8:20AM EST	**Dr. Tim Grey** **Editor, Peanut Science**	**49 Years of Peanut Science**
7:40AM CST 8:40AM EST	**Dr. Timothy Widmer** **National Program Leader** **USDA-ARS**	**Lessons Learned from Covid-19 Can be Applied to Plant Disease Epidemics**

[Break}

Symposium
Complicated and Challenging World Created by Viruses

Moderator: David Jordan
9:00AM - 11:30 AM CST
10:00AM - 12:30PM EST

Time - USA	Speaker	Title
9:00AM CST 10:00AM EST	**Dr. Stephanie Langel** **Duke University**	**Coronaviruses and the Human Body**
9:30AM CST 10:30AM EST	**Dr. Albert Culbreath** **University of Georgia**	**A Brief History of Tomato Spotted Wilt Virus in Peanut**
10:00AM CST 11:00AM EST	**Dr. Mike Deom** **University of Georgia**	**Overview of Groundnut Rosette Disease: Past, Present and Future**
10:30AM CST 11:30AM EST	**Dr. Sudeep Bag** **University of Georgia**	**Approaches to Prevent and Manage Viruses Introduced by Seed**
11:00AM CST 12:00PM EST	**Dr. Hanu Pappu** **Washington State University**	**Tomato Spotted wilt Virus-host Interactions: What is the Host Telling Us?**

[LUNCH BREAK]

Breeding, Genetics & Biotechnology I

Moderator: Jeff Dunne
12:30PM - 4:30PM CST
1:30PM - 5:30PM EST

Time - USA	Speaker	Agenda
12:30PM CST 1:30PM EST	Shyam Tallury	Peanut Germplasm Resources and Genetic Vulnerability Considerations
12:45PM CST 1:45PM EST	David Bertioli	Benefits of International Seed Exchange of Peanut Wild Species: The *Arachis cardenasii* Case
1:00PM CST 2:00PM EST	Carolina Chavarro	A Tree Of Relationships Of Section *Arachis* of Unprecedented Scope And Detail
1:15PM CST 2:15PM EST	Soraya Leal-Bertioli	Mobilizing the Multiple Resistance of *Arachis stenosperma* for Peanut Improvement
1:30PM CST 2:30PM EST	Carolina Ballen-Taborda	Learning from Using Wild Relatives to Incorporate Nematode Resistance in Peanut
1:45PM CST 2:45PM EST	Xuewen Wang	Construction Pan-genome Graph for Peanut species
2:00PM CST 3:00PM EST	**[BREAK]**	**[BREAK]**
2:15PM CST 3:15PM EST	Sudhansu Dash	PeanutBase: Mining genetic and genomics data using the PeanutMine
2:30PM CST 3:30PM EST	Josh Clevenger	Fast, Accurate, Low Coverage Sequencing for Genome Wide Genotyping Large Populations for Genetic Improvement
2:45PM CST 3:45PM EST	Walid Korani	An Efficient Means for Calling Moderate to Long Structural Variations through Pairwise Genomic Comparison and Kmers
3:00PM CST 4:00PM EST	Ye Chu	Genetic Recombination in a New Magic Population of Peanut
3:15PM CST 4:15PM EST	Baozhu Guo	High Resolution Genetic and Physical Mapping of a Peanut Spotted Wilt Disease Resistance Locus, Pswd-1, to Tomato Spotted Wilt Virus (Tswv)
3:30PM CST 4:30PM EST	Charles Chen	Characterization of a New Virginia-type Peanut Cultivar "AU14-34"
3:45PM CST 4:45PM EST	Jianping Wang	Using Crispr/Cas9 In Hairy Roots System to Explore The Gene Functions During Peanut Nodulation
4:00PM CST 5:00PM EST	Daniel O'Connor	Successful Implementation of Speed Breeding Techniques in a Peanut Breeding Program

July 14, 2021
Schedule of Events

Joe Sugg Award Competition

PhD. Student Division

Moderator: Bob Kemerait
7:00AM - 2:00PM CST
8:00AM - 3:00PM EST

Sponsored by:
North Carolina Peanut Growers Association and National Peanut Board

Time - USA	Speaker	Title
7:00AM CST 8:00AM EST	Esther Achola	Genome Wide Association Studies Reveal Novel Loci For Resistance To Groundnut Rosette Disease In Cultivated Peanut (*Arachis Hypogaea* L.)
7:15AM CST 8:15AM EST	Lutangu Jethrow Makweti	Understanding the Genetics of Resistance to Groundnut Rosette Disease
7:30AM CST 8:30AM EST	Stephen Arthur	Growth and Yield Response of Peanut to Pest and Crop Management Packages in Ghana -or- Benefits of Peanut – Cereal Rotation and Inputs Systems on Maize Growth and Yield in Northern Part of Ghana
7:45AM CST 8:45AM EST	Ahmed Seidu	Influence of Geographical Location and Time of Planting on Pest Densities and Yield of Peanut Varieties in Ghana
8:00AM CST 9:00AM EST	Chad Abbott	Peanut Variety Response to Brake®
8:15AM CST 9:15AM EST	Samuele Lamon	Estimation of Double Reduction in Segmental Allotetraploid Peanut
8:30AM CST 9:30AM EST	Mahesh Bashyal	Do Belowground Peanut Plant Parts Contribute N credits to Subsequent Crops?
8:45AM CST 9:45AM EST	Hope Becton	Dispersal Of *Nothopassalora Personata* from an Inoculum Source
10:00AM EST	**[BREAK]**	**[BREAK]**
9:15AM CST 10:15AM EST	Justin Calhoun	Determining Residual Length of Control for Soil-Applied Herbicides in Peanut
9:30AM CST 10:30AM EST	Yi-Ju Chen	Thrips and Tomato Spotted Wilt Orthotopsovirus Resistance on Wild Relatives by Greenhouse Evaluation

Joe Sugg Award Competition-PhD. Student Division, Continued

Time - USA	Speaker	Title
9:45AM CST 10:45AM EST	Leslie Commey	Insoluble polyphenol mediate Aspergillus flavus resistance in peanut
10:00AM CST 11:00AM EST	Maricel Gonzales	Introgression of wild Arachis cardenasii Alleles into Cultivated Peanut to Confer Resistance to Early and Late Leaf Spot
10:15AM CST 11:15AM EST	Marco Goyzueta	Utilizing QTLseq pipeline to identify genetic regions linked to the black pod trait.
10:30AM CST 11:30AM EST	Nick Hurdle	Response of Non-irrigated Peanut to Multiple Rate Delayed Flumioxazin Applications
10:45AM CST 11:45AM EST	Naveen Kumar	Phenotyping and genotyping RIL population of Virginia type peanut for drought tolerance in Virginia Carolina region
11:00AM CST 12:00PM EST	**[LUNCH]**	**[LUNCH]**
12:00PM CST 1:00PM EST	Pin-Chu Lai	Spatial and Temporal Spread of Tomato Spotted Wilt Orthotospovirus (TSWV) in Two Runner Type TSWV-Resistant Peanut Cultivars
12:15PM CST 1:15PM EST		
12:30PM CST 1:30PM EST	Cassondra Newman	Genomic Characterization of North Carolina State University's Germplasm and Breeding Lines
12:45PM CST 1:45PM EST	Alan Peper	Survey, Isolate and Apply Calcite Dissolving Bacteria as a New Form of Calcium Source.
1:00PM CST 2:00PM EST	Chiara Rossi	Photosynthetic Efficiency and Yield of Peanut Plants Treated with Dodine
1:15PM CST 2:15PM EST	Cheng-Jung Sung	Genome-Wide Association Study on Peanut Water Deficit Stress Tolerance Using the U.S. Minicore to Develop Improvement for Breeding
1:30PM CST 2:30PM EST	Yun-Ching Tsai	A Novel Source of Resistance to Peanut Stem Rot from Wild-derived Allotetraploid ValSten1 Identified by Greenhouse and Field Evaluation Methods
1:45PM CST 2:45PM EST	Xing Wei	Comparison of standard and newly registered peanut fungicides against Athelia rolfsii through a laboratory bioassay using detached plant tissues
2:00PM CST 3:00PM EST	**[BREAK]**	**[BREAK]** **Breakout Sessions Resume at 3:30**

CST = USA Central Time
EST = USA East Coast Time

Economics

Breakout Session

Moderator: David Jordan
2:30PM - 3:15PM CST
3:30PM - 4:15PM EST

Time - USA	Speaker	Title
2:30PM CST 3:30PM EST	Marshall Lamb	Cost of Aflatoxin to the United States Peanut Industry
2:45PM CST 3:45PM EST	Audrey Luke-Morgan	Risk Management Decisions from an Economic Perspective: The Case of Crop Insurance for U.S. Peanut Enterprises
3:00PM CST 4:00PM EST	Amanda Smith	Valuing Disease Resistance: A Comparison of the Florunner and GA16HO Cultivars

FOOD SCIENCE

Breakout Session

Moderator: David Jordan
3:15PM - 4:00PM CST
4:15PM - 5:00PM EST

Time - USA	Speaker	Title
3:15PM CST 4:15PM EST	Lisa Dean	Peanuts as a Source of Vegetable Protein: Past Successes and Future Challenges.
3:30PM CST 4:30PM EST	Julie Marshall	Proteomic Analysis of Raw and Roasted *Arachis hypogaea* Seeds

July 15, 2021
Schedule of Events

Breeding, Genetics & Biotechnology II

Breakout Session

Moderator: Jeff Dunne
7:00AM - 10:15AM CST
8:00AM - 11:15AM EST

Time - USA	Speaker	Title
7:00AM CST 8:00AM EST	Justus Chintu	Release of Two Early Maturing Spanish Peanut Varieties for Production in Malawu
7:15AM CST 8:15AM EST	Japheth Neindow	Genetic Variation for Drought Tolerance and Oil Quality Traits in a Groundnut Population Using Sensing Technologies
7:30AM CST 8:30AM EST	Richard Oteng-Frimpong	Enhancing the Efficiency in Data Collection in Peanut Through Whole-Plot Data Capture: the Case of Above Ground Biomass and Foliar Diseases
7:45AM CST 8:45AM EST	Nino Brown	Evaluating the potential of UAV-based imagery for detailed measurement of above-ground growth characteristics in a peanut breeding application
8:00AM CST 9:00AM EST	Barry Tillman	The Effects Plant Type and Seeding Density on Plant Growth and Pod Yield
8:15AM CST 9:15AM EST	Ryan Andres	Understanding Variation in Oleic Acid Content of High-Oleic Virginia-type Peanut
9:30AM EST	**[BREAK]**	**[BREAK]**
8:45AM CST 9:45AM EST	Alexandre-Brice Cazenave	Using Multispectral Drone Camera to Differentiate Drought Tolerant Recombinant Inbred Lines of Peanut Grown under Rainout Shelters
9:00AM CST 10:00AM EST	Mark Burow	Field Measurements, Yield, and Grade of the U.S. Minicore under Water Deficit Stress.
9:15AM CST 10:15AM EST	Phat Dang	Phenotyping the US Mini-core Collection to Identify Drought Tolerant Peanut Genotypes Using Environmental Control Plots
9:30AM CST 10:30AM EST	Alicia Massa	Progress in the Evaluation of Peanut Germplasm to Enable Selection for Aflatoxin Resistance
9:45AM CST 10:45AM EST	Jeffrey Dunne	Characterize leaf spot resistant loci through image analysis of advanced breeding lines in the NCSU peanut breeding program
10:00AM CST 11:00AM EST	C. Corley Holbrook	Release of Peanut Germplasm Lines with Resistance to Late Leaf Spot

Thursday, July 15, 2021, Continued

Harvesting

Breakout Session

Moderator: David Jordan
10:30AM - 11:00AM CST
11:30AM - 12:00PM EST

Time - USA	Speaker	Title
10:30AM CST 11:30AM EST	Daniel Anco	Sound Splits as Influenced by Seed Size for Runner and Virginia Market Type Peanut Graded on a Reciprocating Sheller
10:45AM CST 11:45AM EST	Renee Arias	The White Stuff on Properly Stored Peanuts Identified, Need to Reassess Boundaries?

LUNCH BREAK
12:00PM - 1:00PM EST

Extension

Breakout Session

Moderator: David Jordan
12:00PM - 1:00PM CST
1:00PM - 2:00PM EST

Time - USA	Speaker	Title
12:00PM CST 1:00PM EST	Kathryn Beasley	Chayote Contests and Tamarind Butter: The Natural Agricultural Range of Florida and its Role in Home Demonstration Programming, 1915-1930
12:15PM CST 1:15PM EST	Kaylyn Groce	Measuring Peanut Sustainability Production Practices Using the Field to Market Fieldprint Calculator in Georgia
12:30PM CST 1:30PM EST	Bill Tyson	Comparison of Peanut White Mold Fungicide Programs in Bulloch County, Georgia
12:45PM CST 1:45PM EST	Kris Balkom	Evaluation of Twin Row Spacings and Seeding Rates for Runner Peanuts

Weed Science

Breakout Session

Moderator: David Jordan
1:00PM - 1:15PM CST
2:00PM - 2:15PM EST

Time - USA	Speaker	Title
1:00PM CST 2:00PM EST	Eric Prostko	Peanut Response to Soil-Applied Liberty (Glufosinate)

Thursday, July 15, 2021, Continued

Entomology

Breakout Session

Moderator: David Jordan
1:15PM - 1:30PM CST
2:15PM - 2:30PM EST

Time - USA	Speaker	Title
1:15PM CST 2:15PM EST	Sally Taylor	Honey Bee Foraging in a Mixed Crop Landscape

Plant Pathology

Breakout Session

Moderator: David Jordan
1:30PM - 4:00PM CST
2:30PM - 5:00PM EST

Time - USA	Speaker	Title
1:30PM CST 2:30PM EST	Timothy Brenneman	Effects of Dynasty and Rancona Seed Treatments and In Furrow Sprays on Peanut Plant Stands, Diseases and Pod Yield
1:45PM CST 2:45PM EST	Robert Kemerait	Assessment of Inpyrfluxam as a Component of a Program for the Management of Peanut Diseases
2:00PM CST 3:00PM EST	Tucker Price	2020 Peanut White Mold Fungicide Program Comparison in Cook County, Georgia
2:15PM CST 3:15PM EST	Emran Ali	Molecular Detection, Gene Expression and Phylogenetic Analyses of Aflatoxin Producing of Aspergillus flavus Strains Isolated from Peanut Seeds in Georgia
2:30PM CST 3:30PM EST	Jake Fountain	New Reference Genomes and Comparative Genomics Analyses in *Aspergillus flavus*
2:45PM CST 3:45PM EST	Jennifer Chagoya	In Vitro Fungicide Sensitivity of Pythium and Rhizoctonia Isolates Associated with Peanut Pod Rot
3:00PM CST 4:00PM EST	Austin Hagan	Comparison of Fluopyram and Aldicarb for Root-Knot Nematode and Disease Control along with Yield Response of Peanut, 2013 to 2020
3:15PM CST 4:15PM EST	Amanda Strayer-Scherer	Evaluation of Alternatives to Chlorothalonil for Peanut Disease Control in Southeast Alabama

July 16, 2021
Schedule of Events

Physiology, Seed

Breakout Session

Moderator: David Jordan
7:00AM - 8:30AM CST
8:00AM - 9:30AM EST

Time - USA	Speaker	Title
7:00AM CST 8:00AM EST	Alain Audebert	High Throughput Phenotyping Methods on Peanuts Fields
7:15AM CST 8:15AM EST	Li Yang	Are Calcite Dissolving Bacteria a New Player in the Soil Calcium Cycle?
7:30AM CST 8:30AM EST	James Rhoads	A Comparative Analysis of Peanut Seed Systems: Searching for Innovation to Sustainably Unlock Improved Genetics
7:45AM CST 8:45AM EST	Cristiane Pilon	Water Management Strategy in Peanut for Improved Seed Physiological Quality
8:00AM CST 9:00AM EST	Christopher Butts	Fruit Initiation Response to Early Season Water Stress
8:15AM CST 9:15AM EST	Maria Balota	Vegetation Indices Enable Indirect Phenotyping of Peanut Physiologic and Agronomic Characteristics.

Production

Breakout Session

Moderator: David Jordan
8:30AM - 9:30 AM CST
9:30AM - 10:30AM EST

Time - USA	Speaker	Title
8:30AM CST 9:30AM EST	Wezi Mhango	Effects of Fungicides application and Weed Management Methods on performance of groundnut (Arachis hypogea)
8:45AM CST 9:45AM EST	W. Scott Monfort	Impact of fungicide programs and delayed harvest on yield and quality of peanut (*Arachis hypogaea* L.).
9:00AM CST 10:00AM EST	R. Scott Tubbs	Replanting of Gaps in Peanut Rows
9:15AM CST 10:15AM EST	Simerjeet Virk	On-Farm Evaluation of Nozzle Types for Peanut Pest Management Using Commercial Sprayers

APRES Business Meeting

July 16, 2021

10:00AM - 11:00AM CST
11:00AM - 12:00PM EST

Time - USA	Speaker	Agenda
10:00AM CST **11:00AM EST**	**Gary Schwarzlose APRES President 2020-21**	**Call To Order**
		Awards Announcements
		*NPB Graduate Student Poster Competition Winner
		*Joe Sugg Award - M.S. Student Division
		*Joe Sugg Award - PhD. Student Division
		*Corteva Agriscience Award for Excellence in Education
		*Coyt T. Wilson Distinguished Service Award
		*Fellow of the Society
		Announcement of 2021-22 Board of Directors
		Outgoing Board Member Recognition
		Closing Remarks
		Passing of the Gavel
	David Jordan APRES President 2021-22	**President's Award Presentation**
		Goals for 2021-22 **Committee Chair Leadership**
		Nominating Committee Assignment -SW Rep Nominee to Serve Mark Burow Remaining Term -Industry Rep Nominee to Replace Retiring Bob Sutter
		2022 Annual Meeting -July 12-14; Omni Las Colinas Resort, Dallas, TX
		Program Committee Assignment -Task Program Committee Chair to Fill His Committee
		Formation of ad hoc Committee to Review APC Proposal
		Closing of 53rd Annual Meeting

Posters

APRES Online Content

Posters will be Available for Viewing July 12, 2021
www.apresinc.com

General Posters

Last Name	First Name	General Poster Title	Links
Abney	Mark	The Reliability of DAS-ELISA for Detecting Tomato Spotted Wilt Orthotospovirus in Leaf and Root Tissue from Symptomatic and Asymptomatic Peanut Plants	PDF / YouTube Video
Arthur	Stephen	Benefits of Peanut – Cereal Rotation and Inputs Systems on Maize Growth and Yield in Northern Part of Ghana	PDF / YouTube Video
Bennett	Rebecca	Response to Drought Stress in a Subset of the U.S. Peanut Mini-core Evaluated in Three States	PDF / YouTube Video
Bowen	Samantha	Quantifying Acetochlor Thermal Stability	PDF / YouTube Video
Brandenburg	Rick	Enhancing the Peanut Value Chain through Peanut Innovation Lab Partnerships: Examples of a Production Guide in Malawi using Research Results from Ghana	PDF / YouTube Video
Buol	Greg	Contrasts of Peanut Risk Management Tools for Peanuts in Argentina, Ghana, India, Malawi, and North Carolina	PDF / YouTube Video
Campbell	Howard	Disease and Yield Response of Selected Peanut Cultivars to Low and High Input Fungicide Programs in Southeast Alabama	PDF / YouTube Video
Carter	Ethan	2021 Panhandle Row Crops Update Series: Connecting Producers Virtually to Research from Three Land Grant Institutions	PDF / YouTube Video
Cason	John	Screeing for Amino Acid Content in Peanut (*Arachis hypogaea* L.) Using Raman Spectroscopy	PDF / YouTube Video
Chamberlin	Kelly	Identification of U.S. Germplasm Resistant to Peanut Smut	PDF / YouTube Video
Rossi	Chiara	Plant Growth and Leaf Spot Control of Peanut Plants Treated with Different Fungicide Programs	PDF / YouTube Video
Danso	Benjamin Aboagye	Validation and Utilization of SNP Markers for Introgression of Late Leaf Spots Resistance Genes in Peanut	PDF / YouTube Video
Devota	Pratap	Response of Peanut to Exposure Timing and 2,4-D plus Glyphosate Rate	PDF / YouTube Video
Dotray	Peter	Peanut Response to Multiple Exposures of Low Rates of Enlist Duo®	PDF / YouTube Video
Edwards	Phillip	Assessment of Peanut Fungicide Programs and Sulfur in Irwin County, GA, 2020	PDF / YouTube Video

Last Name	First Name	General Poster Title	Links
Faye	Issa	Analysis of Vegetative and Reproductive Traits Revealed Positive Transgressions and Strong Correlations Between Traits in a Population of Recombinant Inbred Lines in Groundnut (*Arachis Hypogaea* L.)	PDF / YouTube Video
Foote	Bill	Interesting Issues Associated with Varieties and Seed Quality in North Carolina and Virginia over the Past Decade	PDF / YouTube Video
Fountain	Jake	Identification of Peanut Late Leaf Spot Resistance locus, pRPP13-like, using Nested Association Mapping Approach	PDF / YouTube Video
Grichar	W. James	Peanut Response to Diclosulam in the Texas Peanut Growing Areas Pyroxasulfone	PDF / YouTube Video
Hayes	Brian	Evaluating Peanut Fungicide Programs in Mitchell County, Georgia	PDF / YouTube Video
Hoisington	Dave	Feed the Future Innovation Lab for Peanut Employs Novel Approach to Research During Pandemic Travel Restrictions	PDF / YouTube Video
Hollifield	Stephanie	Grower Education on the Effect of Tillage Practice Related to Peanut Water Availability and Usage	PDF / YouTube Video
Hopkins	Mark	Genesis and Characterization of New Interspecific Hybrids to Increase Genetic Diversity in Cultivated Peanut.	PDF / YouTube Video
Ingram	Sydni	Effect of Insecticide, Sodium Chloride, and Fertilizer Solutions on the Invasive Snail, *Bulimulus sporadicus*	PDF / YouTube Video
Jordan	David	Developing Weed Management Risk Tools for Crops in North Carolin a	PDF / YouTube Video
Jordan	David	Influence of Heat Unit Accumulation and Low Temperatures on Pod Maturation: An Example from North Carolina during the 2020 Growing Season	PDF / YouTube Video
Li	Steve	Integrated Weed Management Practices To Control als and ppo-Inhibitor Resistant Palmer Amaranth In Peanut	PDF / YouTube Video
Marshall	Julie	Analysis of Total Fat and Total Protein Percentages from 2018-2020	PDF / YouTube Video
Marshall	Michael	Evaluation of Selected Herbicide Programs for Broadleaf Weed Management in Peanut.	PDF / YouTube Video
Miller	Jennifer	Economic Impact of Increased Seeding Rates in Single Row Peanut in Southeast Georgia	PDF / YouTube Video
Nboyine	Jerry	Developing Risk Management Tools to Help Farmers Minimize Risk in Peanut Production in Two Agro-ecologies in Ghana	PDF / YouTube Video
Pham	Hanh	Marker Analysis of Breeding Lines for High Oleic Oil and Nematode Resistance	PDF / YouTube Video
Ravelombola	Waltram	Unmanned Aerial System (UAS) Phenotyping for Organic Peanuts	PDF / YouTube Video
Ravelombola	Waltram	Field Evaluation for Organic Peanuts in North Texas	PDF / YouTube Video
Royals	Brian	Thrips and Peanut Response to Imidacloprid and Fluopyram Applied at Planting	PDF / YouTube Video
Sanchez-Dominguez	Samuel	Evaluation of Fifteen Peanut lines and Commercial Varieties under Dry Conditions in Summer 2019, in State of Morelos, Mexico	PDF / YouTube Video

Last Name	First Name	General Poster Title	Links
Shumaker	Jaime	Potential Use of RAMAN Spectroscopy for Trait Indetification in Peanut (*Arachis hypogaea* L.)	PDF / YouTube Video
Sine	Bassirou	High Throughput Functional Traits to Screen Peanut Productivity and Adaptation in Senegal	PDF / YouTube Video
Sobolev	Victor	Simple Non-Destructive Method for Quantification of Aflatoxins in Individual Peanut (*Arachis* spp.) Seeds	PDF / YouTube Video
Yahaya	Iddrisu	Impact of Adoption of Improved Varieties on Household Share of Peanut Income in Northern Ghana	PDF / YouTube Video
Zurweller	Brendan	Peanut Cultivar Response to Residual Soil Test Potassium Amounts in North Mississippi	PDF / YouTube Video

National Peanut Board

Graduate Student Poster Competition

Last Name	First Name	Graduate Student Poster Title	Links
Aigner	Benjamin	Effects of Landscape Context and Environmental Factors on Injury to Peanut Caused by the Subterranean Pest *Pangaeus bilineatus* in South Georgia.	PDF / YouTube Video
Bediako	Kwabena Asare	Response of Peanut Genotypes to Pre-Harvest Aflatoxin Contamination in Ghana	PDF / YouTube Video
Campbell	Rebecca	Aroma Profile of Nineteen Cultivars of Roasted Peanuts	PDF / YouTube Video
Carrillo	David	Breeding Spanish Peanuts (*Arachis hypogaea* L.) for Organic Peanut Production In West Texas	PDF / YouTube Video
de Souza Rodrigues	Juliana	The Effects on Peanut Seed Germination Using Plant Growth Regulators Under Different Temperatures	PDF / YouTube Video
Dudak	Jennifer	Weed Management Programs in Peanut	PDF / YouTube Video
Kemigisha	Daisy	Drivers of Youth Participation in Groundnut Value Chains in Nwoya and Tororo Districts, Uganda	PDF / YouTube Video
Luo	Ziliang	Identifying Genomics Regions And Evaluating The Epistasis Controlling Stem Rot Resistance In Cultivated Peanut (*Arachis Hypogaea*)	PDF / YouTube Video
Mirembe	Ruth Martha	Use of Photovoice to Assess Quality and Safety of Peanuts along the Value Chain: A case of Youth in Nwoya and Tororo districts, Uganda	PDF / YouTube Video
Moreno	Leticia	Physiological Quality of Peanut Seeds Impacted by Drought During the Reproductive Development	PDF / YouTube Video
Skipper	April	Evaluating Sampling Methods for Two Rootworm Pests, *Diabrotica undecimpunctata* and *Diabrotica balteata*, and Determining Their Relative Abundance in Georgia Peanut Fields	PDF / YouTube Video

Last Name	First Name	Graduate Student Poster Title	Links
Ssendagire	Henry	Identifying Alternative Host(s) of Groundnut Rosette Disease Virus Complex	PDF / YouTube Video
Treadway	Zachary	Anthem Flex Use in Peanut	PDF / YouTube Video
Wang	Yichun	Epigenetic Gene Expression Regulation of Nsp2, A Gras Family Transcriptional Factor Controlling Peanut Nodulation	PDF / YouTube Video
Whittenton	Joseph	Using Remote Sensing to Predict Peanut Pod Maturity and	PDF / YouTube Video
Yang	Xinlei	QTL Mapping and QTL×Environment Interaction Analysis of Pod and Seed Related Traits in Cultivated Peanut (*Arachis hypogaea* L.)	PDF / YouTube Video

Complicated and Challenging World Created by Viruses

APRES 53 Invited Speakers || July 13, 2021

Dr. Tim Grey, University of Georgia

Professor and Interim Department Head, University of Georgia
Department of Crop and Soil Sciences

Ph.D. Auburn University, Soil Science and Agronomy, 1996
M.Sc – Auburn University, Agronomy and Crop Science, 1992
B.Sc – University of Kentucky, 1986

Dr. Grey's duties include research into herbicide dissipation from soil and polyethylene mulch covers used in vegetable production, physiological crop and weed responses to herbicides in field, greenhouse, and laboratory experiments, and using rotational practices for the production of field and vegetable crops.

He is editor of the journal *Peanut Science* since 2011, and an associate editor of *Weed Science* since 2008.

Dr. Grey received the Coyt T. Wilson Distinguished Service Award (2019), Dow AgroSciences Award for Excellence in Teaching (2016), Dow AgroSciences Award for

Dr. Tim Widmer, USDA-ARS

Dr. Widmer is the USDA/ARS National Program Leader for Plant Health. He is the point of contact for all USDA/ARS projects related to plant health and is involved also with antimicrobial resistance, soil health, invasive species and issues related to agricultural biosecurity. He has been with USDA/ARS since 2000, working previously as a research plant pathologist at the European Biological Control Laboratory in Montpellier, France and the Foreign Disease and Weed Science Research Unit Ft. Detrick, Maryland.

Dr. Widmer received his PhD in Plant Pathology at the University of Florida, Gainesville, Florida in 1996 and had a post-doctoral position at Cornell University, Geneva, NY.

Stephanie Langel, PhD

Dr. Stephanie Langel, Duke University

Medical Instructor, Duke University School of Medicine
Ph.D. - The Ohio State University 2013-2018
M.S. - Virginia Polytechnic and State University (Virginia Tech) 2011-2013
B.S. - The Ohio State University 2007-2011

Research focuses on understanding maternal and neonatal immune responses in order to prevent neonatal viral infections. Current research efforts focused on maternal oral influenza and SARS-CoV-2 vaccination for generation of potently neutralizing secretory IgA antibodies in breast milk, which is part of an awarded Gates Foundation grant for which Stephanie is the principal investigator

Host of podcast 'Immune' - a monthly podcast about the host defense systems that protect against disease.

Dr. Albert Culbreath, University of Georgia

Professor, University of Georgia
Department of Plant Pathology
Ph.D. North Carolina State University, 1989. Major: Plant Pathology. Minor: Plant Breeding
M. S. Auburn University, 1985. Major: Plant Pathology (Nematology)
B. S. Auburn University, 1982. Major: Botany
Assoc. Sci. Roane St. Community College, 1980. Major: Science

Current research efforts are directed toward epidemiology and management of foliar fungal diseases and tomato spotted wilt virus (TSWV) of peanut. Particular areas of emphasis include determining the effects of partial resistance to TSWV on disease progress of spotted wilt and the effects of partial resistance to Cercospora arachidicola and Cercosporidium personatum on disease progress of early and late leaf spot of peanut. We work closely with several peanut breeders programs in efforts to develop cultivars with resistance to these pathogens. Substantial efforts are directed toward fungicidal control of early and late leaf spot diseases of peanut, with particular emphasis on fungicide resistance management.

Dr. Mike Deom, University of Georgia

Professor, University of Georgia
Department of Plant Pathology

Ph.D. in Microbiology, Saint Louis University, 1985
M.A. in Microbiology, Southern Illinois University, 1978
B.A. in Microbiology, Southern Illinois University, 1974

Virus-host interactions: genetic, biochemical, and molecular mechanisms required for understanding how geminivirus C4 proteins induced hyperplasia.

Development and dissemination of improved groundnut varieties with traits to mitigate biotic and abiotic stresses, while simultaneously adding traits to improve nutrition and marketability.

Dr. Sudeep Bag, University of Georgia

Assistant Professor, University of Georgia
Department of Plant Pathology

Ph.D. in Plant Pathology, Washington State University, Pullman, 2013
M.Sc. in Biotechnology, Indira Gandhi Agricultural University, Raipur, India, 2001
B.Sc. in Microbiology, Bilaspur Central University, Bilaspur, India, 1999

Research interest is in the development of management strategies for virus diseases on economically important crops using interdisciplinary approaches.

The primary focus is currently on etiology, epidemiology, and genomics of emerging and re-emerging viruses in vegetable crops; understanding the crosstalk between the host-virus-vector system and utilizing it to mitigate disease; and application of recent advances in genomics and molecular biology tools for virus disease management.

Dr. Hanu Pappu, Washington State University

Professor, Washington State University
Department of Plant Pathology

Ph.D. - University of Alberta, Edmonton, Canada
M.Sc. - Indian Agricultural Research Institute, New Delhi, India
B.Sc. - (Ag). A.P. Agricultural University, Agricultural College, Bapatla, India

Pappu leads a highly productive and internationally recognized research program in genomics and biotechnology of RNA and DNA viruses that are economic constraints to the production of several horticultural and field crops.

Citrus tristeza virus (CTV) is considered one of the most important viral pathogens of tree fruits, and Pappu was the first to decipher its genome structure and organization and structure–function relationships. His work laid the foundation for subsequent research on the molecular biology and host–CTV interactions.

Pappu is especially noted for his research on thrips-transmitted tospoviruses. Globally, these viruses cause more than $1 billion in crop losses annually to field and horticultural crops. Pappu developed an internationally recognized research and extension program on *Tomato spotted wilt virus* (TSWV), the most common and economically important tospovirus in the United States.

APRES

AMERICAN PEANUT RESEARCH & EDUCATION SOCIETY, INC.

Business Meeting & Awards Ceremony
July 16, 2021

Program Committee

- Thanks to the Entire Program Committee
- Chairman – David Jordan
- Technical Committee – Jeff Dunne
- Local Arrangements – Dan Anco
- Spouses’ Activities – David Langston
- Fun Run – David Langston
- Sponsors who made this all possible

Nominating Committee

- Chairman, Past President Barry Tillman
- New Board Members:
  - David Jordan, President
  - Mark Burow, President-elect
  - Gary Schwarzlose, Past President
  - Kira Bowen, SE University Rep
  - William Pearce, Industry Rep-Sheller
  - Cassie Newman, APRES GSO Rep

Nominating Committee

- Chairman, Past President Barry Tillman
- Recognition of retiring Board members:
  - Barry Tillman
  - Henry Mclean
  - Bob Kemerait
  - Bob Sutter

Awards Ceremony

- Coyt T. Wilson Distinguished Service Award
- Bailey Award
- Joe Sugg Graduate Student Award Competition
- Corteva™ Agriscience Award for Education
- APRES Fellow

Coyt T. Wilson Distinguished Service Award

This award recognizes an individual who has contributed two or more years of distinguished service to the American Peanut Research and Education Society, given annually in honor of Dr. Coyt T. Wilson who contributed freely of his time and service to the organization in its formative years. He was a leader and advisor until his retirement in 1976.

The award shall consist of a $1,000 cash award and a bronze and wood plaque both provided by the Society and presented at the annual meeting.

Coyt T. Wilson Distinguished Service 20 Award Recipient

- Bob Kemerait

Joe Sugg Graduate Student Competition

- Chairman, Bob Kemerait
- 22 Papers submitted
- 18 Presented
- Largest number of competitors in APRES history
- New Masters and PhD Divisions
- Sponsored by North Carolina Peanut Growers Association and National Peanut Board

Joe Sugg Award Graduate Student Competition – PhD. Division

- 1st Place
- $500 Award
- Jake Fountain, University of Georgia
- Paper Title:

  Potential Roles of Environmental Oxidative Stress in Aflatoxin Production Revealed in the Aspergillus flavus Transcriptome

Joe Sugg Award Graduate Student Competition – M.S Division

- 1st Place
- $500 Award
- Claire Klevorn, North Carolina State University
- Paper Title:

  Variation in O/L Ratio Demonstrated among High-Oleic Spanish-type peanuts

National Peanut Board
Graduate Student Poster Competition

- 1st Place
- $500 Award
- Claire Klevorn, North Carolina State University
- Paper Title:

  Variation in O/L Ratio Demonstrated among High-Oleic Spanish-type peanuts

Corteva™ Agriscience Education Award

- Chairman, David Jordan

The award will recognize an individual or team for excellence in educational programs. The award may recognize an individual (team) for career performance or for an outstanding current educational achievement of significant benefit to the peanut industry. One award will be given each year provided worthy nominees are nominated. The recipient will receive an appropriately engraved plaque and a $1,000 cash award. In the event of team winners, one plaque will be presented to the team leader and other team members will receive framed certificates. The cash award will be divided equally among team members.

Corteva Agriscience Education Award
2021 Recipient – Team

- Bob Sutter
- Dell Cotton
- Marianne Catalano

APRES Fellow

- Chairman, David Jordan

Fellows are active members of the Society who have been nominated to receive the honor of fellowship by other active members, recommended by the Fellows Committee, and elected by the APRES Board of Directors. Up to three active members may be elected to fellowship each year.

APRES Fellow
2021 Recipient

- Bob Sutter

Past President's Award

Gary
Schwarzlose

Peanut Variety Response to Brake®

C.C. ABBOTT*, E.P. PROSTKO, Dept. of Crop & Soil Sciences, The University of Georgia, Tifton, GA 31793.

Brake® (fluridone), manufactured by SePRO Corporation, is an herbicide under evaluation for potential preemergence (PRE) use in peanut. Brake® was recently registered for PRE use in cotton and has been sold for numerous years in the aquatic weed control market as Sonar®. Therefore, the objective of this research was to determine the effects of Brake® 1.2SL on the growth, development, and yield of several peanut varieties when applied PRE at 0, 16, 32 and 64 oz/A. Irrigated, small-plot field trials were conducted in 2019 and 2020 at the UGA Ponder Research Farm near Ty Ty, Georgia. Treatments were arranged in a randomized complete block design with a three (variety) X four (rate) factorial arrangement with four replications. Peanut varieties included GA-06G, GA-16HO, and GA-18RU. All plot areas were maintained weed-free using a combination of labeled herbicides and hand-weeding. Data collected included Brake® effects on peanut density, foliar bleaching, plant stunting, and yield. All data were subjected to ANOVA using PROC GLIMMIX and means separated using the Tukey-Kramer Method (P=0.05). Peanut density was significantly reduced by 19% at the 32 oz/A rate and by 46% at the 64 oz/A rate. Foliar bleaching ranged from 11 to 35% with all rates above 0 oz/A. GA-16HO had significantly more bleaching when compared to GA-18RU, but was not significantly different from GA-06G. Brake® at 32 oz/A and 64 oz/A caused significant peanut stunting (17% and 44%, respectively). When averaged over variety, peanut yield was not significantly reduced at the 16 oz/A or 32 oz/A rate. However, significant yield losses of 33% occurred when Brake® was applied at 64 oz/A. Based upon these results, Brake® 1.2SL should not be recommended for use in peanut at rates greater than 16 oz/A.

The Reliability of DAS-ELISA for Detecting Tomato Spotted Wilt Orthotospovirus in Leaf and Root Tissue from Symptomatic and Asymptomatic Peanut Plants

P.-C. LAI, G.D. BUNTIN, R. SRINIVASAN, Department of Entomology, The University of Georgia, Griffin, GA 30223, S. BAG, Department of Plant Pathology, The University of Georgia, Tifton, GA 31793 AND **M.R. ABNEY***, Department of Entomology, The University of Georgia, Tifton, GA 31793

Thrips-transmitted tomato spotted wilt orthotospovirus (TSWV) causes spotted wilt disease in peanut. Double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) is commonly used to detect TSWV. Previous studies detected higher rates of TSWV infection in peanut root tissue than leaf tissue using DAS-ELISA and suggested that root tissue might be a better sink for TSWV than leaf tissue. Nevertheless, the mechanism(s) responsible for higher TSWV detection rates in root tissue than leaf tissue in these studies remains unknown. Asymptomatic TSWV infection has been documented in peanut, and it is not clear if TSWV detection in asymptomatic plants is affected by the type of tissue tested. To address these questions, TSWV detection using DAS-ELISA in leaf and root tissue from symptomatic and asymptomatic plants was cross-validated with reverse transcription polymerase chain reaction (RT-PCR) and quantitative RT-PCR (qRT-PCR). TSWV was also quantitated by qRT-PCR in leaf and root tissue. TSWV was detected by DAS-ELISA, RT-PCR, and qRT-PCR at similar rates in leaf and root tissue from symptomatic plants and in leaf tissue from asymptomatic plants. However, TSWV was detected at a significantly higher rate in root tissue from asymptomatic plants using DAS-ELISA compared to RT-PCR and qRT-PCR. This indicates that using DAS-ELISA for TSWV detection in root tissue from asymptomatic plants can result in overestimation of TSWV infection. Leaf tissue had higher TSWV loads than root tissue from symptomatic plants, while TSWV loads in leaf and root tissue from asymptomatic plants did not differ and were low relative to symptomatic plants. These findings suggest that leaf tissue is a better choice than root tissue for TSWV detection in peanut using DAS-ELISA.

Assessment of Genetic Purity of Commercially Cultivated Peanut Varieties in Ghana

J. ABOGOOM* and R. AKROMAH, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana and D.L. JORDAN, North Carolina State University, Raleigh, NC 27695.

Simple Sequence Repeat (SSR) markers were used to determine the genetic purity of two commercially cultivated peanut varieties in Ghana using farmer-saved seeds. Twenty-eight farmer-saved seeds comprising twenty ‘Chinese’ and eight ‘Yenyawoso’ seeds, collected from farmers across five regions of the country were assessed in this study. A sample of the ‘Chinese’ variety collected from CSIR-SARI while samples of the ‘Yenyawoso’ variety collected from CSIR-SARI and CSIR-CRI, were used as the controls for this study. DNA was extracted from 10 individual plants of each sample and bulked for PCR amplification. After screening 25 pairs of SSR markers for their ability to discriminate between the two varieties, 4 polymorphic primer pairs were subsequently selected to test for genetic purity. Amplified products from 5µl of the PCR reaction were separated by a 6% polyacrylamide gel electrophoresis run for 75 minutes at 80 V and 300 amh. After electrophoresis, the gels were stained with ethidium bromide (10 mg/ml) for 30 minutes and visualized using an Alpha Imager TM 2200 gel documentation system. All genotypes were scored for the presence (1) and absence (0) of SSR bands manually and the band scores were used to generate a similarity data matrix using Simple Matching (SM) coefficient. Subsequently, the pair-wise similarity coefficients were used to construct a dendrogram following the unweighted pair-group method with arithmetic average (UPGMA) in NTSYS-pc version 2.20v. The Sequential Hierarchical and Nested (SAHN) method was adopted. Genetic similarity values ranged from 43% to 100%. Overall, cluster analysis put the seed lots into one group at 43% similarity but subsequently separated them into two clusters at 60% coefficient of similarity. At 60% similarity index, the 2 ‘Yenyawoso’ seed lots from SARI and CRI were grouped in a cluster along with 8 farmer-saved ‘Yenyawoso’ seed lots and 1 farmer-saved ‘Chinese’ seed lot. Similarly, the ‘Chinese’ seed lot obtained from SARI, 19 farmer-saved ‘Chinese’ seed lots and one 1 farmer-saved ‘Yenyawoso’ seed lot were grouped in one cluster. Out of the 20 seed lots reported by the farmers to be the ‘Chinese’ peanut variety in this study, only 5 were found to be 100% genetically similar to the reference ‘Chinese’ seed in Cluster I. With regards to ‘Yenyawoso’ farmer-saved seeds, only 2 of them were found to be 100% similar to the reference ‘Yenyawoso’ seed samples in Cluster II. The results showed that there is a significant deterioration in the genetic purity of these two peanut varieties in the hands of farmers.

Genome Wide Association Studies Reveal Novel Loci for Resistance to Groundnut Rosette Disease in Cultivated Peanut (*Arachis hypogaea* L.)

E. ACHOLA*, Makerere University Regional Center for Crop Improvement, Kampala, Uganda; D.A. ODENY, International Crops Research Institute for the Semi-Arid Tropics–Nairobi, Kenya; J. CLEVENGER, HudsonAlpha Institute for Biotechnology, Alabama, U.S.A; P. WASSWA, School of Agricultural Sciences, Makerere University, Kampala, Uganda; C.M. DEOM, Department of Pathology, The University of Georgia, Athens GA,30602, USA; R. EDEMA, P. Gibson, Makerere University Regional Center for Crop Improvement, Kampala, Uganda; D.K. OKELLO, National Semi-Arid Resources Research Institute, Serere, Uganda

Groundnut Rosette Disease (GRD) is the most devastating biotic stress of peanut in Africa. The disease is widespread in Sub-Saharan Africa (SSA) and its off-shore islands resulting in 100% yield loss in severe cases. GRD is caused by a complex of three viral agents, transmitted by an aphid, *Aphis craccivora* Koch. Host plant resistance towards aphids or the virus is the most effective approach in the management of the disease for resource limited farmers across Africa. Efforts from breeding programs across Africa have resulted in the release of tolerant varieties however, the genetic basis of GRD resistance is not fully understood. Insights into the genetic control of GRD resistance will guide breeding approaches and facilitate marker assisted-breeding.

Two hundred genotypes representative of the diversity of peanut across breeding programs in Africa were phenotyped in two seasons; across two GRD hotspots (Serere and Nakabango) in Uganda. Data was collected on Percentage Disease Incidence and GRD severity at 4, 8 and 12 weeks after planting. Genotyping was performed using the Axiom Arachis Vs2 SNP array. BLUPs for percentage disease incidence in each location were generated in R version 4.0.3. GWAS analysis was done using MLM methods in TASSEL 5.2.20 with a Bonferroni cut off of $P<6.15E-06$ as the significance threshold. Candidate genes within 6Kb of the associated SNPs were identified on Peanutbase. Consistent and significant SNP associations with GRD resistance were observed across locations and seasons with 90% of the significant SNPs located on either Chromosome A04 or B04. Several putative genes were identified including a disease resistance protein of the TIR-NBS-LRR whose role is to provide signal transduction and elicit defense response against pathogens in the plant and an Argonaute family protein which plays a central role in RNA silencing of the Virus. Results reported in this study provide insight into the genetic architecture of GRD resistance and thus the basis for development of molecular markers for Marker assisted selection for GRD resistance.

Effects of Landscape Context and Environmental Factors on Injury to Peanut Caused by the Subterranean Pest *Pangaeus bilineatus* in South Georgia.

B.L. AIGNER*, M.R. ABNEY, J.M. SCHMIDT. Entomology Department, The University of Georgia, Tifton, GA 31793-0748.

The peanut burrower bug (PBB), *Pangaeus bilineatus* Say (Hemiptera: Cydnidae), is a serious economic pest of peanut, Arachis *hypogaea* L., in the Southeast U.S., especially in Georgia. Factors driving the distribution of this historically sporadic native pest are unknown and annual losses have been reported throughout the region since 2010. Records of all PBB injury occurring in the 2016-2018 GA crop years were acquired from the Georgia Federal-State Inspection Service. Preliminary analyses were conducted using data from 2016 to test for significance of land use land cover (LULC) proportions in peanut, cotton, other agriculture, wetland, forest, and non-agricultural land with PBB injury. Other factors of irrigation, soil texture, field size, average roughness, and cumulative days of rain were inspected as potential predictors for PBB injury using a stepwise regression model in R. Preliminary results suggest significant factors of PBB injury to peanuts include irrigation, cumulative days of rain, average roughness, field size, and proportion of peanut in the surrounding landscape (1km).

Molecular Detection, Gene Expression and Phylogenetic Analyses of Aflatoxin Producing of *Aspergillus flavus* Strains Isolated from Peanut Seeds in Georgia

E. ALI *, M. GUNN, S. WALIULLAH, T. STACKHOUSE, A. K. CULBREATH, and T. B. BRENNEMAN. Dept of Plant Pathology, University of Georgia, Tifton, GA 31794.

Aspergillus flavus infects peanuts and produces a mycotoxin called aflatoxin, a potent human carcinogen. In infected peanuts it can also affect peanut seed quality by causing seed rot and reducing seed viability, resulting in problems establishing plant stands. In 2020, peanut seeds in Georgia had lower than expected germination and a high frequency of *A. flavus* contamination. A total of 102 *Aspergillus* isolates were collected from seven seed lots and their identity, aflatoxin contamination and expression of the aflatoxin regulatory genes were studied. The isolates were confirmed as *A. flavus* by morphological characteristics and a PCR-based method using species-specific primers. Aflatoxin-producing strains identity and expression were assayed by targeting four genes involved in the aflatoxin biosynthetic pathway: *nor*1, *ord*1, *omt*A, and *afl*R. In all examined strains, 80 out of 102 (78%) were successfully amplified using all four genes, indicating aflatoxigenic activity. ELISA analysis further confirmed that the isolates produced high levels of aflatoxins (B1). A real-time PCR was used to analyze the level of expression of these regulatory genes in all collected *A. flavus* isolates. Our results showed a significant gene expression variation between aflatoxigenic and non-aflatoxigenic *A. flavus* isolate (Aflaguard). The variation of gene expression may be related to seed storage conditions as well as aflatoxin production. Overall, these studies presented that the 4 out of 25 biosynthesis-related genes may play an important role in the regulation of aflatoxin production in peanuts during storage. More detailed studies are needed to predict the potential risk of aflatoxin production and the functional importance of specific regulatory genes in stored commercial peanut seed.

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Sound Splits as Influenced by Seed Size for Runner and Virginia Market Type Peanut Graded on a Reciprocating Sheller

D.J. ANCO*, Department of Plant and Environmental Sciences, Clemson University – Edisto Research and Education Center, Blackville, SC 29817; M. BALOTA, School of Plant and Environmental Sciences – Tidewater Agricultural Research and Extension Center, Virginia Tech, Suffolk, VA 23437; and J.C. DUNNE, Crop and Soil Sciences Department, North Carolina State University, Raleigh, NC 27695.

The objective of this study was to examine peanut (*Arachis hypogaea* L.) kernel percent sound splits as a function of sound mature kernel seed size when graded on a reciprocating sheller. Data was compiled from a total of 137 field trials conducted in the Virginia-Carolina region from 2005 to 2020. Runner and Virginia peanut market types were graded according to USDA standards using sheller screens with upper (red) grid sizes of 26/64 x 3/4” and 34/64 x 1”, respectively. Grade data per market type was analyzed separately. Among runner market types, percent sound splits increased linearly with increasing seed size at the rate of 1.3% per 100 seed/lb ($P < 0.0001$). While the estimated slope parameter for this relationship among Virginia market types was not significantly different from zero ($P = 0.92$), corresponding extra large kernels linearly increased with seed size at 7.1% per 100 seed/lb ($P < 0.0001$). Runner market types with 600 seed/lb were estimated to have a 50% probability of a 2.9% or greater increase in sound splits compared to runner seed with a count of 830/lb, equivalent to a potential deduction increase of $\geq$\$2.40/ton. For both Virginia and runner market types, seed weight linearly increased with pod weight at 16.8 and 15.8% ($P < 0.0001$), respectively. Results from these studies may be used as a starting point to suggest runner seed sizes above which larger sheller screen size utilization in line with USDA grading practices may be warranted to reduce mechanical sound splits during grading on a reciprocating sheller.

Understanding Variation in Oleic Acid Content of High-Oleic Virginia-type Peanut

R. J. ANDRES*, J. C. DUNNE, Department of Crop and Soil Science, North Carolina State University, Raleigh, NC 27607.

Bailey II is a high-oleic (HO) version of the commercially successful cultivar Bailey. In recent tests, the oleic acid content of Bailey II averaged 74%, barely meeting the requirements of a high oleic cultivar. Furthermore, this is below that of other HO Virginia-type peanut cultivars and breeding lines within the NC State program that typically measure 79-81%. We posit three possible explanations exist for this discrepancy: 1) differences in days required to achieve optimum maturity 2) seed contamination via either seed mixing or inadvertent cross-pollination, or 3) differences in genes with minor effects on oleic acid content.

To investigate, four cultivars and four breeding lines were grown in 2019 and 2020 at the Peanut Belt Research Station in Lewiston, NC. Two plots per entry were dug at three different digging dates: very early (131 days after planting (DAP), optimum (145 DAP), and very late (159 DAP). Ninety-six seeds from each plot were run on a Brimrose Luminar 3076 Seedmeister to determine oleic acid content. In order to assess genetic purity, all 96 seeds per plot were genotyped for the *FAD2B* causal mutation.

Genotyping revealed extensive contamination of Bailey II at the *FAD2B* allele, however contamination was not exclusive to Bailey II. This indicates that more rigorous standards should be employed for seed increases in order to ensure purity at the *FAD2B* locus in our program. However, pure lots of Bailey II should not differ in oleic acid content from other cultivars. To this end, higher oleic acid thresholds will be adopted for screening with the Seedmiester and the purchase of a Qualysense QSorter Explorer should enable more efficient screening of large seed lots.

The White Stuff on Properly Stored Peanuts Identified, Need to Reassess Boundaries?

R.S. ARIAS*, C. BUTTS, V.S. SOBOLEV, A.N. MASSA, V.A. ORNER, M.C. LAMB,
National Peanut Research Laboratory (NPRL), Agricultural Research Service, U.S.
Department of Agriculture, Dawson, GA 39842

Peanuts stored under low humidity (a_w 0.77) and high carbon dioxide (≥ 9000 mg/m^3) conditions which normally would not support life, were exhibiting a white powder coat. This was identified at the NPRL as an extremophile fungus that had never been reported on peanuts before. Environmental conditions that effectively prevent growth of *Aspergillus flavus*, *A. parasiticus* and *A. niger* are not sufficient to stop growth of this extremophile which can thrive at much lower humidity than *Aspergillus* and in the absence of oxygen. Appropriate storage conditions for peanuts might need some adjustments to prevent extremophiles and preserve seed quality, those conditions are discussed.

Benefits of Peanut – Cereal Rotation and Inputs Systems on Maize Growth and Yield in Northern Part of Ghana

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One important benefit of including legumes in crop rotations is their ability to make nitrogen available to the next crop through biological nitrogen fixation. However, this soil benefit becomes unavailable, because most farmers in Northern Ghana collect peanut haulm as animal feed after each season. To demonstrate the benefit of leaving peanut haulm to the next crop, two separate 2 × 2 × 3 factorial experiments were conducted in 2020 at Tamale and Wa in the Northern and Upper West Regions of Ghana respectively, following crop rotations initiated in 2019. Peanut or maize was planted in 2019 depending on the rotation system and the integrity of the plots were maintained for follow up cropping of maize in the 2020 season. The experiments comprised two levels of crop rotation (peanut–maize versus maize–maize), two levels of maize varieties (hybrid 'CRI Ahof3' versus the open pollen variety (OPV) 'CRI Omankwa'), and three levels of production and pest management inputs [low input (LI) that included high quality seed, timely planting, and 1 manual weeding; moderate input (MI) that included high quality seed, timely planting, 2 manual weedings, 1 time insecticide treatment, and urea fertilizer applied 5–6 weeks after planting (WAP) for maize; or high input (HI) that included high quality seed, timely planting, preemergence application of pendimethalin followed by 1 manual weeding, 2 applications of insecticide, NPK (15:15:15) applied 2 WAP followed by urea application at 6 WAP for maize]. A wide range of data were recorded associated with pest and crop response. Cost for all inputs was recorded to enable benefit:cost analysis. Data were analyzed using Statistix 9 data software; ANOVA was generated and means separated by SED at 5%. In both locations, the interaction between peanut–maize rotation and all input systems produced taller maize plants at 3 WAP than the maize–maize rotation and input systems when data were pooled over varieties. In addition, the application of HI, MI, or LI on peanut–maize rotation resulted in significantly taller maize plants at 12 WAP than their corresponding input systems on the maize–maize rotation in both locations when data were pooled over varieties. When data were pooled over varieties and production systems, the peanut–maize rotation produced greater yield (1.4 metric tons/ha at Tamale and 2.5 metric tons/ha at Wa) than the maize–maize rotation (0.9 metric tons/ha at Tamale and 2.0 metric tons/ha at Wa). Grain yield of hybrid maize was greater in the peanut–maize rotation (1.6 metric tons /ha at Tamale and 3.2 metric tons/ha at Wa) than the maize–maize rotation (0.9 metric tons/ha at Tamale and 2.5 metric tons/ha at Wa) when data were pooled over production input systems. In Tamale, hybrid maize yielded more grain in the HI system (3.0 metric tons/ha) or the MI system (1.8 metric tons/ha) in the peanut–maize rotation than their corresponding input systems on the maize–maize rotation (2.0 or 0.6 metric tons/ha) or the first year (2019) maize (2.6 or 0.8 metric tons/ha). In addition, the HI system in peanut–maize rotation for the OPV also significantly produced much grain yield (2.4 metric tons/ha) than the same system for the first year maize (1.8 metric tons/ha) or maize–maize rotation (1.5 metric tons/ha). At Wa, the HI system increased hybrid grain yield when applied in the peanut–maize rotation (4.7 metric tons/ha) or maize-maize rotation (4.4 metric tons/ha) than the HI system of the first year maize (2.6 metric tons/ha). The application of MI in the peanut–maize rotation (4.3 metric tons/ha) also increased hybrid maize grain yield more than the MI system for the maize–maize rotation (2.9 metric tons/ha) or the first year of maize (1.6 metric tons/ha). Peanut will be established following both of these rotations in 2021 in both locations

Growth and Yield Response of Peanut to Pest and Crop Management Packages in Ghana

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Peanut peasants in Ghana realize yields of up to 76% lower than the minimum potential yield of 2.5 metric tons/ha. The shortfall is attributable to use of varieties without adequate tolerance to diseases, low quality seed, delays in planting, limited fertility and low soil pH, negative impacts of weeds and other pests, ineffective drying and storage practices, and limited financial resources to invest in inputs to address these issues. Most pest and crop management recommendations addressing these have not been developed into production packages for adoption by farmers in Ghana. Three experiments were conducted in Ghana at Kumasi, Tamale, and Wa in the Ashanti, Northern, and Upper West Regions of Ghana, respectively, to ascertain the benefit of pest and crop management packages on peanut growth, pest reaction, and yield. These packages were included in three-year rotation trail. Treatment factors included 2 levels of peanut variety [the improved variety Yenyawso and the traditional variety Chinese] and 3 levels of input systems [low input package (LIP) that included high quality seed, timely planting, and 1 manual weeding; moderate input package (MIP) that included high quality seed, timely planting, 2 manual weedings, 3 applications of local soap and application of NPK fertilizer 3 weeks after planting (WAP); and high input package (HIP) that included high quality seed, timely planting, pre emergence application of pendimethalin followed by 1 manual weeding, 2 applications of fungicide (azoxystrobin plus difenoconazole), application of NPK at 3 WAP, and application of calcium fertilizer at 6 WAP]. A wide range of data were recorded associated with pests and crop response. Cost for all inputs was recorded to enable cost: benefit analysis. Data were analyzed with Statistix 9 data analysis software; ANOVA was generated and means separated by SED at 5%. At 3 WAP, weed density was reduced by 58 to 70% in Kumasi, 75 to 84% in Tamale, and 61 to 73% in Wa in the HIP compared with the LIP. When data were pooled over locations, weed density was reduced by approximately 28% for both varieties in the HIP compared with the LIP. Severity of leafspot disease was lower when in the HIP for both varieties compared with the MIP and LIP; severity was lower in the MIP compared with the LIP. Peanut plants were taller for the variety Chinese in the MIP and HIP at 6 WAP compared with the LIP. In Kumasi, kernel yield of Chinese was greater for the HIP (1.7 metric tons /ha) followed by the MIP (1.2 metric tons/ha) and then the LIP (0.7 metric tons/ha). Kernel yield of Yenyawoso at Tamale was greater in the HIP (2.4 metric tons/ha) followed by the MIP (1.7 tons/ha) and then the LIP (1.2 metric tons /ha). Likewise, kernel yield of Chinese was greater in the HIP (1.8 metric tons/ha) compared with the MIP (0.8 metric tons/ha) and LIP (0.6 metric tons/ha); yield was greater for the MIP than the LIP. At Wa, peanut kernel yield for both Yenyawoso and Chinese was greater for the HIP (1.4 or 1.7 metric tons/ha, respectively) followed by the MIP (1.1 or 1.2 metric tons/ha, respectively), and the LIP (0.8 or 0.8 metric tons/ha, respectively). When data was pooled over locations, When pooled locations, both Yenyawoso and Chinese produced greater kernel yields in the HIP (1.7 and 1.7 metric tons/ha, respectively) followed by the MIP (1.3 and 1.1 metric tons/ha, respectively), and the LIP (1.0 or 0.7 metric tons/ha, respectively). Haulm yield was higher in the HIP compared with LIP or MIP for both the traditional variety Chinese and the improved variety Yenyawoso at all locations

High Throughput Phenotyping Methods on Peanuts Fields

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Meeting the food demand for the growing population will require an increase in crop production despite of the changing climate and the increased risk of drought. Breeding programs are using new technologies based on genetics and phenotyping through marker assisted selection. The traditional methods to evaluate agronomic and morphological plant traits in the field are cost expensive and time consuming. During the last decade, the miniaturization of new performing sensors allowed a breakthrough the phenotyping bottleneck, by remotely trait estimation using vegetation indices. The objective of this study was to compare two high throughput field phenotyping methods, one using onboard multispectral camera on an unmanned aerial vehicle (UAV) and second one using handheld equipment at ground level. The handheld sensors, GreenSeeker crop sensor (Trimble Inc., USA) and SPAD-502 (Konica-Minolta Corp, Japan), are affordable, easy-to-use and quick measurement devices to assess the health and vigor of a crop (biomass, chlorophyll content). UAV flights were performed with a hexacopter UAV (FeHexaCopterV2, MikroKopter Company, Germany). The onboard multispectral Airphen camera (Hyphen, France) included six individual cameras equipped with filters centered on 450, 530, 560, 675, 730 and 850 nm, with a spectral resolution of 10 nm.

For this study we used a randomized complete block design with 4 blocks and 21 peanut varieties. The experiment was performed at two sites in Senegal (Bambey and Nioro).

The varieties were representative to the agronomic and morphological traits observed in west Africa. The results showed a significant association between the two methods. The normalized difference vegetation index (NDVI) measured by the GreenSeeker and the NDVI from the UAV camera presented an average correlation coefficient (r) around 0.8. We observed similar good relationships between the SPAD relative chlorophyll content and green normalized vegetation index (GNDVI). These relationships were less straightforward when the plants have not yet reached full plant cover (leaf area index (LAI) ≤ 1). This is probably due to the presence of weeds during the early growth stages.

Differences were observed in the implementation of these methods. For the use of the handheld sensors, one hour was necessary to phenotype the whole experiment. With the UAV a complete overview of the experiment took 10 minutes.

The strong technological advances of the last few years give the possibility of phenotyping populations at lower cost and in narrow time windows. The different methods are largely comparable. The choice of their use depends only on the objectives and the investment desired by the research teams.

Effect of Different Winter Cover Crops on Peanut in Rotation with Cotton

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Winter cover crops can potentially decrease inputs on crop production, improve yield and soil health, reduce soil erosion, conserve moisture. and protect water quality. They can also be harvested to supply biomass used to feed livestock or for bio-based fuels. Row crops such as peanut (*Arachis hypogaea L.)* and cotton (*Gossypium hirsutum L.*) are important summer crops in Georgia and could benefit from the use of winter cover crops. The objectives of this study are to evaluate three winter crops, lupin (*Lupinus sp.*); narrow-leaf lupin (*Lupinus angustifolius L.*)*;* cereal rye (*Secale cereale L.*) and their combination for biomass production and crop quality, and their subsequent effect on the production of peanut in rotation with cotton. The study was conducted at three sites in South Georgia: Tifton, Fort Valley, and Shellman in the years of 2018, 2019 and 2020. The experimental design is a split-split-plot, with peanut and cotton as the main plot treatments, cover crop as subplot treatments and winter cover crop termination (harvest, rolled) as sub-sub-plots. Measurements for cover crops included percent ground cover, mid-season biomass and biomass yield. Measurements for peanuts included final yield, imagery of canopy coverage and final biomass. Results for the year of 2018, did not show a clear relationship between the yield of peanuts and cotton with the cover crops and the crop termination system. Winter cover crops showed significant biomass differences, with lupin and narrow-leaf-lupin having the largest final biomass production, and rye the lowest for the first two years of the study. Yields for peanut were lower during the second year of the rotation due to a hot and dry season. Differences were not observed between treatments for 2019 year as well. For 2020

Approaches to Prevent and Manage Viruses Introduced by Seed

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With the globalization and widespread exchange of plant materials across the borders, and the ability of seeds to act as a carrier of virus and vectors increases the risk of introduction of disease in to a new geographical region.

The two species of pecluviruses, Peanut clump virus (PCV) and Indian peanut clump virus (IPCV) are currently restricted to the regions of African and Asian continents respectively. APHIS designated them as quarantine pests for peanuts. We initiated a study to develop a robust, and accurate diagnostic assay to detect the presence of PCV and IPCV on peanuts. Due to availability of numerous serotypes, two TaqMan multiplex assays were developed separately for IPCV and PCV for accurate detection. Freeze-dried plant tissues infected with two different IPCV strains (Durgapur (D) and Hyderabad (H)) from India and one PCV strain were collected from Senegal. Specific primers and probes were designed targeting the conserved regions (coat protein-CP; triple gene block-TGB; and RNA dependent RNA polymerase-RdRp) of viral genome. Total RNA was used for RT-PCR to amplify the targeted genes (IPCV H CP, IPCV D CP, IPCV D TGB, IPCV H TGB, PCV CP, PCV RdRP) followed by sequencing for virus confirmation. SYBR-Green-based qRT-PCR was designed and standardized separately for the IPCV D CP, IPCV H CP, IPCV RdRP, PCV CP and PCV RdRP genes along with plant genes (*ADH3* and *ACT11*) as internal controls. Analysis of thermal curves confirmed the specificity of each targeted gene amplification. One-step TaqMan singleplex assays were developed separately for all targeted regions, with the efficiencies and R^2 values within the expected ranges of 90-110% and 0.98.-0.99 respectively. One-step Triplex assay which detects CP, RdRP and Actin genes was developed for PCV. Detection of IPCV D CP, IPCV H CP, IPCV RdRp, Pecluvirus specific RdRp and Peanut Actin gene were successful resulting a five-plex assay for IPCV. As a conclusion, optimized One-Step SYBR Green qRT-PCR and One-step TaqMan based triplex qRT-PCR were developed for an accurate and rapid detection of Pecluviruses to be used for quarantine purposes. The next step is to validated these tools with multiple samples.

Evaluation of Twin Row Spacings and Seeding Rates for Runner Peanuts.

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Research was conducted at the Wiregrass Research and Extension Center in Headland, Al from 2017-2019. The trial design was a complete randomized block design. We evaluated Ga 16 HO in three different twin row patterns plus a single row pattern with three different seeding rates and evaluated Tuf 511 in comparison with the standard row spacing and seeding rate in 2018 and 2019. Row spacing treatments were three different twin row spacings of 8”, 10”, and 12” with three different seeding rates of 6, 8, and 10 sd/ft. We wanted to test our standard seeding rate of 3 sd/ft for each twin row to total 6 sd/ft with both rows per linear foot the same as 6 sd/ft in single row to see if it is still sufficient or economical for producers today. For the twin row there was no difference between yields for 8”, 10”, and 12” spacing. However, seed rate did differ with 6 sd/ft yielding less than either 8 or 10 sd/ft. The Ga 16HO twin vs. single statistically out yielded the Tuf 511 for both years 2018 and 2019. Comparison of varieties separately indicated Tuf 511 had a statistically higher yield in twins over single for both years but the Ga 16HO showed only a significantly higher yield in twins over single in 2019. In summary, three out of four times twin out yielded single rows. In 2019, regardless of variety, twin out yielded single and in 2018 twin row Tuf 511 out yielded single of the same variety. Our research indicates a benefit to planting twin rows over single as well as an increase in yield with increased seeding rate. A cost analysis comparison was performed to determine if an economic benefit was achieved with increased seeding rate.

Learning from Using Wild Relatives to Incorporate Nematode Resistance in Peanut

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Peanut is an allotetraploid species characterized by a very low genetic diversity and is extremely susceptible to peanut root-knot nematode (PRKN) *Meloidogyne arenaria*. Near-immunity has been found in the peanut wild relative *A. stenosperma*, and the two new loci (A02 and A09) providing strong resistance, have been mapped and validated in a tetraploid background using F_2 and backcross populations. These chromosome segments were incorporated in elite breeding lines through marker-assisted backcrossing approach. In 2020, progeny (BC_3F_2s) of 251 genotypically characterized third backcrossed lines were field tested, advanced and selected in Midville, GA. These lines are on average 90.7% elite genetics, with wild segments across the genome, including the two loci for PRKN resistance from *A. stenosperma*. During the field experiment, phenotypic information for plant architecture, plant size, disease resistance (LLS and TSWV) and overall performance was recorded. Additionally, genome-wide genotyping of 80 high performing BC_3F_2 lines was completed and correlated with the phenotypic information. BC_3F_3 progeny was phenotyped for pod weight per plant, constriction, reticulation, total number of pods, percentage of double pods and 100-seed weight. Overall, many lines performed as well as the cultivar controls, with outstanding yield and great pod and seed characteristics. Although, the lines were selected for the PRKN resistance alleles, other wild introgressions were unintentionally inherited and are controlling other important traits, such as resistance to LLS and we also observed resistance to TSWV on a heavily infested field. Finally, a greenhouse bioassay allowed us to successfully validate PRKN resistance from *A. stenosperma* in a set of BC_3F_3 lines. In the future, field selections and advancement will be taking place for germplasm release. This present work represents an important step towards the development of new high-yielding peanut cultivars harboring new and strong resistances.

Vegetation Indices Enable Indirect Phenotyping of Peanut Physiologic and Agronomic Characteristics.

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Identification of sources of resistance to biotic and abiotic stress is key for the development of improved cultivars, but direct phenotyping is slow. Vegetation Indices (VIs) derived from aerially-collected canopy reflectance in the red, green, and blue (RGB) and near infra-red (NIR) spectra enable indirect phenotyping. Accessions of the US mini-core peanut (*Arachis hypogaea* L.) germplasm collection were grown in RCBD replicated trials in 2017 and 2018 at the Tidewater Agricultural Research and Extension Center, in Suffolk, VA. Phenotyping included the following: stand count; plant height; lateral branch growth; normalized difference vegetation index (NDVI); canopy temperature depression (CTD); wilting; thrips damage; tomato spotted wilt virus (TSWV) (caused by *tomato spotted wilt virus*, genus *Tospovirus*; family *Bunyaviridae*); southern stem rot (SSR, caused by *Athelia rolfsii* (Curzi) C.C. Tu & Kimbr.), Sclerotinia blight (caused by *Sclerotinia minor* Jagger), Cylindrocladium black rot (CBR, caused by *Calonectria ilicicola* Boedijn & Reitsma); post digging in-shell sprouting, and yield. These characteristics were evaluated at 4, 5, 6, 7, 9, 10, 11, 12, 14, and 16 weeks after planting (WAP). A total of 48 VIs including reflectance in red, blue, green, and NIR, RGB color space indices and combinations of them, taken by an octocopter drone at the same time with the ground measurements were correlated with the physiologic and agronomic characteristics. Correlation coefficients up to 0.8 were identified for several VIs, indicating their suitability to indirect phenotyping. Broad-sense heritability (H^2) was further calculated to assess the suitability of particular VIs to enable genetic gains. For example, the normalized difference CIELab (NDLab) and CIELuv (NDLuv) indices were significantly correlated with yield within all botanical types in the mini-core collection in 2017, i.e. N = 104; r = 0.43 to 0.57 ($p \leq 0.001$). But while H^2 for yield was 0.14, H^2 for the NDLab and NDLuv evaluated during pod development ranged from 0.43 to 0.54, showing that the vegetation indices could be used successfully as surrogates for the physiological and agronomic trait section in peanut.

Do Belowground Peanut Plant Parts Contribute N credits to Subsequent Crops?

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Farmers in the US southeast are often recommended to reduce nitrogen (N) fertilization after peanut (*Arachis hypogaea* L.) by co-operative extension services. Although these recommendations are not supported by the scientific literature, the literature has never taken into account potential N credits from belowground plant parts and undug pods. An experiment was conducted to quantify potential N credits from peanut plant parts to subsequent crops using field litterbag decomposition studies. The objective was to quantify fertilizer replacement value of peanut hay, taproots and undug pods. A two factor (4 plant parts: leaves, stems, roots and pods × 9 retrieval periods) randomized complete block study was conducted during 2020-2021 season in Jay, FL. All residues were buried at 10 cm depth. Based on preliminary results, root biomass net N mineralization was 10% at 56 days after deployment. Pod biomass net N mineralization was 7% at 56 days after deployment. Results after 56 days will be presented and will inform peanut N synchronicity to summer crops. Traditional decomposition studies utilizing above-ground residue only may underestimate N credits, as preliminary results highlight the small but potentially significant contribution of peanut roots and pods to N synchronicity to subsequent crops.

Chayote Contests and Tamarind Butter: The Natural Agricultural Range of Florida and its Role in Home Demonstration Programming, 1915-1930

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Between 1915-1930, the natural agricultural range and climate in Florida lent itself to economic opportunities for women involved in home demonstration programming. The differences between the vegetables and nuts in the panhandle of north Florida, to the citrus groves and home dairies of central Florida, to the tropical fruits of southern Florida, all coalesced into creating marketing and business prospects for the state's rural women. Florida became advantageous for home demonstration programming, as Floridian women and girls throughout the 1920s used this natural diversification in climate and environment to enhance agricultural and horticultural varieties to help their own financial situations. Using Florida's resources became part of the home demonstration agent's early plans, to which rural women responded with enthusiasm. These women would also capitalize on the tourist and "snow bird" economies of the 1920s, by selling and marketing their Florida-grown foods through a variety of methods, including their own businesses, contests which encouraged growing specific produce, local events, and other avenues. They marketed the "Florida" name by using the agricultural climate to their benefit and through the support of home demonstration programming, which resulted in rural Floridian women utilizing what Florida's environment had to offer.

Dispersal of *Nothopassalora personata* from an inoculum source

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Late leaf spot, caused by *Nothopassalora personata*, is the most economically important fungal foliar disease of peanut (*Arachis hypogaea* L.) in South Carolina. Inoculum is spread by wind and rain and is believed to be able to travel over many kilometers. The objectives of this study were to evaluate the dispersal of *N. personata* inoculum using spore traps positioned at 4, 10, 30, 50 and 70 m from three infected peanut fields in SC and to examine this data for relationships with weather data. Stainless steel rods were coated in vacuum grease and were collected at 48, 96, and 168 hours on a weekly interval from July to October. Crude DNA extraction and qPCR using *N. personata*-specific primers were performed on all samples, with individual rods (i.e. subsamples) assessed separately. Cycle threshold (ct) values were recorded and log transformed to estimate spore counts. Weather data was collected from Edisto REC and Barnwell Regional weather stations. Detection incidence and spore quantity were analyzed using generalized linear mixed model with location as a random effect. Correlation between weather events and incidence of detection was examined.

N. personata was detected in early August through the end of the growing season in October. There was detection at each distance, with greater quantities of spores collected at traps placed at 4 and 10 m from inoculum source ($P = 0.0433$). Spore quantities from the three locations were fit to exponential growth models ($P < 0.0001$). Detection incidence and log spore quantities correlated with wind speed ($P = 0.0002$ and $P < 0.0001$, respectively) and air temperature ($P = 0.0032$ and $P = 0.0018$, respectively).

Response of Peanut Genotypes to Pre-Harvest Aflatoxin Contamination in Ghana

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Peanut production is predominant in rain-fed regions of the semi-arid tropics with a characteristic unpredictable drought. This exposes the crop to end-of-season drought, resulting in pre-harvest *Aspergillus* infection and subsequent aflatoxin accumulation. As a consequence, the potential for aflatoxin post-harvest management becomes limited, leading to further accumulation in farmers' stores. Development of varieties with reduced *Aspergillus flavus* infection and aflatoxin contamination in the field is critical in addressing the groundnut aflatoxin contamination menace. It is imperative to identify groundnut genotypes with resistance or tolerance to infection by local strain of *A. flavus* and aflatoxin production to facilitate development of resistant varieties. The objective of the study was to identify groundnut genotypes with reduced *A. flavus* infection and aflatoxin contamination in the field. The experiment was conducted at Fumesua (Deciduous Forest) and Nyankpala (Guinea Savanna) with 27 genotypes (22 from ICRISAT and 5 adapted varieties from CSIR-CRI, Ghana). The experimental design was a 9 × 3 alpha lattice with 3 replications. Plot size was 4 rows (50 cm apart) with a length of 3 m. *A. flavus* strain inoculum was isolated from peanut and toxigenicity determined at the Mycotoxin Laboratory of the Kwame Nkrumah University of Science Technology, Kumasi, Ghana. Inoculum of *A. flavus* was prepared using the organic-matrix method. Planting was delayed at both locations to expose genotypes to 27-30 days terminal drought. *A. flavus* infested corn was broadcasted to groundnut plots at rate of 200 kg/ha at 60 days after planting. Fertilizer (NPK, 15:15:15) at 130 kg/ha was applied at 2 weeks after planting. Ground oyster shells (100 kg Ca/ha) was also applied at 40 days after planting. Manual weeding was done twice at three and six weeks after planting. Kernel infection by *A. flavus* (%), aflatoxin concentration (ng/g) at harvest, haulm yield (kg/ha), and pod yield (kg/ha) were recorded. Data for aflatoxin and kernel infection were log [log (y + 1)] and angular transformed, respectively. Analysis of variance was performed for each location and across locations following homogeneity of variance test using PROC GLM of SAS version 9.4.

Significant genetic variation existed among groundnut genotypes for aflatoxin contamination, seed infection by *A. flavus*, pod yield and haulm yield, indicating possible selection for improvement of these traits. Genotypes ICGV 03331, ICGV 03401, and ICG 4729 consistently showed low aflatoxin levels (<20 ng/g) and low to moderate seed infection by *A. flavus* across contrasting locations, suggesting that their use as parents for improvement of adapted varieties for the aflatoxin reduction traits is possible. Genotypes ICGV 03331 and ICGV 03401 had low aflatoxin levels and appreciable pod and haulm yields and could serve as potential varieties in Ghana following further evaluation in multiple locations.

Sensitivity of *Athelia rolfsii* from Commercial Peanut Fields in Georgia to Tebuconazole and Flutolanil

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For over 20 years in Georgia peanut production, the control of *Athelia rolfsii* has been largely dependent on fungicides, with flutolanil and tebuconazole among the most widely used. With the frequent application of these fungicide classes to peanuts and rotational crops, the development of fungicide resistance has been an issue of concern. Through in vitro assays, we assessed the sensitivity of 256 *A. rolfsii* isolates to flutolanil and tebuconazole using the discriminatory doses 0.03 ppm and 0.02 ppm, respectively. The screened isolates were collected from 14 different locations across Georgia (research sites and grower fields) where *A. rolfsii* control was sometimes less than expected. Significant differences in percent inhibition for both fungicides were seen across the 14 locations, demonstrating variance in fungicide sensitivity between grower fields. The range of percent inhibition for tebuconazole across all locations was 14.78-21.36 (LSD=4.19), with a mean value of 20.40, whereas the range for flutolanil was 15.39-24.98 (LSD=3.61), with a mean value of 18.08. Flutolanil percent inhibition had the most variability and consisted of six significantly different groups, whereas tebuconazole only contained two significantly different groups.

To assess the possibility of fungicide resistance developing over time, our results were compared to a similar study conducted in Georgia in 1998 that used the same fungicides and discriminatory doses. In this study, the average mean percent inhibition for flutolanil and tebuconazole was 30.08 and 28.07, respectively. Our assessment shows a reduction in average percent inhibition of 32.2 % for flutolanil and 35.6 % for tebuconazole over the past 22 years, demonstrating a significant loss in fungicide sensitivity over time. The implications of this change for disease control in the field are uncertain, but need to be explored further.

Response to Drought Stress in a Subset of the U.S. Peanut Mini-core Evaluated in Three States

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Climate change and limited water availability are significant challenges to the future of peanut production, and much work remains in developing drought- and heat-resistant cultivars. To this end, we evaluated 22 accessions from the U.S. peanut mini-core for three years (2017-2019) under drought conditions in Oklahoma, Texas, and Virginia. The accessions were selected to represent extremes in phenotypes for soil plant analysis development (SPAD) chlorophyll, wilting, paraheliotropism (leaf folding), flower production, normalized difference vegetation index (NDVI), canopy temperature, and yield. The replicated trials also included C7616, New Mexico Valencia, Tamrun OL-11, Tamspan 90, Tamval OL-14, Walton (08x09-3-14-1), and Wynne as reference genotypes. Preliminary analyses indicate significant differences among entries for most measurements in all locations. Drought responses of the entries and their associations with yield will be presented.

Benefits of International Seed Exchange of Peanut Wild Species: the *Arachis cardenasii* Case

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The narrow genetics of most crops is a fundamental vulnerability to food security. Wild crop relatives thus are a strategic resource of genetic diversity for crop improvement and adaptation to new agricultural challenges. We uncovered the previously unknown scale of contribution of one wild species, *Arachis cardenasii*, to the peanut crop. *Arachis cardenasii* originates from Bolivia, was transferred to the USA and used for hybridizations initiated in the 1960s in NC and TX, using the hexaploidy and tetraploid route, respectively. Subsequent multiple germplasm transfers, breeding cycles and unrecorded genetic mixing between lineages obscured the widespread dispersal of genetic contributions from this wild species. By genetic analysis and pedigree research, we identified *A. cardenasii*-enhanced, disease resistant cultivars in Africa, Asia, Oceania and the Americas. In the USA, the most notable examples are: the only source of root-knot nematode resistance derived from the amphidiploid TxAG6, present in several commercial cultivars (through the tetraplod route) and also the cultivar Bailey and Bailey II that carries resistance to ELS (through the hexaploidy route). Most recently, advanced lines with very strong resistance to LLS made their way back into the USA and were used for two germplasm releases: TifGP3 and TifGP4. These cultivars provide widespread improved food security, and environmental and economic benefits. This study highlights the importance of wild species and collaborative networks of international expertise for crop improvement.

Quantifying Acetochlor Thermal Stability

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Using a thermal gradient table, acetochlor (formulated as Warrant) stability over temperature and time was evaluated. Abstract will be updated.

Enhancing the Peanut Value Chain through Peanut Innovation Lab Partnerships: Examples of a Production Guide in Malawi using Research Results from Ghana

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The development of accurate and practical crop production information for farmer training and education is dependent upon effective applied research programs. These research programs must be addressing problems that impact the profitable and sustainable production of crops such as groundnuts. Equally important, is that the data from these research projects be packaged into manuals and guides that help farmers understand improved methods for production and profitability. The Peanut Innovation Lab and its predecessors has been conducting research in Ghana for 25 years through the Crops Research Institute in Kumasi and the Savanna Agricultural Research Station in Tamale. These research finding have been critical in developing production programs that help farmers. The research program in Malawi has been of much shorter duration (less than ten years) and while great progress has been made, there are still a number of research gaps to be addressed. The current agricultural transformation occurring in Malawi as farmers move away from tobacco requires a significant effort to develop educational materials and manuals for farmers to use as they cultivate new crops such as groundnut. Since 2019, we have been involved in a process to develop a comprehensive groundnut production manual for Malawi and the first version was produced in late 2019 with a revised version in late 2020. We assembled all of the research findings form the Peanut Innovation Lab and our own global experiences with groundnut production and constructed a manual that started with seed selection and guided farmers through until harvest. However, during the development of the project, it became obvious there were significant gaps in our complete understanding of cost effective and sustainable groundnut production in Malawi. Fortunately, our years of experience and research in Ghana allowed us to carefully select research findings from that country and modify and adjust them to fit into the agroecosystems in Malawi. Some of this input could be very specific, while other information had to be somewhat "generic" since it had not been evaluated specifically in Malawi (but will be in the future). As the final version of the manual was completed, the collaborative value of the project in Ghana to help us make a high quality groundnut production guide for Malawi was obvious. The role that the long-term research program played in supporting our efforts in Malawi cannot be overstated.

Effects of Dynasty and Rancona Seed Treatments and In Furrow Sprays on Peanut Plant Stands, Diseases and Pod Yield.

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Peanut seed treatments were compared in field trials in 2019 and 2020 for their effects on seedling diseases, plant stands, and pod yield. The treatments evaluated were Rancona V PD and Dynasty PD, both applied as a wettable powder formulation to Tifguard seed at 4 oz per 100 lb of seed. The in-furrow treatments were Abound (6.0 fl oz/A), Velum Total (18.0 fl oz/A), Proline (5.7 fl oz), or nontreated. The seeding rate was 6 seed/ft. Lower germination seed lots (about 80% germination) were selected and the field sites were previously planted to peanut to increase seedling disease pressure in the trial. With no in furrow spray, the untreated, Rancona and Dynasty treatments had 0.9, 4.1 and 3.8 plants per foot (LSD=0.5) in 2019, and 0.6, 3.0 and 2.4 plants per foot (LSD=0.5) in 2020, respectively. Severe Aspergillus crown rot developed by early June of both years with 44, 1 and 9% of the emerged plants killed in the nontreated, Rancona and Dynasty plots, respectively in 2019, and 46, 1, and 4% killed in 2020. Pod yields were about 2000 lb/A both years with nontreated seed, and increased by greater than 100% with both seed treatments. Yields were not significantly different between the two seed treatments. Velum Total was the only in furrow treatment to increase both plant stands and yield with nontreated seed. Pod yields were higher by 2746 and 2432 lb/A in 2019 and 2020, respectively, where Velum Total was applied. Both Velum Total and Proline were highly effective on Aspergillus crown rot, whereas Abound had no effect. This was presumably due to the presence of QoI-resistant *Aspergillus niger*. The effects of Proline and Abound on plant stands and yield when applied to fungicide-treated seed were inconsistent, but they were significantly higher than the seed treatments alone in some cases.

Evaluating the Potential Of UAV-Based Imagery for Detailed Measurement of Above-Ground Growth Characteristics in a Peanut Breeding Application.

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Stand establishment, early-season seedling vigor, and mid-season canopy closure ensure a grower's timely and efficient achievement of a vigorous crop that can resist weeds, take advantage of available moisture and nutrients, and produce optimal yield. In large breeding trials however, direct measurement of these traits is prohibitively time consuming. Estimations based on visual ratings are prone to high levels of variation and low accuracy. Thus, the utility of using unmanned aerial vehicles (UAV) for the measurement of plant growth-related traits is currently being evaluated in replicated yield trials and early generation trials. In 2019 at the University of Georgia's Gibbs Research Farm in Tifton, GA, images were taken by UAV at 43 DAP. Visual rating of mid-season vigor were assessed the same day, and plant height collected 53 DAP. In 2020, images were taken by UAV at 16 DAP, 33 DAP, and 47 DAP. Visual rating of stand establishment and seedling vigor were taken 15 DAP; plant height was directly measured and mid-season vigor visually estimated approximately 56 DAP and 58 DAP, respectively. Moderate correlations were achieved for early-season measurements, however, high correlations were evident comparing UAV-derived mid-season growth characteristics and visual vigor ratings as well as direct plant height measurements. Individual plants within an F2 nursery were assessed in 2020, and the resulting F2:3 progeny rows were planted in 2021 for comparison. Adoption of UAV-based imaging for high throughput phenotyping of above-ground growth characteristics in cultivated peanut is promising.

Contrasts of Peanut Risk Management Tools for Peanuts in Argentina, Ghana, India, Malawi, and North Carolina

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Effectively managing risk is important for success in establishing and maintaining sustainable farming systems. Part of managing risk is knowing how farming practices affect a wide range of pests. A risk tool for North Carolina peanut production (https://peanut.ces.ncsu.edu/peanut-risk-tool-and-field-log/) was developed using Microsoft Excel software. Individual risk indices were developed for over 10 peanut pests commonly found in North Carolina. The risk tool allows practitioners to simultaneously observe the aggregate risk of all practices related to these pests. The main goal of the tool is to assist farmers and their advisors in identifying practices to minimize pest risk. Cost of each practice is included in the risk tool to demonstrate the financial impact that can be observed when practices are adjusted to reduce risk. Similar tools have been developed for Ghana and Malawi production systems. A risk tool is currently under development for India and plans are to develop a risk tool for Argentina. The North Carolina, India, and the planned Argentina risk tools evaluate multiple pest risk indices with a range of tools or practices impacting each pest. In contrast, the Ghana and Malawi risk tools evaluate risk indices for yield and aflatoxin. These risk tools can be downloaded at https://cropmanagement.cals.ncsu.edu/risk-tools/default.html. The tools have also been beneficial in formal classroom instruction and in conversations among collaborative teams of researchers and extension faculty and staff in modifying production recommendations. These interactions have helped researchers identify knowledge gaps on particular pests or pest complexes. Finally, the risk tools are designed to be living tools that can be modified to incorporate new pests or new practices affecting existing pest indices.

Field Measurements, Yield, and Grade of the U.S. Minicore under Water Deficit Stress.

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The U.S. minicore collection was grown in replicated trials under water limiting conditions in Virginia, Oklahoma, and Texas in 2017, and in Virginia in 2018. Data on grade were taken in TX in 2017, and on 100 seed weight in TX and OK. Data collected during the growing season included flower count, SPAD chlorophyll meter reading (SCMR), normalized difference vegetation index (NDVI), canopy temperature, leaf closure rating, wilting rating, plant height and plant width. Pod yield was measured after harvest. Additional data on harvest index and ground penetrating radar were taken in 2018 and 2019. Significant differences were observed among genotypes for all traits measured. Many minicore accessions had consistent phenotypic responses across environments, and significant correlations among traits across locations were observed. Accessions with high yield, grade, and 100 seed weight were identified. Stepwise regression models to explain yield based on ground-based measurements were developed.

Fruit Initiation Response to Early Season Water Stress.

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Daily plant water needs change in response to crop growth stage and water availability. Peanut uses very little water during the early vegetative growth and consequently requires very little supplemental irrigation. The irrigation scheduling tool, Irrigator Pro, does not recommend irrigation during the first 30 d after planting except to promote uniform emergence. Irrigator Pro uses daily water use to forecast irrigation events in association with maximum soil temperature at a 5-cm depth. The developers of Irrigator Pro define the fruit initiation date (FID) as the date that the plants initiated an average of 6 fruit indicators (pins + pegs + pods) per plant. Research indicates that mid-season drought stress may suspend flowering. Therefore, does early season drought affect flowering and the resultant FID?

AU-NPL 17 was planted in two rainout shelters at the National Peanut Research Laboratory in Dawson, GA into a well-watered sandy loam soil at 20 seed/m in rows spaced 0.91 m apart. Each 12-m rainout shelter was divided into two 6-m plots and irrigated based on the average soil water potential measured at 20 and 41 cm. Treatment 1 or control plot applied water when the average soil water potential reached -40 kPa. Treatment 2 (Trt 2) was irrigated when the average soil water potential reached -100 kPa. In irrigation treatment 3 (Trt 3), the first two irrigation events were triggered when the soil water potential reached -100 kPa then irrigated at -40 kPa thereafter. Treatment 4 (Trt 4) triggered the first two irrigation events when the average soil water potential reached -200 kPa then -40 kPa thereafter. Each irrigation event applied enough water to bring water potential to field capacity (-10 kPa).

Between 32 and 55 days after planting (DAP), six plants were removed daily from each plot and the number of flowers, pins, pegs, and pods were counted and the above ground biomass was dried and weighed. The FID was calculated daily using the formula presented in Irrigator Pro. Remaining peanut plants in each plot were taken to yield and harvested by hand.

The average FID for all irrigation treatments occurred 41 DAP (July 01). However, the standard deviation of the FID tended to decrease as the soil water potential to trigger irrigation decreased. The standard deviation of the FID in Trt 1 was ±3.1 d, Trt 2 was ±1.8 d, Trt 3 was ±2.2 d, and Trt 4 was ±0.8 d. The above-ground dry biomass (g/plant) on the FID decreased with increasing water stress and was 17.62, 13.05, 7.95, and 5.48 for Trt 1 to 4, respectively. The final yield for Trt 1, 2, and 3 were similar at 5320, 5099, and 5233 kg/ha, respectively. The final yield for Trt 4 was 4423 kg/ha. The trends in this data are inconclusive and this research should be repeated for multiple years and with current commercial peanut cultivars to verify results.

Determining Residual Length of Control for Soil-Applied Herbicides in Peanut

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Herbicide resistance development among weed species has impacted the sustainability and profitability for many cropping systems across the United States including peanut. In order to prevent herbicide resistance development, the use of preemergence (PRE) herbicides have been a foundational necessity for any program across the US. The utilization of PRE herbicides allows producers the option of more herbicide mechanisms of action (MOAs), reducing selection pressure on any one post-emergent chemistry. The use of herbicides producing long residual periods of control could lead to peanut production with decreased number of applications, mitigation of resistance development, and an overall reduced environmental impact. Therefore, studies were conducted in 2020 and 2021 at the R.R. Foil Plant Science Research Center in Starkville, MS, the Coastal Plain Branch Experiment Station in Newton, MS, and at a research field site in Tillar, AR to determine the length of residual control of common soil applied herbicides used in peanut production. Two treatments of herbicide combinations were also investigated to determine if the use of multiple MOAs in a single application resulted in greater duration of residual control. Visual weed control evaluations were taken weekly beginning 7 days after application and lasting until 50% weed control occurred for each treatment. Data were subjected to ANOVA using RStudio and means separated using Fisher's protected LSD ($\alpha=0.05$) were significance was observed. Regression analysis was also conducted with time as a factor to estimate week control exhibited by individual treatments following application. Data analysis of 2020 some differences among herbicide treatments with respect to residual duration, however 2021 data has not been collected at the time of writing this abstract.

Disease and Yield Response of Selected Peanut Cultivars to Low and High Input Fungicide Programs in Southeast Alabama

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The reaction of twelve peanut cultivars to early leaf spot *Passalora arachidicola,* late leaf spot *Novopassalora personatum*, and rust *Puccinia arachidis* along with white mold *Athelia rolfsii* as influenced by fungicide program was assessed in southeast Alabama at the Wiregrass Research and Extension Center (WREC). Leaf spot intensity was evaluated using the Florida 1-10 leaf spot scoring system and rust was evaluated using the ICRISAT 1-9 rating scale. Stem rot incidence was assessed immediately after plot inversion by counting the number of disease loci per row. Yields were reported at <10% moisture.

For the no-fungicide control, leaf spot-incited defoliation differed significantly across cultivars with AU-NPL 17, and Georgia-14N, and TifN/V High O/L having lowest defoliation. While rust was sporadic throughout the plots, highest rust intensity was with Georgia-16HO. With the standard fungicide program, Georgia-18RU, TUFRunner 511, AU 16-28, TUFRunner 297, and Georgia-09B had significantly greater defoliation levels than AU-NPL 17 and TifN/V High O/L. While significant differences in defoliation were noted with the intensive fungicide program, defoliation levels were low across all cultivars. White mold incidence was greater for Georgia-09B than Georgia-16HO along with TifN/V High O/L, Georgia-12Y, FloRun 331, and Georgia-14N with the latter four cultivars having similarly low disease indices. The intensive fungicide program greatly reduced this incidence of this disease compared with the standard fungicide program and the nontreated-fungicide control. While the high yield recorded for Georgia-14N was equaled by Georgia-16HO, Georgia-06G, and TifN/V High O/L, similarly low yield was recorded for Georgia-09B, TUFRunner 511, and TUFRunner 297. Pod yield reported for the intensive fungicide program was significantly greater compared with the standard and no fungicide control with the latter having the lowest yield.

Aroma Profile of Nineteen Cultivars of Roasted Peanuts

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The aroma profile of 19 commercially available peanut cultivars was determined. There were 12 runner (10 high-oleic [HO] varieties), 5 virginia (2 HO varieties) and 2 spanish cultivars (both HO varieties). The aroma volatiles of the peanut samples roasted to medium roast levels were extracted using headspace solid-phase microextraction (HS-SPME) technique. A gas chromatograph coupled to a mass spectrometer (Model 7890A/5977A, Agilent Technologies, Santa Clara, CA) was used to separate and identify 14 volatile aroma compounds in the samples. A one-way analysis of variance with cultivar as the main factor revealed differences in aroma volatiles among the cultivars. The four runners – Georgia 13M (HO), TUFRunner™ '297' (HO), AU-NPL 17 (HO), and Georgia 06G (normal-oleic [NO]) had the most amounts of total aroma volatiles. Georgia 16HO (HO) and FloRun™ '331' (HO), both runners, and the two spanish cultivars (TamNut OL06 and OLé; HO) had intermediate amounts of total aroma volatiles. The five virginia cultivars, along with the rest of the runners (mostly HO) had low amounts of aroma volatiles. The principal components analysis (PCA) biplot also reiterated the findings above, where Georgia 13M (HO) and TUFRunner™ '297' (HO) were characterized by having the most volatiles. These were followed by AU-NPL 17 (HO), Georgia 06G (NO), and the two HO spanish cultivars (TamNut OL06 and OLé; HO). It can be inferred from this study that runner and spanish cultivars have higher contents of aroma volatiles than virginia cultivars. It would be interesting to determine the relationships of the aroma volatiles with sensory characteristics.

Breeding Spanish Peanuts (*Arachis hypogaea* L.) for Organic Peanut Production In West Texas.

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Organic peanut production is centralized in West Texas, with estimates indicating as much as 98% of all organic peanuts in the U.S are produced in this region. Organic producers have limited options with regards to fungicides, herbicides, and seed treatments in order to control several key production issues. Without the use of commercial products, organic fields often have poor germination and stand establishment, as well as weed and disease control issues throughout the season. The Texas A&M AgriLife Research Peanut Breeding Program initiated an evaluation of current germplasm in 2020 in an on-farm trial in Terry Co. Texas. Twenty breeding lines and cultivars were evaluated. Each entry was replicated 3 times without any commercially available seed treatment. Plots were arranged in a randomized complete block and stand counts were taken by hand at 7, 14, 21 and 28 days. In addition, plot data was collected and evaluated for plant height, visual greenness, pod rot, yield, and grade. Visual differences were observed based on date of stand counts and plant height. Statistical differences were found in kg/ha, %TSMK and %DK. Of particular interest was that the location had heavy pod rot infestation with 2 entries showing statistically significantly reduced %DK. Data will be presented. This project will be replicated in 2021, and expanded on, in order to develop breeding lines specifically suited for the unique needs of organic peanut producers as an objective.

2021 Panhandle Row Crops Update Series: Connecting Producers Virtually to Research from Three Land Grant Institutions

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Situation: The project aimed to move traditional, in class educational opportunities to a virtual world for producers due to Covid 19. By offering four winter educational row crop production programs through Zoom, UF/IFAS Extension agents wanted to continue to teach farmers in a safe way. The weekly February series covered the following topics: Cotton, Peanuts, Corn/Soybeans, and Precision Agriculture. Agents filmed videos with Florida, Auburn, and Georgia specialists in Fall/Winter, then edited them to show for the winter meetings.

Objectives: To educate 125-200 producers on row crop management practices and acquire skills related to integrated pest management and best management practices (at least 80% of participants will increase knowledge); at least 50% of participants will adopt behavior changes in one or more of these areas; 100-125 producers and industry personnel would receive training in utilizing restricted use pesticides (80% of participants would receive certification or recertification through FDACS or CCA).

Evaluation: An initial survey was developed before the series began to be used at the very end of each learning session to gather baseline data for the project. A follow up Qualtrics survey has been developed and will be distributed to growers who participated in mid-Summer.

Results: Webpage with 24 YouTube videos and presentations for farmers to review the series, 284 people from 17 Florida, 3, Georgia, and 4 Alabama Counties, 263 pesticide applicators for points, 15 CCA CEUs, 229/231 (99%) of respondents reported a knowledge gain, 168/232 (72%) of respondents reported an anticipated practice change, 11/43 (26%) of survey respondents expect cost reductions on farm from their anticipated change. **Conclusion**: Ag business representatives were pleased with the opportunity to address clientele through this innovative meeting approach. Farmers sent texts and emails relaying that it was good to see what new research had come out from 2020 work. The people who needed CCAs were particularly satisfied in the ease of the process. Extension agents were pleased with the number of participants who used Zoom for the first time to get the information. Protocol

Screening for Amino Acid Content in Peanut (*Arachis hypogaea* L.) Using Raman Spectroscopy.

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Nutritional enhancement of plant-based proteins is becoming increasingly important in the quest to feed our increasing population. Peanut is an excellent protein source but is lacking in the amino acids Lysine and Methionine. Although produced at low levels these two essential amino acids (EAA) are in amount below nutritional requirements. We are using Raman Spectroscopy (RS) to compile chemometric fingerprints of the Texas A&M AgriLife wild and cultivated germplasm collection. Raman Spectroscopy is a noninvasive, nondestructive laser-based scan that provide phenotypic information. Raman spectroscopy uses a laser to interact with the chemical bonds present in the sample. The initial phase of the project involves collecting spectra from cultivated breeding lines (2n=4x=40) and validating the amino acid content using Gas Chromatography-Mass Spectroscopy (GC-MS). Once RS is correlated to GC-MS in cultivated germplasm, we will collect additional scans from wild Arachis accessions (2n=2x=20) to validate the finding in the diploid relatives. The final portion of phase one will be screening our entire germplasm collection for elevated levels of the limiting EAA. Phase two of the project will be to determine where the genetic pathways in question are affected to develop a plan for incorporating the trait into cultivated germplasm. We will then use traditional introgression, Marker Assisted Selection, Raman Based Selection or Gene Editing to transfer the elevated EAA levels into elite breeding material.

Using Multispectral Drone Camera to Differentiate Drought Tolerant Recombinant Inbred Lines of Peanut Grown under Rainout Shelters

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Peanut (*Arachis hypogaea*, L.) yield and quality are limited by drought worldwide. Peanuts require a minimum of 600 mm of water regularly distributed throughout the growing season. The summer months often lead to precipitation deficits, with recurrent drought events leading to limited availability of water that may impact pod yield. Producers are supplementing water through irrigation but, with only 35 % of the peanut acreage in the U.S. equipped of such systems, most of the fields are rainfed. Therefore, peanut producers will need to adopt drought tolerant cultivars improved in yield and quality, to maintain the competitiveness of the U.S. peanut stakeholders in the marketplace. To achieve this, phenotyping is generally used to screen lines within the breeding pipeline, resulting in the development of new cultivars. However, manual ground measurement of the field traits is laborious, time-consuming and sometime subjective. Unmanned aerial vehicles (UAV), equipped with sensors, are fast development technologies, and can acquire data quickly, repeatedly, with increased resolution and reliability. In this study, 56 recombinant inbred lines (RIL) were selected from a population of 340 [developed from the cross of N08086olJCT: a large seeded Virginia-type and high yielding line and ICGV 86015: an early-maturing drought tolerant Spanish-type line coming from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)]. They were grown at the Tidewater AREC in Virginia under rainout exclusion shelters to mimic drought as well as in irrigated field plots. Regularly throughout the growing season, aerial data were collected using a multispectral camera to more reliably differentiate and identify drought tolerant RILs. Drought tolerant RILs would be defined as not displaying a loss of growth and yield caused by the use of the shelters and also a fast recovery once the shelters were removed. This first-year experiment has shown an existing variability between RILs among the different traits analyzed.

Identification of U.S. Germplasm Resistant to Peanut Smut.

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Peanut smut, caused by *Thecaphora frezzii*, is an emerging threat to global peanut production. Found in 100% of Argentinian peanut growing regions, smut infestation can result in substantial yield reductions. Although peanut smut has not been reported outside of Brazil and Argentina, immediate proactive measures must be taken so that global peanut production will not be threatened. The first step in preventative breeding for resistance to peanut smut is to identify key sources of resistance. Therefore, the objective of this study was to identify sources of resistance to *T. frezzii* that can be used to incorporate smut resistance into cultivars optimized for key areas of U.S. peanut production. In this study, peanut genotypes, including accessions from the USDA Peanut Germplasm collection purified by single-seed descent and U.S. cultivars, were screened for resistance. Trials were planted in test plots where peanut smut is prevalent near General Deheza (Córdoba Province), Argentina, and arranged in an augmented grid design with three replicates. For screening purposes, entries were retained for future testing if they scored 10% or less disease incidence. Among the entries tested in the 2017-2020 growing seasons, potential new sources of peanut smut resistance were noted. Eight USDA peanut mini-core accessions were identified as near-immune, demonstrating 0% incidence for three years. Proven resistant sources are being used to incorporate this resistance into peanut cultivars suitable for production in all growing regions of the U.S.
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APRES
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~~Abstract~~

High-Throughput Phenotyping Enables Indirect Selection f~~F~~or Leaf Spot a~~A~~nd Groundnut Rosette Disease Resistance i~~I~~n Peanut Breeding Program In Uganda

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Late leaf spot (LLS) caused by *Cercosporidium personatum* (Berk. & Curt.) and groundnut rosette disease (GRD) (genus *Umbravirus;* family *Tombusviridae*) present the most important biotic constraints to groundnut production in Uganda. Acquisition of high-quality phenotypic data is important for effective selection for resistance for LLS and GRD in groundnut breeding. The application of traditional phenotyping methods like visual scores and manual counts for assessing the incidence and severity of disease symptoms is resource-intensive and subjective. Remote sensing methods for high-throughput phenotyping are readily available for the identification of stress symptoms in plants but have not been tested for effective deployment for LLS and GRD resistance selection in groundnut breeding. In this study, we evaluated whether high-throughput phenotyping (HTP) can replace visual assessments of LLS and GRD disease symptoms. HTP involves the use of advanced technologies for fast and accurate collection and extraction of phenotypic data by automation. A field experiment of 50 genotypes was planted under rain-fed conditions across two breeding locations; NaSARRI, Serere, and Nakabango, Jinja; both locations are LLS and GRD hotspots. Data was collected using both visual assessment and HTP sensors; red-green-blue (RGB) camera for the images, GreenSeeker for normalized difference vegetation index (NDVI), and FLIR thermal camera for canopy temperature (CT). Results from the Pearson correlation analysis indicated that NDVI (r = -0.88), Greener area (GGA) (r = -0.75), and Green area (GA) (r = -0.7) were negatively correlated with LLS scores. CSI (r = 0.87) and CT (r = 0.69) were positively correlated with the LLS scores. NDVI, GA, and GGA (r = -0.69, -0.69, -0.68, respectively) were negatively correlated with GRD percentage disease index (PDI), and a*, u*, CT, and CSI (r = 0.7, 0.7, 0.65, 0.6 respectively) were positively correlated with GRD PDI. Our findings indicated that HTP indices are highly correlated with LLS and GRD visual scores and can be applied for indirect selection for GRD and LLS resistance in groundnut breeding. Further studies will aim at the development of prediction models using the HTP indices to be applied for routine selection in the peanut breeding program in Uganda.

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A Tree of Relationships of Section Arachis of Unprecedented Scope and Detail

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The 33 described species within the botanical section Arachis, the wild species most closely related to cultivated peanut (*Arachis hypogaea*), are of particular interest because they can be used as sources of diverse alleles in breeding. They have been the subject of intense collection and characterization. Here we studied 659 germplasm samples representing deposits in national collections in EMBRAPA (Brazil), IBONE (Argentina), USDA (USA) and seeds from active research programs in Texas A & M, North Carolina State and the University of Georgia. These 659 samples represent 296 accessions, virtually all collections of wild peanuts within the Arachis section ever made. The DNA of these germplasm samples was characterized with 14K informative SNPs after the genotyping using the Axiom Arachis Array with 48K SNPs. This matrix of data was used to generate a phylogenetic tree of relationships of the 588 diploid germplasm samples after curation and a tree with 287 germplasm accessions with a unique sample per accession. These trees broadly supported the division of the section into the six genome types with almost all accessions assigned to A genome species forming a well-defined clade. The non-A species form another clade with clear separation of genome types; the most derived B genome clade being associated with the F, D, K and 2n=18 clades in increasing genetic distance respectively. *A. hoehnei*, a species of as yet undefined genome type, is positioned at the periphery of this non-A group. Some species classifications were well-supported: for instance, *A. duranensis* and *A. stenosperma* accessions cluster in well-defined monophyletic clades. The genetic structure of the 35 accessions of *A. stenosperma* strongly supporting the theory of its use and transport by Amerindians prior to the European discovery of South America. Other species showed clear polyphyletic groupings, for instance *A. kuhlmanni* clustering in at least four distinct groups. Still others, such as *A. correntina* form paraphyletic groups. A group of miscellaneous and new collections positioned between the A and non-A clades may represent undescribed species. In summary, this analysis of unprecedented scope and resolution gives a powerful tool to confirm accession identities, and explore and revise the species structure of the section Arachis.

APRES
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Characterization of a New Virginia-type Peanut Cultivar “AU14-34”

Charles Chen*, Kris Balkcom, Austin Hagan Auburn University, Auburn, AL 36849; Lisa Dean, Phat Dang, Marshall Lamb, USDA-ARS National Peanut Research Lab, Dawson, GA 39842; Ming Li Wang, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA 30223.

The original pure breeding line ‘AU14-34’ originated as an F_6 single-plant selection from the cross of FL-07 xVa98R. ‘Florida-07’, a runner-type peanut with high oleic fatty acid trait, was developed from a breeding line 89xOL14-11-1-1-1-b2-B and C99R by Gorbet et al. (2009) and VA98R (PVP 9,900,419), a Virginia peanut, developed at the Tidewater Agricultural Research and Experiment Station in Suffolk, VA (R. Walton Mozingo et al. 2000). The new cultivar is a Virginia-type peanut. It has a prostrate growth habit with a main stem. Seeds of ‘AU14-34’ are pink testa seed coats. ‘AU14-34’ flowers approximately 35 days after planting and is of medium maturity of 140 days in the Southeastern growing region. It is high-yielding, tomato spot wilted virus (TSWV) resistant, leaf spots tolerant, high grade, and superior shelling characteristics. It has high oleic fatty acid content and good flavor. The hundred seed wight of ‘AU14-34’ is 95.5 g. The foundation seeds will be produced in 2021.

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Characterization of a New Virginia-type Peanut Cultivar “AU14-34”

C. CHEN*, K. BALKOM, A. HAGAN Auburn University, Auburn, AL 36849; L. DEAN, P. DANG, M. LAMB, USDA-ARS National Peanut Research Lab, Dawson, GA 39842; M.L. WANG, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA 30223.

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Thrips and Tomato Spotted Wilt Orthotopsovirus Resistance on Wild Relatives by Greenhouse Evaluation

Y-J. CHEN*, R. SRINIVASAN, Entomology Department, The University of Georgia, Griffin, GA 30223; and S. LEAL-BERTIOLI, Department of Plant Pathology, The University of Georgia, Athens, GA 30602.

Tomato spotted wilt orthotopsovirus (TSWV) is transmitted by thrips in propagative and persistent manner. Tobacco thrips, *Frankliniella fusca* (Hinds), is the major vector of tomato spotted wilt disease in peanut. Wild species are the potential sources of resistant peanut. 14 diploid or induced allotetraploid genotypes were screened by the thrips-mediated transmission assays in greenhouse during 2019 and 2020. TSWV infection rate and severity of thrips feeding injury on foliage were evaluated. Two years results showed that diploid *Arachis stenosperma* V10309 and induced tetraploid BatDur1 and ValSten have potential resistance to TSWV. Since thrips resistance was conducted by feeding injury overtime, only BatDur1 showed lower feeding damage index (FDI) after 14 days inoculation; Valida, Villosa, and BatDur1 showed lower FDI after 21 days inoculation. The heritability of resistance to TSWV and thrips in wild genotypes was discussed.

Release of Two Early Maturing Spanish Peanut Varieties for Production In Malawi

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Early maturity in peanut is an important trait which enables its production in places where seasons are short and prone to end season drought. In order to improve peanut productivity in these areas, sixteen elite spanish groundnut genotypes were selected from the ICRISAT's regional breeding nursery and evaluated alongside two released check varieties in Malawi. The trials were done in three seasons and laid out in an incomplete block design with 3 replications. Significant differences were observed in terms of yield among the genotypes in all sites. On average, across the test sites, the following test genotypes out yielded the check Kakoma; ICGV-SM 03530 by over 12.9%, 31.3 % and 13.3% in 2014/15, 2015/16 and 2016/17 seasons respectively; ICGV-SM 08528 by over 34.1%, 17.5%, 8.2% and 35 % in 2014/15, 2015/16, 2016/17 and 2017/18 seasons respectively; and ICGV-SM 08538 by over 41.3%, 18.7%, 16.5% and 11.3% in 2014/15, 2015/16, 2016/17 and 2017/18 seasons respectively.

The genotypes ICGV-SM 08538 and ICGV-SM 03530 were among the most stable genotypes. Because of the excellent performance of these two Spanish genotypes, they were released for use by farmers in Malawi in the year 2020.

Genetic R~~r~~ecombination in a N~~n~~ew MAGIC P~~p~~opulation of P~~p~~eanut

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In order to overcome the limitation of allele diversity in bi-parental based inbred populations, a multi-parent advanced generation intercross (MAGIC) population of peanut is under construction. To maximize diversity, 18 founder parents with highly diverse characteristics including morphological, disease resistance, responses to drought stress and aflatoxin accumulation have been intercrossed in a partial MAGIC scheme. Three rounds of crossing are being completed before generation advance. The first round of 9 crosses was accomplished by random 2-way pairings among the founder parents. The second round of 4-way crosses aimed to pair once among the two-way F_1 hybrids which yielded 169 4-way F_1s from 32 combinations. The genetic materials involved in this study were genotyped by the version 2 *Arachis* SNP array. Known introgressed regions from *Arachis cardenasii* on chromosomes A02, A03, A08 and A09 were mapped among 4-way F_1 hybrids. These introgressed regions have been reported to confer disease resistance to peanut root-knot nematode, early leafspot, late leafspot and rust. F_1 hybrids with all introgressed regions could be used to test the effect of pyramiding alleles on these major peanut diseases. In addition, unique alleles extracted among the founder parents enable the counting of recombination events and determining allele contributions among these genetic materials.

Fast, Accurate, Low Coverage Sequencing for Genome Wide Genotyping Large Populations for Genetic Improvement

J. CLEVENGER*; W. KORANI. Hudson Alpha Institute for Biotechnology, 601 Genome Way Huntsville, AL 35806

Genetic improvement using genomics relies on the quality, quantity, and cost of genome wide molecular markers. Marker types have evolved dramatically since the advent of the peanut genome initiative and subsequent release of a high-quality reference genome for peanut. Currently, there are two large scale single nucleotide polymorphism (SNP) arrays that provide a cost effective and accurate set of markers for researchers. However, these SNP arrays were designed using only a small population of peanut genotypes with available sequence and as such the arrays suffer from strong ascertainment bias. The most effective marker system uses genome-wide sequencing to theoretically assay all DNA sequence variation within a population, but sequence cost and informatics has been a limiting factor. We have recently developed an informatics pipeline, Khufu, that is highly accurate calling alleles in peanut with very low coverage sequencing (1X coverage). Using published datasets and sets of known true SNPs, we show that Khufu exhibits higher than 99% allele call accuracy in peanut using as low as 0.5X coverage whole genome sequencing. Additionally, more than 90% of the possible SNPs are recovered with 3X coverage sequencing. The cost of sequencing and accuracy with low coverage reduces per sample cost to that of fixed arrays. The combination of population-specific, *de novo* SNP sets, with low cost and high throughput makes genotyping with Khufu the best option for genetic mapping, diversity studies, and other genomics analyses.

Insoluble Polyphenols Mediate *Aspergillus Flavus* Resistance in Peanut

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Aspergillus flavus invasion in peanut has been a major drawback in the peanut industry with most of the infection occurring in the post-harvest stage. At the postharvest stage, the seed coat is the only outer layer protecting the endosperm from pathogen infection. The seed coat is made up of secondary metabolite called polyphenols which are important determinants of color, taste and flavor of foods. These polyphenols can be grouped into soluble and insoluble polyphenols. We sought to identify which component of these biochemicals present in peanut seed coat plays a role in *A. flavus* resistance. Soluble polyphenol was extracted using acetone, acetic acid and water. Insoluble polyphenols were freed from the wall bound compounds using alkaline hydrolysis and HCL complementation, followed by extraction with acetone, acetic acid and water solution. The radial growth bioassay using these compounds showed that insoluble polyphenols showed a greater resistance to *A. flavus* growth as compared to soluble polyphenols. Solid phase extraction (SPE) techniques were used to fractionalize the polyphenols into phenolic acids, flavanols and anthocyanin groups. We have identified 8 phenolic acids by complimenting the SPE techniques with the HPLC.

The results observed indicates that the seed coat biochemicals contains certain biochemicals which could be used to regulate *A. flavus* contamination in peanut.

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A Potential New Source of Rust (*Puccinia arachidis*) Resistance from Wild Peanut Relatives *Arachis stenosperma* and *Arachis batizocoi*

K.M. COSTELLO*, S.C.M. LEAL-BERTIOLI, C. BALLEN-TABORDA, M. HOPKINS, Department of Plant Pathology, University of Georgia, Athens GA 30602, D.J. BERTIOLI, Department of Crop and Soil Sciences, University of Georgia, Athens GA 30602

Due to its low genetic diversity, cultivated peanut (*Arachis hypogaea*) is susceptible to many pathogens and pests and relatively few sources of resistance have been found in the cultivated gene pool. *Puccinia arachidis* (peanut rust) is a pathogen that plagues many peanut farmers around the world. Wild peanut relatives have been found to be resistant to various pathogens including rust. This project focuses on a population that has been produced by backcrossing *A. hypogaea* with an allotetraploid derived from the wild peanut relatives *A. batizocoi* and *A. stenosperma,* called GA-BatSten1. Segregant lines have been found to have resistance to rust along with other pathogens. The goal of this work is to genetically identify wild segments that confer the resistance to rust to enable the production of new resistant lines using marker assisted selection. For this, lines were phenotyped for rust and genotyped using the Thermofisher Arachis Array with 36K SNP markers. Two highly resistant families from this population have been identified. This information will be used to breed a new peanut cultivar with rust resistance peanut that will be beneficial for peanut farmers around the world.

Phenotyping the US Mini-core Collection to Identify Drought Tolerant Peanut Genotypes Using Environmental Control Plots

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Drought is a major abiotic stress in peanut that can cause significant yield loss and reduce seed quality. Breeding for drought tolerance has been challenging due to multi-allelic affect and variable environmental factors. The US mini-core peanut germplasm collection provides a small and diverse genetic panel that can be evaluated to identify potential drought tolerant genotypes. This research aims to associate physiological, agronomic, and molecular plant responses to identify drought tolerant lines by evaluating 162 peanut accessions, including the US mini-core collection. Peanuts were evaluated during the 2017 and 2018 growing seasons, utilizing environmental control rainout shelters (Dawson, GA). A middle-season 30-day drought was applied at 70 days after planting followed by re-irrigation until harvest. Physiological measurements, such as specific leaf area (SLA), relative water content (RWC), and leaf dry matter content (LDMC) were taken every week during drought and one week following irrigation. Drought was rated on a scale of 1 (no wilting) to 5 (complete wilting) taken just before irrigation. Pod yield (pod weight and number) was measured at the end of the growing season. Correlation of measured traits was utilized to identify drought tolerant genotypes. A genome wide association study (GWAS) is in progress to identify quantitative trait loci (QTLs) associated with drought tolerance. Results will facilitate development of drought tolerant peanut varieties for the US peanut industry.

Validation and Utilization of SNP Markers for Introgression of Late Leaf Spots Resistance Genes in Peanut

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Late leaf spots disease (LLS) causes over 70% yield loss to peanuts in Ghana by reducing plant area available for photosynthesis. Host-plant resistance offers a safe and efficient way in controlling LLS. Molecular markers such as Single Nucleotide Polymorphism (SNP) markers promote selection efficiency and genetic gain in breeding. Four SNP markers have been proposed by INTERTEK Laboratory, Sweden but have not been validated in West Africa. The most popular variety of peanut in Ghana known as 'Shitauchi' is susceptible to LLS and needs to be improved. The objective of this research was to validate four SNP markers for identification of LLS resistant plants. A total of 150 F_2 seeds were generated from hybridization of LLS resistant 'CS16' variety and susceptible 'Shitauchi' variety. A small portion of seed cotyledon was sampled from each of the 150 F_2 seeds and genotyped with four SNP markers at INTERTEK laboratory in Sweden. The F_2 generation seeds were planted in pots and inoculated with conidia suspension of *Phaeoisariopsis personata* (causal agent of LLS). A 9-point rating scale was used to phenotypically screen the F_2 plants. SNP marker GKAMA02GL779 was not polymorphic, indicating it could not distinguish between the resistant and susceptible parents. The other 3 markers were polymorphic. SNP markers GKAMA02GL582, GKAMA02GL975 and GKAMA02GL829 had R^2 values greater than 0.5 which indicates strong effects of the markers on LLS suggesting that these markers can be used effectively in early generation selections for LLS resistance. Availability of validated SNP markers have enabled accelerated introgression of LLS resistance genes into a susceptible variety of peanut. Three out of the 4 proposed markers for LLS resistance breeding have been validated and can be used to aid the introgression of LLS resistance genes in a marker assisted backcross breeding program

PeanutBase: Mining Genetic and Genomics Data Using the PeanutMine

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PeanutBase was started in 2013 to serve as the primary repository for peanut genetic and genomic data generated by the International Peanut Genomics Initiative. The website and database, which has been supported by The Peanut Research Foundation over this period, has matured in concert with the Genomics Initiative, and now provides tools that allow researchers to explore the diploid ancestral genomes (A. *duranensis* and A. *ipaensis*) and the cultivated peanut (Tifrunner) genome.

The website integrates most major data types involved in peanut genetics and genomics, including: genetic markers from numerous genetic maps and from the main genotyping chip (Affy 48k SNP set); images of accessions/varieties in the U.S. peanut collection; an interactive map of the geographic origins of all Arachis material in the U.S. collection; mapped traits; and gene expression data for all genes and for a wide range of tissues and developmental stages. The current efforts are directed to keep PeanutBase current with rapidly-progressing research in peanut.

Tools are also being developed in parallel to visualize such data and aid in its utilization in crop improvement. In this presentation we will focus on using the PeanutMine for ease in mining genomic and genetic data.

Peanuts as a Source of Vegetable Protein: Past Successes and Future Challenges

L. L. Dean*, Food Science and Market Quality and Handling Research Unit, USDA, ARS, SEA, Raleigh, NC 27695-7624.

The current interest in nonanimal sources of protein in the human diet has increased exponentially in past few years. Peanuts are well positioned to benefit from this phenomenon. Defatted roasted peanuts have been used to produce flours and powders with high levels of protein that are used in a range of food products. Marketing strategies to emphasize these aspects have brought renewed attention to these products. Recent research has reported on improvements to human health related to consumption of these products.

As a legume, peanuts which are processed by operations other than roasting can be the source of peanut protein with different functionality and applications that can put them on par with more typical sources of vegetable protein such as peas and beans. Higher value products can be produced from peanut that can serve as ingredients in meat substitutes, extruded snacks, bioactive peptides, and other nutraceuticals. Investigations into possibilities for new directions for applications of peanut protein are available and their focus will be discussed.

Overview of Groundnut Rosette Disease: Past, Present and Future.

C.M. DEOM*, Department of Plant Pathology, University of Georgia, Athens, GA 30602-7274; D.K. OKELLO, National Semi-Arid Resources Research Institute (NaSARRI), Serere, Uganda, P.O. Box 56

Groundnut rosette disease (GRD) is the most destructive viral disease and arguably the most important pathogen of groundnut in Sub-Saharan Africa (SSA). GRD is endemic to, and ubiquitous in, SSA and its off-shore islands. The disease causes significant economic losses, up to 100% yield losses if infection occurs before flowering and during severe epidemics, and routinely jeopardizes food security and livelihoods of groundnut farmers. Groundnut was introduced into Africa from Brazil by the Portuguese explorers in the 1600s. The disease was first reported on groundnut in Tanzania in 1907.

GRD results from an intimate interaction between groundnut rosette assistor virus (GRAV, member of the genus Enamovirus), groundnut rosette virus (GRV, member of the genus Umbravirus), and the satellite RNA (satRNA) of GRV. The disease is transmitted persistently by the aphid, *Aphis craccivora* Koch. (cowpea aphid or groundnut aphid). Host plant resistance is the most economical way of minimizing losses due to GRD. Presently, almost all cultivars developed in Uganda have resistance to GRD. Research efforts have endeavored to breed GRD resistance varieties that are high yielding, drought tolerant, have resistance to other pathogens and pests, have a short to medium maturity period, as well as other agronomic important traits. While GRD presently is endemic to SSA, the aphid vector is found worldwide. So, the potential for GRD to emerge and spread over groundnut growing regions of Asia and the Americas is a legitimate concern. Future research will better define the genetic architecture of GRD resistance that will allow marker assisted selection for rapid development of GRD resistant production packages. Better understanding the etiology and molecular pathology of the disease will also allow for a better understanding of GRD resistance and how to optimize disease control strategies.

Development of Taqman Assay for the Detection of Groundnut Bud Necrosis Orthotospovirus on Peanut: A Quarantine Pathogen in the USA

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It is extremely important to avoid the entry of exotic pests while allowing the safe exchange of plant propagation material, which is important for genebanks and breeding programs. Groundnut bud necrosis orthotospovirus (GBNV) is a thrips-transmitted virus restricted to southeast Asian countries. The presence of major hosts (peanut, tomato and potato) and the vectors (*Frankliniella schultzei, Scirtothrips dorsalis* and *Thrips palmi*) within the USA make GBNV an important quarantine pathogen. The objective of the current study is to develop sensitive and specific, diagnostic assay to detect GBNV facilitating quarantine and phytosanitary procedures and transfer the work instruction to USDA-APHIS-PPQ. For assay optimization isolates of GBNV collected from ICRISAT, Hydrabad and IARI New Delhi, in India. Specific primers and probe sets were designed to target conserved regions of the nucleocapsid (NP) and movement protein (MP) genes using the GBNV complete NP (54) and MP (47) sequences which were available in NCBI GenBank till April 2019. Plant gene Actin 11 (*act11*) specific primers and a probe were used as internal control. Using conventional RT-PCR the presence of the virus was confirmed in the received samples. The amplification of NP and MP genes were successful using SYBR Green based qRT-PCR. The specificity and qualitative ability of the assays were confirmed using amplification profiles and melting curve analysis. Disassociation curves with a single peak were obtained for the targeted NP and MP regions of GBNV genome and *ACT11*. In singleplex TaqMan assays, the efficiencies observed were 91.6% and 90.6 % for NP and MP, respectively. The assays were sensitive to detect GBNV in a minimum of 0.05ng/µl of total RNA. For all the specific reactions, high fluorescence signals were observed, and no significant non-specific amplification plots were obtained with other orthotospoviruses GRSV, TCSV, and TSWV present within US. As a conclusion, optimized TaqMan based triplex qRT-PCR was developed for detection of GBNV.

Response of Peanut to Exposure Timing and 2,4-D choline plus Glyphosate Rate

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Peanut is commonly grown in close proximity to Enlist cotton, soybean, or corn fields in the southeastern US. 2,4-D choline plus glyphosate is primarily applied for weed control in Enlist system, so there is potential for herbicide drift to adjacent peanut. A field research was conducted to evaluate response of peanut exposure timing (at 25, 50, and 75 days after planting) to different rates of 2,4-D choline plus glyphosate applied at: 2.1 plus 2.2; 8.4 plus 8.8; 33.6 plus 35.2; and 134.4 plus 140.8 g ae ha^{-1}, respectively. Significant interaction was observed between peanut exposure timing and 2,4-D choline plus glyphosate rate on peanut injury, and canopy width, height, and yield reduction. The interaction illustrated that peanut injury, canopy height or width reduction was higher when exposed during early growth timing with the higher herbicide rate. At 2 WAT, peanut injury was ≥14% when exposed at 25 DAP compared to 75 DAP. Similar result was observed at 4 or 8 WAT where injury was higher on peanut exposed to 2,4-D choline plus glyphosate at 25 compared to 75 DAP. Herbicide rate effect was observed for peanut injury where higher rate resulted in greater injury at all the evaluation timings. 2,4-D choline plus glyphosate exposure at 25 DAP resulted higher peanut canopy (≥13%) and height (≥6%) reduction compared to 75 DAP exposure. Difference in peanut canopy and height reduction was observed with herbicide rate. Yield reduction was not influenced by peanut exposure timing; however, significant difference was observed with 2,4-D choline plus glyphosate rate. This research highlighted that 2,4-D choline plus glyphosate drift can cause significant injury on peanut depending on herbicide rate and exposure timing, and yield reduction could depend on the 2,4-D choline plus glyphosate exposure rate.

Peanut Response to Multiple Exposures of Low Rates of Enlist Duo®

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Cotton was planted on 6.8 million acres in Texas in 2020. Although the majority of these acres were planted to XtendFlex® cotton varieties, Enlist™ cotton made up approximately 15% or 1 million acres. The increase in Enlist™ cotton acres would suggest an increase in the number of applications of Enlist Duo® (2,4-D Choline + glyphosate) with Colex-D® technology. Peanut tolerance studies were conducted in 2019 and 2020 in Gaines County, TX and in south Texas near Yoakum under weed-free conditions. Enlist Duo® was applied at 0.0195 (1/100X) or 0.039 (1/50X) lb ae/A at 30 and 60 days after planting (DAP) or at 30 followed by (fb) 60 fb 90 DAP. Peanut visual injury was scored on a scale of 1-5 (1=no injury, 2=25% of leaves exhibiting symptoms, 3=50% of leaves exhibiting symptoms, 4=75% of leaves exhibiting symptoms, and 5=100% of leaves exhibiting symptoms). Plant stunt, yield, and grade were determined. Georgia 09B was planted at both locations in both years.

In Gaines County, a visual injury scores up to 1.88 and 2.8 was observed following the low and high rate of Enlist Duo®, respectively, but no injury was observed 100 days DAP. In 2020, no visual injury was observed following the low rate of Enlist Duo® and no injury score exceeded 2 following the high rate regardless of the number of sequential applications. No peanut stunt was observed in either year. Peanut yield ranged from 6933 to 7588 lb/A in 2019 and from 3238 to 3619 lb/A in 2020 and were not different from the non-treated control. No difference in peanut grade (SMK, SS, SMK+SS, OK) was observed in either year at Gaines County.

At the south Texas location near Yoakum, a visual injury score up to 2 was observed in 2019 regardless of Enlist Duo® rate and number of sequential applications. In 2020, no visible injury was observed following the low rate of Enlist Duo®, but an injury score as great as 3 was observed following the high rate. No peanut stunt was observed in 2019 and 2020. Peanut yield ranged from 2661 to 3230 lb/A in 2019 and from 2184 to 2698 lb/A in 2020 and were not different from the non-treated weed-free control. No difference in peanut grade (SMK, SS, SMK+SS, OK) was observed in either year at Yoakum.

Weed Management Programs in Peanut

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Weed control in peanut is crucial. Yields losses attributed to competition with weeds can be as high as 60%. A diversified herbicide program is key to weed management in peanut, this includes both preemergence (PRE) and postemergence (POST) applications. The objectives of this project were to evaluate the efficacy of various herbicides combinations to determine best management options for weed control in peanut.

This multi-state research was conducted in Georgia, Mississippi, and Oklahoma in 2020. Treatments included Valor (2 oz/A), Outlook (12.8 fl oz/A), and Pursuit (4 fl oz/A) applied PRE alone and in combination. Pursuit was applied PRE or as a split application PRE (2 fl oz/A) followed by At-Crack (2 fl oz/A). All PRE applications were applied with Prowl H2O (32 fl oz/A). These were all followed by Gramoxone (16 fl oz/A) + Zidua SC (1.75 fl oz/A) + Agridex (1% v/v) At-Crack and Cobra (12.5 fl oz/A + 2,4-DB (21 fl oz/A) + Agridex (1% v/v) early POST. The Georgia location included Storm At-Crack. The Mississippi and Oklahoma locations also included Select Max (16 fl oz/A) + Agridex (1% v/v) late POST. Valor (3 fl oz/A) PRE followed by Cadre (4 fl oz/A) + Dual Magnum (16 fl oz/A) + 2,4-DB (21 fl oz/A) + Agridex (1% v/v) early POST were included as a comparison treatment. All treatments increased yield by 58% over the untreated check at all locations. The PRE application of Pursuit resulted in peanut injury over 21% at Georgia and Oklahoma. However, when applied as a split application injury lowered by 14%. There were still visible injury symptoms reported in late June at both locations, however by July the peanut had recovered at Oklahoma. Most treatments provided over 90% weed control regardless of weed species or location. All treatments provided over 90% control of browntop millet, eclipta, and smallflower morningglory in Mississippi. A few exceptions include early season weed control of wild radish when Valor and Pursuit were applied alone in Georgia. The Oklahoma location resulted in less than 77% mid and late season control of Texas panicum and ivyleaf morningglory when Valor and Outlook were applied alone PRE and yellow nutsedge when Valor was applied alone PRE. This research confirmed that a comprehensive preemergence herbicide program is needed to control a diverse population of weeds.

Characterize Leaf Spot Resistant Loci Through Image Analysis of Advanced Breeding Lines in the NCSU Peanut Breeding Program

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Phenotypic data for leaf spot has historically been collected visually. The subjective nature of evaluating leaf spot resistance on a whole-plot basis may introduce rater, trial and/or environmental biases leading to inaccurate selection. Data collected using a scaled convention limits the evaluation to overall leaf spot symptoms on a whole-plot basis. In addition, efforts to manually count individual lesions, especially while differentiating early versus late leaf spot, have been limited and error-prone. In order to address this issues, a total of 220 genotypes were grown at the Peanut Belt Research Station (Lewiston-Woodville, NC) for the characterization of leaf spot pressure and differentiation in resistance using a low-throughput image-based method. During the evaluation process (August – October), plots were routinely rated visually using the Florida scale (1-9); leaf tissue from each plot was evaluated for percent leaf spot lesions using customized Fiji (ImageJ) scripts; and aerial images were captured using a Mavic 2 Pro drone in order to evaluate percent defoliation. The overall objective of this project was to correlate the visual ratings to the weighted evaluation of percent leaf spot lesions and defoliation and to identify and target introgression blocks associated to resistance. Results after the first year of analysis indicate a distribution of leaf spot ratings, especially among lines that were whole-genome sequenced. The alignment of the whole-genome sequences should reveal resistance blocks that have been selected within the NCSU peanut breeding program stemming from introgressions from plant introductions (PI) and from wild diploid sources, *A. cardenasii* and *A. diogoi*.

Assessment of Peanut Fungicide Programs and Sulfur in Irwin County, GA, 2020

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Disease management is essential for profitable peanut production in Irwin County; however, cost of fungicide programs is among the greatest expenses for our farmers. The objective of this study was to provide peanut growers with information from local data to aid in their selection of a fungicide program. A replicated, large-plot, on-farm fungicide study was conducted in Irwin County, GA in 2020 to assess the efficacy of several fungicide programs for the management of late leaf spot (*Nothopassalora personata*) and southern stem rot (*Scelrotium rolfsii*). The field where the trial was established was cropped to peanut in 2017 and to cotton in 2018 and 2019. The trial was planted to 'Geogia-06G' on 18 May, inverted on 22 Oct, and harvested on 3 Nov. Plots were 18-rows wide by the length of the field and were arranged in a randomized complete block design with four replications. Plots were rated for severity of leaf spot disease and incidence of stem rot immediately prior to harvest. Fungicide treatments included: 1) – Priaxor (6 fl oz/A) – Umbra/Echo (36 fl oz/A, 1 pt/A) – Muscle ADV (2 pt/A) – Umbra/Echo-Muscle ADV; 2) - Priaxor-Umbra/Microthiol Disperss (5 lb/A)-Muscle ADV – Umbra/Microthoil Disperss – 3) - Priaxor – Convoy/Echo (32 fl oz/A, 1.5 pt/A) - Muscle ADV – Convoy/Echo- Muscle ADV and 4) – Lucento (5.5 fl oz/A) – Elatus (9.5 oz/A) – Lucento (5.5 fl oz/A) – Convoy/Equus (21 fl oz/A, 1.5 pt/A) – Muscle ADV. Fungicides were applied on a 14-day interval beginning approximately 45 days after planting. Leaf spot ratings (FLA 1-10 scale) were 4.4 (treatment 1, Umbra program), 3.8 (treatment 2, Umbra sulfur program), 4.4 (treatment 3, Convoy/Echo program), and 4.9 (treatment 4, Lucento/Elatus/Convoy program). Stem rot ratings (hits per 200 ft) were 7.5 (treatment 1), 6.5 (treatment 2), and 8 (treatment 3), 4.5 treatment 4). Average yields from treatments 1 to 4 were 6200, 6161, 6013, and 5989 lb/A, respectfully. From the results of this study, it is apparent that peanut growers have multiple programs of similar efficacy from which to choose for management of leaf spot and stem rot diseases. Perhaps of greatest interest, growers could substitute sulfur (5 lb/A) for Echo (1.0 pt/A) and maintain yield while slightly improving leaf spot control.

Identification and Genetic Mapping of Novel Sources of Resistance to Groundnut Rosette and Late Leaf Spot Diseases in a Collection of *Arachis* Wild Derivatives

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Late leaf spot (LLS) and Groundnut rosette disease (GRD) are the most destructive diseases of groundnut in sub-Saharan Africa. Limited resistance is available therefore, novel sources of resistance are required in cultivated groundnut varieties. Three hundred and sixty-six (366) interspecific lines that bring wild alleles-genetic variation from four different wild species (*A. batizocoi, A. valida, A. duranensis* and *A. ipaensis*) were evaluated in two agro-ecological zones in Uganda at Nakabango and Serere. Phenotyping of the three populations identified several interspecific lines with good agronomic, and disease resistance traits. One genotype, from the population (Fleur11 x (*A. valida* x *A. duranensis*)^{4x}), B7-25-22-8 was particularly useful in combining high yields and disease resistance and could be used as a parent in the groundnut breeding program.

Individuals from population (Fleur11 x (*A. batizocoi* x *A. duranensis*)^{4x}) consisting of 133 lines were genotyped with Axiom_Arachis1 SNP array to generate a genetic map consisting of 1440 markers in four (4) linkage groups (LG). QTL analysis identified four QTLs for GRD on linkage groups B01, B04, B05 and A08 with phenotypic variance explained (PVE) of 11.04, 12.56, 11.51 and 7.90 % respectively. Two QTLs were identified for LLS on linkage group B04 with PVE of 9.43 and 9.60%. QTL analysis allowed us to verify the effect of wild alleles on disease resistance. The QTLs identified for LLS and GRD were contributed by wild parent (*A. batizocoi* x *A. duranensis*) with the exception of GRD severity whose lower values were contributed by the recurrent parent, Fleur 11. The QTLs identified for LLS and GRD resistance provides additional tools for marker-assisted breeding to advance groundnut improvement and for molecular characterization of disease resistance.

Analysis of Vegetative and Reproductive Traits Revealed a Positive Transgression and Strong Correlations Between Traits in a Population of Recombinant Inbred Lines in Groundnut (*Arachis hypogaea* L.)

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In this study, a population of 254 recombinant inbred lines derived from a cross between Fleur 11 and 73-30 was evaluated for agromorphological traits and fresh seed dormancy. The experimental design consisted of an alpha lattice with 17 blocks of 17 entries each, with three replications. Parameters studied were pod weight per plant, number of two-seeded pods per plant, seed weight, percentage of sound mature kernels, sound kernel weight per plant, pod length, above-ground biomass per plant, and percentage of fresh seed germinated. All traits exhibited positive transgression, indicating complementary gene action. Significant and positive correlation ranging from 0.26 to 0.90 was observed between pod weight and secondary traits such as sound kernel weight, one seed weight, number of two-seeded pods per plant, percentage of sound mature kernels, and pod length. The germination rate of fresh seed was not significantly correlated to any agromorphological trait. Lines C1P5-4-7, C1P5-4-5 and C1P28-4-2 had the highest pod weight per plant. Lines C1P28-4-2, C1P11-5-4 and C1P32-2-2 exhibited the highest two-seeded pod number per plant. Lines C1P5-4-7 and C1P24-8-3 had the highest sound mature kernel weight. Lines C1P24-8-3, C1P11-14-3, C1P37-4-4, C1P37-7-9, C1P11-10-1 and C1P23-4-2 had the highest percentage of sound mature kernels, and lines C1P31-11, C1P23-5-4 and C1P23-5-5 had the highest weight per seed. Seven lines (C1P33-6'-1, C1P33-2-2, C1P30-9-8, C1P24-1-1, C1P18-6-6, C1P23-4-1 and C1P18-6-5) exhibited a fresh seed germination percentage similar to that of the fresh seed dormant parent 73-30. From a breeding view, these lines could be used as parental lines to develop new lines with higher yield and with fresh seed dormancy using a marker assisted selection scheme.

Analysis of Vegetative and Reproductive Traits Revealed Positive Transgressions and Strong Correlations Between Traits in a Population of Recombinant Inbred Lines in Groundnut (*Arachis Hypogaea* L.)

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In this study, a population of 254 recombinant inbred lines derived from the cross between Fleur 11 and 73-30 was evaluated for agromorphological traits and fresh seed dormancy. The experiment design consisted to an alpha lattice design with 17 blocks of 17 entries in each, with three replications. Parameters studied were the pod weight per plant, number of two-seeded pods per plant, one seed weight, percentage of sound mature kernels per plant, sound kernels weight per plant, pod length, above biomass per plant and percentage of fresh seed germinated. All traits exhibited positive trangression indicating complimentary gene action. Significant and positive correlation ranging from 0.26 to 0.90 was observed between pod weigth and secondary traits such as sound kernel weight, one seed weigth, two-seeded pod number per plant, percentage of sound mature kernels per plant and pod length. Percentage of fresh seed germinated was not significantly correlated to any agromorphological trait. The lines C1P5-4-7, C1P5-4-5 and C1P28-4-2 revealed highest pod weight per plant. The lines C1P28-4-2, C1P11-5-4 and C1P32-2-2 exhibited the highest two-seeded pod number per plant. The lines C1P5-4-7 and C1P24-8-3 were the best lines for the sound mature kernel weigth. The lines C1P24-8-3, C1P11-14-3, C1P37-4-4, C1P37-7-9, C1P11-10-1 and C1P23-4-2 revealed the highest percentage of sound mature kernels. And lines C1P31-11, C1P23-5-4 and C1P23-5-5 have the highest one seed weight. Seven lines C1P33-6’-1, C1P33-2-2, C1P30-9-8, C1P24-1-1, C1P18-6-6, C1P23-4-1 and C1P18-6-5 exhibited fresh seed germination percentage similar to that of the dormant parent 73-30. From a breeding view, these lines could be used as parental lines to develop new lines with higher yield and with fresh seed dormancy using a marker assisted recurrent selection scheme.

Interesting Issues Associated with Varieties and Seed Quality in North Carolina and Virginia over the Past Decade

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A wide range of issues can develop before and during the growing season that can impact seed quality. In this abstract we present a description of ten of the most prominent issues observed with seed during in recent years. 1) Sheller selling peanuts without certifying, improperly labeled, unknown origin, unknown parent seed, or unknown purity and quality. 2) Sheller selling uncertified seed with excessive foreign matter, low germination, excessive splits, and untreated. The sheller deliberately attempted to circumvent the certified seed system and sell inferior planting stock. 3) High Oleic trait lost in Foundation seed lots. 4) Mixtures of varieties are rare but can occur. For example, seed lots for the variety Sugg were found with pink and red seed coats and may have been adulterated by Bailey. 5) Gregory was first released with variant (bushy off-type) but was purified through Breeder/Foundation seed. 6) Low germination for several lots pf Wynne in the Foundation Class in grower fields and in official grow outs. 7) Poor germination caused by drought in 2006 with gypsum still on soil surface at harvest. 8) Low turn-out due to excessive moisture at harvest and rapid drying and associated moisture stratification in drying trailers. 9) Brantley lost high oleic trait possibly due to outcrossing or contamination at the sheller. 10) Early shelling season dormancy can be an issue. Seed tested November and December and occasionally in early January has an increased occurrence of dormancy. This problem (or non-problem) disappears over time as dormancy is broken later in the season. The past two years have been of particular interest. Current and sporadic issue caused by modern cultural practices may be contributing factors that are not associated with variety.

North Carolina Crop Improvement has been certifying seed for over 50 years. Our certification standards and protocols are used to classify seed, and they are based on uniform-national standards. Proof that the system is working is the rarity of peanut seed complaints brought to the North Carolina Department of Agriculture and Consumer Services Seed Board. The only seed complaint involving peanut seed in the last 7 years was not from a certified lot but rather an illegal farmer-to-farmer transfer. Practically all seed-borne issues are discovered early during field inspections or during seed conditioning. Virtually all of these problems are removed from the seed chain before they make it to the grower field. We have very few examples of non-conforming certified seed lots that made it into the seed supply because the system works. Only one seed lot that made it to the grower with low germination in the last 7 years. Other than this case, the seed supply chain is very stable and reliable. Just to give you scope of the size of the seed supply; NC Crop Improvement certifies over 700 seed lots annually. Only one seed lot in approximately 5,000 seed lots exhibited low quality (0.02%).

Interactions of Foliar Applied Herbicides with Residual Herbicides and Fungicides

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Defining compatibility of pesticides in terms of pest control and crop injury important in developing pest management strategies. Research was conducted at one location in North Carolina during 2000 to compared weed control and peanut injury when Gramoxone SL (paraquat dichloride) at 8 oz/acre plus Basagran (bentazon) at 8 oz/acre was applied alone or with Dual Magnum (*S*-metolachlor) at 16 oz/acre, Outlook (dimethenamid-P) at 12 oz/acre, Warrant (acetochlor) at 48 oz/acre, Zidua (pyraoxasulfone) at 2.0 oz/acre, and Anthem Flex (carfentrazone plus pyroxasulfone) at 2.5 oz/acre when weeds had 1 to 3 leaves and peanut was 4 inches in diameter. Non-ionic surfactant at 0.125% (v/v) was included with all treatments. Peanut injury was greater when residual herbicides were applied with Gramoxone plus Basagran compared with contact herbicides alone but did not differ among residual herbicides 1 week after treatment (WAT) and no injury was observed 3 WAT. Relatively minor differences in common ragweed, common lambsquarters, eclipta, entireleaf morningglory, and Texas panicum control was observed 3 and 6 WAT, although in some instances control was greater when residual herbicides were applied with Gramoxone plus Basagran compared with control by contact herbicides applied alone. In other experiments conducted twice, Texas panicum control by Clethodim (clethodim) at 16 oz/acre was similar when applied alone or with the fungicides Miravis (adepydin) at 3.2 oz/acre, Miravis plus Elatus (azoxystrobin plus benzovindiflupyr) at 9 oz/acre), Miravis plus Convoy (flutolanil) at 32 oz/acre. In a separate experiment also conducted twice, Texas panicum control by Clethodim did not differ when applied alone or with Anthem Flex (2.5 oz/acre), Dual Magnum (16 oz/acre), or Zidua (2.0 oz/acre). Crop oil concentrate at 1.0% (v/v) was applied with all treatments. These results suggest that residual herbicides applied with Gramoxone plus Basagran in most cases will provide similar weed control and crop injury. These results also indicate that Clethodim and Miravis plus either Elatus or Convoy are compatible and that the residual herbicides Anthem Flex, Dual Magnum, and Zidua will not adversely affect grass control. Additional research is needed to determine if these herbicides affect disease control when applied with Miravis plus either Elatus or Convoy.

~~Poster, Genomics and Genetics, 53rd APRES Annual Meeting, Dallas, TX, July 13-15, 2021~~

Identification of P~~p~~eanut L~~l~~ate L~~l~~eaf S~~s~~pot R~~r~~esistance L~~l~~ocus, *pRPP13*-like, using Nested Association Mapping Approach

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Identification of genetic markers linked to resistance to late leaf spot (LLS) in peanut has been a focus of molecular breeding for several years. Efforts have been hindered by limited mapping resolution due to low levels of genetic recombination and marker density available in traditional biparental mapping populations. To address this, multi-parental mapping populations including Nested Association Mapping (NAM) populations have been developed along with high-throughput genotyping SNP arrays. Here, we utilized a subset of two NAM populations, NAM_Tifrunner and NAM_Florida-07, which were genotyped with the *Axiom_Arachis* 58K SNP array and phenotyped for three years for LLS severity. These data were used for quantitative trait locus (QTL) and genome-wide association study (GWAS) analyses. Joint linkage-based QTL mapping in NAM_Tifrunner identified 30 QTLs including a major QTL on chromosome A02 with 42.8 - 65.6% phenotypic variance explained (PVE). Similarly, in NAM_Florida-07, 32 QTLs were detected including a major QTL on chromosome A03 with 28.9 - 61.3% PVE. In parallel, GWAS analysis identified 221 and 293 significant single nucleotide polymorphisms (SNPs; $-\log_{10}(P) > 3.0$) in NAM_Tifrunner and NAM_Florida-07, respectively, associated with LLS resistance. Integration of QTL and GWAS results identified 27 significant SNPs associated with 26 QTLs. These markers were associated with several putative resistance genes and pointed to a prominent role for *Recognition of Peronospora Parasitica 13* (*RPP13*)-like NBS-LRR R-genes in LLS resistance, here named the *peanut RPP13* (*pRPP13*) gene. This gene still requires functional validation and characterization. However, the associated markers are prime candidates for development into selectable markers for molecular breeding. This approach clearly demonstrates the power of NAM populations for marker-trait association in peanut.

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New Reference Genomes and Comparative Genomics Analyses in *Aspergillus flavus*

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Understanding the biology of *Aspergillus flavus* and the causes of isolate-to-isolate variation in aflatoxin production and pathogenicity-related traits is critical to developing targeted efforts in improving host plant resistance. To facilitate this, we present two chromosome-arm reference genomes for *A. flavus* isolates NRRL3357 and AF13, each with eight chromosomes, lengths of 36.996 and 37.439 Mb, respectively, and updated gene annotations. These two isolates contrast phenotypically with AF13 showing greater levels of aflatoxin production, growth on peanut seed, and oxidative stress tolerance compared to NRRL3357. Comparative analyses between these genomes revealed a large 310kb insertion on Chromosome 1 unique to AF13 containing 60 genes including a novel bZIP transcription factor gene, *atfC*, which may be involved in oxidative stress tolerance and aflatoxin production. Comparisons with previously released or concurrently sequenced genomes of *A. flavus* isolates showed that this 310kb insertion is present completely or partially in few isolates. Using this information, isolate collections are currently in progress for a large-scale *Aspergillus* Re-Sequencing Project. To date, 264 genomes of *Aspergillus* isolates from field soils in Georgia and corn plants in Mississippi have been sequenced with additional isolate collection in progress, particularly from the origin of AF13 in Arizona. These data will be used for genome wide association studies (GWAS) for identifying novel aflatoxin regulators, and shedding light on the origin and evolution of the 310kb insertion. These new reference genomes and additional genomics information represent valuable tools for the aflatoxin and peanut research communities for continuing study in this system.

Development of Genomic Resources for Increased Folate Content in Peanut (*Arachis hypogaea*)

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Tetrahydrofolates are essential in gene expression, the synthesis of lipids and proteins along with the formation of other plastids and cellular macromolecules important in plant development and structure. Biofortification of folate in peanut can be achieved through plant breeding efforts, providing an efficient, economical and sustainable method for fighting nutritional deficiencies in humans. Clinical studies have shown that folate deficiencies in humans can lead to an increased risk of cardiovascular disease (CVD), dementia, certain cancers and pregnancy complications due to the occurrence of neural tube defects caused by folate deficiency-anemia. Knowing that peanut can be a rich source of folate, the objective of this research is to identify molecular markers in order to increase the nutritional content in cultivated peanut (*Arachis hypogaea*) through marker-assisted selection; more specifically, focusing on molecular breeding strategies to facilitate an increase in total folate content found in peanut seed. Using information from a previous study evaluating total folate content of the peanut mini-core germplasm collection, we plan to map quantitative trait loci (QTL) important in the folate biosynthetic pathway. Three plant introductions (PI) selected for high levels of folate were used in the development of a nested recombinant-inbred line (RIL) population with a recurrent cultivar parent, Georgia Green. The three populations, representing ~175 RIL lines in each, were genotyped using a filtered set of polymorphic markers between each PI and the recurrent parent in anticipation for mapping total folate. Large effect QTL identified through this analysis will be used to develop single nucleotide polymorphic (SNP) marker assays for marker-assisted selection. These assays will be used more directly for screening existing peanut breeding populations and selecting advanced breeding lines for increased folate content.

Effects of Prohexadione Calcium Application Timing on Peanut (*Arachis hypogaea* L.) Growth and Yield in Mississippi

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Excessive vegetative growth in peanut (*Arachis hypogaea* L.) can lead to decreased reproductive growth and harvest efficiency. Peanut vegetative growth is often managed with the plant growth regulator, prohexadione calcium. Although application of prohexadione calcium is recommended at 50% and 100% canopy closure, research on the optimal application timing has been minimal. The objective of this research was to evaluate the effect of prohexadione calcium application timing based on percent canopy closure. Experiments occurred at three different on-farm sites across Mississippi. Treatments included applications at 50% and 100% (canopy closure), before 50% and after 100%, 2 applications in 1 week at 100%, before 50% and before 100%, and 3 applications in a week at 100%. A non-treated control was included in all experiments. On all sites, prohexadione calcium applications were made at the manufacture recommendation of 140 g ai ha^{-1}. Treatment responses were evaluated based on peanut yield, pod loss, and harvest indices including pod weight, pod count, and dry plant weight. Peanut yield across field sites was evaluated as a percent untreated control.

Average yields by treatment ranged from 6535 to 7000 kg ha^{-1}. On average, control treatments had a lower yield than treatments containing prohexadione calcium. Two applications in 1 week at 100% had the most significant effect on yield with an average of 8.9% increase in yield when compared to control treatments. The lowest performing treatments were the before 50% and after 100% and the 3 applications in 1 week at 100% with an average of 1.4% and 0.9% increase in yield when compared to control treatments. Application timing had little effect on pod count and pod loss. The use of prohexadione calcium in the growing season at optimized timings increased peanut yield and decreased vegetative growth, improving harvest efficiency and reduced harvest losses.

Tractor Planting Speed and Downforce Effect on Peanut Seed Spacing, NDVI, Plant Stand, and Yield

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Planting season for peanut (*Arachis hypogaea* L.) can be one of the busiest parts of many growers' operations. When external forces such as impending rainfall influence producers to try to cover more acreage in a certain time frame, growers may consider increasing planting speed to accomplish this. Planting at faster speeds than recommended may result in reduced or non-uniform plant emergence. Utilizing correct downforce settings can potentially assist in achieving optimal seed depth depending on soil moisture and texture. This experiment was conducted in Tifton and Attapulgus, GA in 2020 to determine an optimal tractor speed and downforce setting to achieve optimum seed spacing, plant stand, yield, and greatest average canopy reflectance. These trials were conducted in a randomized complete block design with a factorial arrangement of four planting speeds (4.0, 6.4, 8.6 and 11.1 km/hr) with four downforce settings (445, 890, 1335 and 1780 N) on the planting unit. Tractor speed and downforce were tested independently and for interactions. Average seed spacing over 300 cm of plot row were similar for 4.0 and 6.4 km/hr speeds (5.4 to 5.9 cm), then increased at 8.6 km/hr (6.8 cm) followed by a drastic increase at 11.1 km/hr (16.4 cm). A decrease in plant stand was observed in plant emergence with each increase in planting speed. Canopy reflectance quantified by Normalized Difference Vegetative Index (NDVI) averaged over the length of the plot in Attapulgus was greatest for both 4.0 and 6.4 km/hr speeds but decreased as speed increased to 8.6 km/hr and was least for 11.1 km/hr planting speed. Yield in Tifton began to decrease as planting speed reached 8.6 km/hr and was least when speed reached 11.1 km/hr. Yield in Attapulgus was maintained up to 8.6 km/hr planting speed and drastically decreased at 11.1km/hr. No differences were observed for any downforce settings tested on NDVI or yield. These results suggest that planting at speeds exceeding 8.6 km/hr will result in reduced plant emergence and yield.

Introgression of Wild *Arachis cardenasii* Alleles into Cultivated Peanut to Confer Resistance to Early and Late Leaf Spot

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Cultivated peanut (*Arachis hypogaea* L.) has low to moderate level of resistance to both Early (ELS) and Late leaf spot (LLS). These diseases can cause tremendous yield loss when not properly managed. Effective fungicide spray programs are currently used to control these diseases but resistant cultivars are still the best way to mitigate them. Hence, this study aims to obtain lines with multiple resistances that combine wild-derived segments that confer long-term, high level of resistance to foliar diseases with resistance to root-knot nematode (also from *A. cardenasii*) and the high oleic property from cultivar 'TifNV H/O'. Crosses were also performed using cultivar 'Bailey', with resistance to various diseases including ELS and an advanced line (IAC 321) with resistance to LLS and rust. Both peanut genotypes have different segments derived from *A. cardenasii*. F_1 seeds were harvested and hybridity was confirmed using Kompetitive Allele Specific PCR (KASP) analysis. Two true hybrids (Bailey x IAC321_F1) were germinated and used as male parents for backcrossing to Bailey and TifNV H/O. BC1F1 seeds were harvested and hybridity was confirmed. Then, BC1F1s with different segments were evaluated for ELS and LLS resistance using a detached leaf bioassay. Four different components of resistance were measured: incubation period (IP), lesion number per leaf area (LN/LA), number of sporulating lesions per leaf area (SL/LA), and percent diseased leaf area (DLA). ELS bioassay results revealed significant differences among hybrids and susceptible controls based on the LN/LA, SL/LA and DLA. On the other hand, results in the LLS bioassay showed significant differences among hybrids and susceptible controls based on the IP, LN/LA, and DLA. AUDPC values on both ELS and LLS bioassays also statistically varied between hybrids and susceptible controls. Overall results suggest that hybrids with segments from Bailey and IAC 321 exhibited higher level of resistance to both ELS and LLS than the parents. Development of advanced lines with different alleles conferring various disease resistance segments will provide long-term protection to these fungal diseases.

Utilizing Qtlseq Pipeline to Identify Genetic Regions Linked To The Black Pod Trait.

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The peanut black pod trait has been studied at the University of Florida peanut breeding program in the recent years. Its relationship with maturity has been confirmed, nevertheless, other reasons to include the trait into commercial lines is continuously being explored. There is a need to understand more about the genetics of the trait at a molecular level. Bulk segregant analysis aided by QTLseq analysis has been used extensively to identify genomic regions controlling traits in a vast number of crops in the recent years. A population of peanuts segregating for the BP trait has been developed by crossing the BP line and FloRun '331' in 2016. After, F_1, F_2 and F_3 populations were grown in Marianna FL. DNA of F2 plants was extracted and same plants were sowed the following year in a plant to plot setting. F3 plots were evaluated as only black, white or segregating for pod coloration to confirm F2 plant's identity. Bulked DNA of F2 plants and parental DNA was sent for sequencing at RAPiD genomics. From these sequences it was possible to identify 220,714 single nucleotide polymorphisms (SNP) between the plants expressing the black pod traits and the ones expressing normal pod coloration. Using the QTLseq pipeline the SNP-index for both the black pod bulk and normal pod bulk samples was calculated. Delta SNP-index was calculating by comparing the previously calculated SNP-index of both samples. Based on delta SNP-index the analysis identified three possible regions controlling the black pod trait at a 95% confidence. G-statistics were used to improve the results, this yielded a region of 5.36 mega bases on Chromosome 20 as the responsible of the black pod trait. Effects of the SNPs within this region were analyzed, and four genes were identified as candidates for the black pod trait.

Peanut Response to Diclosulam in the Texas Peanut Growing Areas

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Diclosulam (Strongarm®) is a soil-applied herbicide that may be applied preplant incorporated, preplant surface, or preemergence (PRE) through cracking (CRACK) in peanuts and is labelled in all peanut growing areas except New Mexico, Oklahoma, and Texas. Although no issues were seen in south Texas, when diclosulam was registered for use in peanut over 15 years ago, serious stunting and yield loss occurred in west Texas in the first year of its use. A major factor involved in this injury was believed to have been a very sensitive peanut variety that was introduced during the launch year.

To determine tolerance of some newer peanut varieties to diclosulam, field studies were conducted during the 2018 through 2020 growing season in south Texas near Yoakum and in the High Plains of Texas near Lubbock in 2018 and Gaines County in 2019 and 2020 under weed-free conditions. Treatments were arranged in a randomized complete block design with a 2 (diclosulam rate) X 2 (application timing) factorial arrangement with 3-4 replications. All plot areas were maintained weed-free using a combination of labeled herbicides and hand-weeding. Data collected included peanut stunting (30 and 90 DAP), yield, and grade. All data were subjected to ANOVA and means separated using Fisher's Protected LSD Test ($P<0.05$) when appropriate. In south Texas, Georgia M-13 was planted in 2018 and Georgia 09B was planted in 2019 and 2020 while in the High Plains Georgia 09B was planted all three years. Diclosulam at 0.026 (1X) and 0.053 (2X) kg ai ha^{-1} was applied PRE and CRACK.

No injury (stunting) was noted at Yoakum in any year or at the Lubbock location in 2018 when furrow irrigation was used; however, in 2019 and 2020 when overhead irrigation was used, a diclosulam rate by application timing effect was seen at the Gaines County locations. Stunting increased as diclosulam rate increased and diclosulam applied PRE caused greater injury than the CRACK application. With respect to yield, no diclosulam treatment by application timing interaction was seen at Yoakum in any year or at the Lubbock location in 2018 or Gaines County location in 2020 with yield and grade not different from the untreated check. In 2019 at Gaines County and Yoakum, peanut yield and grade, respectively, decreased as diclosulam rate increased with application timing having no effect on yield or grade.

Based on these results, diclosulam at the 1X rate is safe to use on Georgia M-13 or Georgia 09B peanut in Texas. However, if for some reason a higher than labelled rate is accidently applied, the chance of peanut injury does exist.

High Resolution Genetic and Physical Mapping of a Peanut Spotted Wilt Disease Resistance Locus, *PSWD-1*, to *Tomato Spotted Wilt Virus* (TSWV)

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Quantitative trait loci (QTLs) for resistance to *Tomato spotted wilt virus* (TSWV) in peanut were previously mapped on chromosome A01 in the recombinant inbred line (RIL) mapping population derived from SunOleic 97R X NC94022 using SSR markers and whole genome resequencing. Using the recently released complete genome sequences for both diploid and tetraploid peanut, and the high-density peanut SNP arrays (58K 'Axiom_ *Arachis*_v1' and the haplotype-based 48K 'Axiom_ *Arachis*_v2' arrays), we developed high-resolution genetic and physical maps of the peanut TSWV resistance locus *PSWD-1*. QTL analysis of five years' TSWV disease ratings identified two major QTLs on chromosome A01 explaining 41.43% and 43.69% of phenotypic variance, within 3.7 cM and 0.3 cM in the same region of the genetic maps, respectively, using these two versions of peanut SNP arrays. These QTL intervals corresponded to a 490-kb physical interval. Comparison of the genetic map and the reference genome revealed a 'cold spot' region from 12,040,521 bp to 12,528,768 bp (488 kb) recombination being observed only in two RILS, S1 and S17, which also had clear, contrasting TSWV phenotypes. The recombination "cold spot" was confirmed using re-sequencing data from these two RILs. Therefore, based on the genetic and physical maps we named the resistance locus as the peanut spotted wilt disease 1 (*PSWD-1*) resistance locus. Within this locus there were three candidate genes including an NBS-LRR disease resistance gene, a glutamate receptor, and an MLO-like protein. The strongest candidate resistance gene is the *TIR-NBS-LRR* R-gene with the gene ID *arahy.1PK53M*, which is a prime candidate for future functional characterization and use in genetic improvement of peanut resistance to TSWV.

Comparison of Fluopyram and Aldicarb for Root-Knot Nematode and Disease Control along with Yield Response of Peanut, 2013 to 2020

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Except for 2019, the efficacy of fluopyram and aldicarb for control of the peanut root-knot nematode, non-target effects on leaf spot diseases and stem rot, along with the yield response was compared from 2013 to 2020 on an irrigated site with an established population of *Meloidogyne arenaria* Race 2 at the Wiregrass Research and Extension Center in Headland, AL. A factorial design arranged in a split-plot with year as the whole plot, and nematicide program as the split-plot treatment was used. Plots consisted of four 30-ft rows spaced 3-ft apart. Fluopyram at 18.5 fl oz/A was applied over the seed in the open seed furrow (IF) with a single drop nozzle as a standalone treatment or was followed by an at-pegging broadcast application of fluopyram + prothioconazole at 13 fl oz/A. Aldicarb at 7 lb/A was applied in-furrow. A no-nematicide control was included. At-plant and at-pegging treatments were watered in with 0.5 in. water delivered with a lateral irrigation system. The peanut root-knot susceptible cultivar 'Georgia-06G' was cropped behind one year of cotton (*Gossypium hirsutum* L.) in 2013, 2017, 2018, and 2020; one year of sunn hemp (*Crotalaria juncea* L.) in 2015; and peanut (*Arachis hypogaea* L.) in 2014 and 2016. Leaf spot defoliation, stem rot incidence, root-knot-related pod and root galling, final root-knot juvenile counts, and plant vigor were recorded. While similar vigor ratings were noted over the seven study years, greater ratings were recorded for all aldicarb and fluopyram programs compared with the no nematicide control. Significant year × nematicide treatment interactions for leaf spot defoliation and stem rot incidence indicated that the response of these variables to the nematicide inputs differed by study year. In 2016, 2017, and 2020, leaf spot defoliation was greater for aldicarb compared with fluopyram alone or in combination with fluopyram + prothioconazole at-peg program. Stem rot incidence was greater for aldicarb compared with fluopyram alone or with the fluopyram + prothioconazole at-peg program only in 2013. When compared with the no-nematicide control, pod and root galling was significantly reduced with aldicarb but not either of the fluopyram programs. Pod and root galling also differed by study year with 2016 and 2020 having the greatest and lowest damage ratings, respectively. While significant differences in final *M. arenaria* juvenile populations were noted between study years, similar populations were noted for all nematicide programs and the no-nematicide control. When compared with the no nematicide control, significant yield gains were obtained with aldicarb and fluopyram programs with fluopyram + prothioconazole producing greater yield than the aldicarb but not fluopyram alone. Yield also differed by study year with the peanut following peanut rotation in 2014 and 2016 having equally low mean yield.

Evaluating Peanut Fungicide Programs in Mitchell County, Georgia

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In 2018, peanut diseases were reported to reduce crop value by 16.1% and to cost Georgia farmers $160.7 million in terms of management expenses and value of lost yield. White Mold (*Sclerotium rolfssii*) is one of the most destructive diseases that peanut growers face in southwestern Georgia. Leaf spot diseases (*Passalora arachidicola* and *Nothopassalora personata*) are also a chronic problem. Producers in Mitchell County have many fungicide options, but programs vary greatly in cost and efficacy. Since 2019, Mitchell County Extension has conducted large-plot, on-farm field trials in commercial peanut fields. The objective of these trials is to evaluate and compare newer fungicide programs to older standards to provide local growers with additional unbiased, research based data in order to make the best decision for their own operation. Each field trial was planted to a randomized complete block design with three replications. Plots were twelve rows wide by the length of the field, and the center six rows where harvested for yield. Plots were assessed for severity of leaf spot and incidence of white mold immediately prior to harvest. Treatment means were separated using Fisher's Protected LSD and return on investment was calcualted using average cost of each treatment. In both years the newer fungicide programs showed decreased disease incidence and increased yield when compared to older fungicide programs. In 2019 White Mold ratings ranged from 6 to 22 hits per 200 feet of row and yield was between 6258 and 6571 pounds per acre. In 2020 White Mold rating ranged from 7 to 34 hits per 200 feet of row and yields were much lower due to weather issues ranging from 2822 to 3474 pound per acre. Leaf Spot was not an issue in either years. Results from these trials are used by peanut producers in Mitchell County and surrounding counties to make fungicide selections for future crops.

Feed the Future Innovation Lab for Peanut Employs Novel Approach to Research During Pandemic Travel Restrictions

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Through the Feed the Future Innovation Lab for Peanut (Peanut Innovation Lab), researchers from a dozen US and overseas institutions work to solve global hunger and food security by increasing resilience to shocks and focusing on nutrition and market-led development.
The five-year program suffered a major disruption in 2020, when international travel and transit within partner countries was curtailed in response to the covid-19 pandemic. Using a multi-pronged approach that included innovations in research design and enhanced digital communication, the program continued to accomplish research findings in the areas of genetics, plant breeding, nutrition, gender dynamics, economics and other areas to address limitations in production, processing and consumption of peanut.

Release of Peanut Germplasm Lines with Resistance to Late Leaf Spot

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Late leaf spot (LLS), caused by *Nothopassalora personata*, is a foliar disease that plagues peanut production worldwide. Chemical control is expensive, sometimes inaccessible, and can be difficult to apply. One effective solution to control this disease would be the development of resistant cultivars. We are releasing four runner-type peanut germplasm lines with resistance to LLS. TifGP-3 and TifGP-4 were selected from the cross of 'TifNV-High O/L' with IAC 322, a breeding line from Brazil with high resistance to late leaf spot due to alien introgressions from *A. cardenasii*. TifGP-3 has introgressed segments from *A. cardenasii* on top of chromosome A02, the bottom of A02 and the bottom of A03. TifGP-4 has the introgressed segments on the top of A02 and the bottom of A03. TifGP-3 and TifGP-4 exhibited a very high level of resistance to LLS. KASPar assays can be used to determine the presence or absence of each introgressed segment.

Previously, a recombinant inbred population from Florida-07 x GP-NC WS 16 segregating for both late leaf spot resistance and high oleic traits was used to perform genetic mapping for late leaf spot resistance by QTL-seq analysis. Kompetitive allele specific PCR (KASP) markers associated with major QTL conditioning resistance to LLS were developed and validated. Two recombinant inbred lines with top levels of field resistance to late leaf spot were selected from this population for release. Both lines possess the resistance alleles of all the genetic markers. One line (TifGP-5) has high oleic acid content and the other (TifGP-6) is normal oleic.

Releasing these four germplasm lines packaged with molecular markers provides the peanut breeding community with genetic resources that can be utilized through marker assisted breeding.

Grower Education on the Effect of Tillage Practice Related to Peanut Water Availability and Usage

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Strip-till cultivation is the most commonly used minimum tillage systems implemented in Brooks County conservation tillage planting programs. Benefits of strip-till production include: improved soil health, decreased soil erosion, and reduced trips across the field, resulting in savings of both time and money. Strip-till systems have been applied in the production of numerous crops, including peanuts. However, peanut producers have questioned yields achieved with strip-till programs compared to typically higher harvestable peanut yields acquired through conventional tillage systems. In addition, the role of season long water availability, consumption, and usage by the peanut plant has not been defined in a strip-till management system. A commercial peanut field research trial was conducted for analysis of the comparison between soil moisture in conventional tillage compared to conservation tillage and the resulting peanut yields. The main objective of study was to implement an applied research trial in both irrigated and dryland commercial peanut fields to evaluate the effect of conventional tillage and conservation tillage, as it relates to: plant water availability, usage, consumption, and yield. The information obtained from this trial will serve as a grower educational tool for peanut production in conservation tillage systems. Peanuts were planted with two field cultural practices; bottom plow utilized for the conventional tillage treatment and strip-tillage for the conservation tillage treatment. Plots were replicated as strips three times within each field. AquaCheck capacitance soil moisture sensors (SMS) were installed in each replicated plot to monitor the difference in soil moisture at soil depths of 8, 16, and 24 inches. Soil moisture data were collected hourly during the entire season. Plots were mechanically harvested and weighed by treatment strip to determine yield.

The trial results revealed an increase in yield with the bottom plow tillage treatments over the strip-tillage treatments. However, no significant differences in season long soil moisture was observed or recorded between the conventional and conservation tillage systems. Nonetheless, there were variations in available soil moisture within replicated plots located across the field. Therefore, peanut yield increase with conventional tillage was not attributed to available soil moisture and usage. In addition, soil moisture data indicates that differences in soil type and variations within a field are closely associated with soil water availability, independent of cultural practice implemented at planting.

Screening Various Peanut (*Arachis hypogaea* L.) Genotypes for Aflatoxin Contamination using *in vitro* Seed Colonization of *Aspergillus flavus*

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Aflatoxin is a fungal mycotoxin produced by certain *Aspergillus* species. Contamination of this toxin from aflatoxigenic isolates of the fungi negatively impact global health, food production, and economy. Peanut (*Arachis hypogaea* L.) is a primary host for aflatoxigenic strains of the fungi and aflatoxin contributes to some of the largest economic losses in the peanut industry. Genotypic differences in peanut can cause varying levels of contamination. This study examines the differences in aflatoxin production between several different peanut genotypes to examine variation in contamination levels. Several varieties and genotypes from experimental populations were inoculated in vitro with a transgenic isolate of A. flavus, AF70-GFP, and screened for aflatoxin contamination.

Lines from a recombinant inbred line population developed from crosses of an aflatoxin resistant genotype, ICG 1471, and aflatoxin susceptible cultivar, Florida-07, were included in this study to validate resistance and susceptibility in respective lines from a previous study. Black-skinned peanut genotypes were also included in this study based on previous evidence which suggested some toxicity resistance. Several other genotypes with proposed resistance were also screened. Certain genotypes in this study have been utilized in crosses to develop populations for additional aflatoxin research. In addition, a few lines in this study are being utilized for genetic analysis of the aflatoxin resistance trait with the goal of identifying genetic regions which contribute to resistance.

Genesis and Characterization of New Interspecific Hybrids to Increase Genetic Diversity in Cultivated Peanut

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Peanut *A. hypogaea* (L.) underwent a significant bottleneck with regards to genetic diversity in its origin and domestication. Wild relatives harbor significant genetic diversity and useful alleles, but they are sexually incompatible. The development of greenhouse induced wild derived allotetraploid hybrids is a way to harness these alleles. We undertook a process that includes crossing wild species representing both A and B genomes, germinating and growing the hybrids, testing for hybridity, and using colchicine to induce chromosome doubling. The resulting synthetic allotetraploids would then be available to begin a breeding program to introgress valuable traits into cultivated peanut. We were able to produce 26 hybrids utilizing 17 accessions from 11 different wild species. Hybrids were confirmed using six primer sets and performing Kompetitive Allele Specific PCR ensuring the presences of both genomes. These hybrids varied with respect to branching patterns, leaf size, shape, and coloration along with other morphological differences. Viable pollen counts for hybrids ranged between 0 and 42% as compared to parentals which were consistently above 98% viable pollen. There was also variation at the cellular level. Stomata and epidermal cells as well as trichomes were counted. Based on the variation seen in all of these morphological characteristics, it is easy to see how these hybrids can be beneficial to increase the genetic diversity within cultivated peanut, and provide resistance to specific diseases and insects, as well as incorporating other value added traits.

Response of Non-irrigated Peanut to Multiple Rate Delayed Flumioxazin Applications

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Flumioxazin is a crucial tool for weed management in Georgia, and across the United States peanut producing region. Over 75% of Georgia hectares are treated with flumioxazin to control troublesome weed species. It is crucial weed control is achieved during weeks three through eight of the nearly 22-week long growing season. Lack of weed control can be detrimental to peanut yield and quality. Though flumioxazin is heavily utilized, peanut injury has been noted under unfavorable environmental conditions after planting. This is often reported for irrigated peanut during cool and wet springs, after growers use water to establish a uniform stand. However, there is minimal information about peanut establishment when growers apply flumioxazin under non-irrigated production. Research was conducted in Georgia at Tifton and Plains, investigating the response of non-irrigated peanut to multiple rates and timings of flumioxazin applications. Flumioxazin at 0, 27, 54, and 107 g ai ha^{-1} was applied at 0, 3, 5, 7, 10, and 14 d after planting (DAP) on GA-16HO. For the 0, 3, 5, 7, 10, and 14 DAP, 1.3 cm of accumulated rainfall was reached on 4, 1, 0, 13, 10, and 6 d after treatment (DAT) for Plains, and 2, 1, 15, 13, 10, and 6 DAT for Plains, respectively. Data collected included crop width, stand counts, percent injury to the non-treated control, and final yield. Data was analyzed using Tukey's HSD for means separation. In Tifton, the overall trend indicated as rate and time after application increased, yield, stand counts, and plant width decreased, with injury increasing. Plains did not indicate a trend for rate, but as application time after planting increased, peanut was negatively affected.

Effect of Insecticide, Sodium Chloride, and Fertilizer Solutions on the Invasive Snail, *Bulimulus sporadicus*

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Bulimulus sporadicus is an invasive, terrestrial snail that has only recently been found in Georgia. Large populations of *B. sporadicus* have been observed in a variety of crops in the state, and the snail has caused problems for pecan and satsuma growers by clogging irrigation emitters. Snails pose a serious risk of crop contamination in peanut when they are present in fields at harvest. Significant economic losses occurred in Thomas County in 2019 when some peanuts had to be cleaned and graded three times at a cost of $72 per acre.

Little is known about snail management in peanut. Aggressive tillage disturbs the soil, and it has been suggested that this could prevent snail populations from increasing. However, tillage is not an option for many Thomas County growers. Bug-N-Sluggo (ai's: iron phosphate and spinosad) is the only commercial product labeled for snails in peanut, but it is expensive and untested. Growers need an effective tool to prevent snails from contaminating peanut at harvest. This project sought to evaluate the effect(s) of insecticide, saline, and fertilizer solutions on *B. sporadicus* in a laboratory bioassay.

Genetic Variation for Drought Tolerance and Oil Quality Traits In A Groundnut Population Using Sensing Technologies

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Drought is the most important abiotic constraint to groundnut production and quality in the world. Approaches to mitigate the effect of drought under rain-fed groundnut production is urgently needed, and as a result, developing drought-tolerant varieties is seen as part of the solution. The study objectives were to; (i) Assess the yield of a population segregation for drought under rainfed conditions. (ii) Determine the oil composition within a segregating population. (iii) Estimate the components of genetic variations within the population. The experiment was conducted at CSIR-SARI during the 2020 rainy season under rainfed conditions. Ninety-four (94) genotypes and three known performing local checks (CHINESE, NKATIESARI and SARINUT 1) were planted in an augmented block design with 19 blocks. Data were recorded for Days to emergence, Days to first flower, Days to 50% flowering, Plant height (PH), Soil and Plant Analysis Development (SPAD), Chlorophyll fluorescence, NDVI readings, Canopy temperature, Early Leaf Spot, Late Leaf Spot, Days to maturity, Fresh weight of haulms/plot/kg, Dry weight of pods/plot/kg and oil composition. All genotypes reached 50% flowering about 31 days after planting (DAP), Days to first flower ranged from 25 to 29 days, NDVI60 showed a weak relationship with ELS ($r^2 = 0.43$) and PH ($r^2 = 0.44$) at 60DAP. Pod yield varied from 533.3 kgha^{-1} (genotype 14GAF1325) to 3,700 kgha^{-1} (genotype 14GAF1385). High pod yield was observed in the genotypes 14GAF1385, SARINUT-1, 14GAF1382, CHINESE, and 14GAF1335. These genotypes can therefore be cultivated in low-rainfall areas and used as parents in breeding programs to produce drought-tolerant groundnut cultivars.

Developing Weed Management Risk Tools for Crops in North Carolina

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Effective weed management is important in protecting crop yield. Evolved resistance to herbicides across many crops has increased the need to integrate non-chemical practices into weed management programs. Cultural practices can include tillage systems, cover crops, cropping sequence, row spacing and plant population, planting date, and cultivar selection. A risk management tool to evaluate risk of over ten North Carolina peanut pests was developed using Microsoft Excel software. One component in this risk tool is weed management and risk to yield. Based on the approach used in the peanut risk tool, similar risk management tools have been developed for weeds in blueberry, corn, cotton, soybean, sweetpotato, and tobacco. Within a risk management tool, a numerical value associated with risk is assigned to each production practice that can affect weed populations and their subsequent impact on crop yield. The risk tool also includes estimates of cost for each practice and can demonstrate the financial investment needed to decrease risk. These tools are currently being modified based on NC State Extension agent input and will be released for public use in late 2021.

Influence of Heat Unit Accumulation and Low Temperatures on Pod Maturation: An Example from North Carolina during the 2020 Growing Season

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The number of heat units accumulated during the growing cycle can directly impact growth, development, and maturation of peanut. Additionally, low temperatures that are not lethal can slow maturation down to a point where further crop development is unlikely to progress unless a prolonged period of warming occurs. Historically, practitioners have indicated that when daily temperatures are below 50 F for two consecutive days, pod maturation slows to a point at which further development even when temperatures moderate. Data supporting this assessment are limited. Temperatures during the harvest cycle of 2020 in North Carolina allowed researchers to observe whether or not cooler night temperatures prevented further development and increased pod maturation. Observations at Lewiston-Woodville with the cultivar Bailey II showed that when temperatures on September 22 and 23 were slightly below 50 F, pod maturation did not increase appreciably throughout the remainder of September and October based on pod mesocarp color. Additional time periods with nighttime temperatures between 45 and 50 F were observed over that period of time and most likely contributed to lack of further pod development. These observations support the recommendation that when temperatures drop below 50 F for at least two consecutive days, increases in pod maturation are unlikely.

Assessment Of Inpyrfluxam As A Component of a Program for Management Peanut Diseases.

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Leaf spot (*Passalora arachidicola* and *Nothopassalora personata*) and stem rot (*Sclerotium rolfsii*) are among the most important diseases of the peanut crop in the southeastern United States. Inpyrfluxam (FRAC Group 7) is a new active ingredient for management of stem rot that will be a component of a total disease management program. The objective of this study was to compare efficacy of ipyrfluxam (2.0, 2.65, 3.0, and 4.0 fl oz/A) to flutolanil (16 and 32 fl oz/A), solatenol (7.3 and 9.5 fl oz/A), and penthiopyrad (16 fl oz/A) when each is integrated into a complete fungicide program. Results from studies conducted at the University of Georgia's Tifton Campus and Attapulgus Research and Education Center between 2018 and 2020 are reported. Trials were planted to 'Tifguard' or 'Georgia-06G' and managed according to guidelines from UGA Extension. The experimental design in each trial was a randomized complete block with four replications. Fungicides were applied with a CO_2 backpack sprayer at 15 gal/A. Plots were assessed for leaf spot (Florida 1-10 scale) and stem rot (reported as hits per plot) severity prior to harvest and were taken to yield (reported in lbs/A). Data were analyzed using ANOVA and Fisher's protected LSD.

In 2018, leaf spot ratings, stem rot ratings, and yield from the untreated control were 6.8, 4.8, and 5076, respectively. Leaf spot ratings, white mold ratings, and yield from treatments that included inpyrfluxam ranged from 3.5 to 3.8, 1.0 to 3.3, and 5624 to 6356, respectively. Ratings from treatments that included flutolanil, solatenol, or penthiopyrad ranged from 2.9 to 3.9, 0.8 to 4.3, and 5611 to 6192, respectively. In 2019, leaf spot ratings, stem rot ratings, and yield from the untreated control were 6.3, 16.5, and 3892, respectively. Leaf spot ratings, stem rot ratings, and yield from treatments that included inpyrfluxam ranged from 3.0 to 3.5, 2.8 to 4.2, and 4824 to 5330, respectively. Ratings from treatments that included flutolanil or solatenol ranged from 3.2 to 4.4, 3.2 to 9.2, and 5071 to 5352, respectively. From trials reported here, fungicide programs that include inpyrfluxam are at least as effective as programs that include flutolanil, solatenol, or penthiopyrad for management of leaf spot diseases, stem rot, and for protecting yield.

Drivers of Youth Participation in Groundnut Value Chains in Tororo and Nwoya Districts, Uganda

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The human capacity of Uganda depends on agriculture and yet most youth (75% of Uganda's population) are still unemployed (at 13.3%). Groundnut is staple in Uganda (253,279mt, covering 4% of all arable land) with new varieties being released often, given Uganda's rich climate and ready market. Employment provision through groundnut value chains could potentially contribute to partial resolve of the youth problem. However, very little has been done to find out the drivers and barriers of youth participation in groundnut value chains. The goal of this study was to establish the incentives and disincentives for youth participation at the different levels of the groundnut value chain utilizing Photovoice. Photovoice is a unique visual research method of collecting qualitative data using photography, captions and follow-up discussions .

Fifteen (15) youth groups aged 20-24 & 25-29 years were purposively selected per district (Nwoya and Tororo). The youth participants were trained in Photovoice and then tasked to take photos that capture the different groundnut value chain activities right from input dealing, production and harvesting practices, post-harvest handling, storage and distribution, processing, marketing and consumption from which themes emerged that highlighted the incentives and disincentives of youth participation in groundnut value chains.

Thematic content analysis was used to summarize the findings of the study using Atlas ti version 6. The preliminary results show that land size, working hours, garden ownership, access to extension services, gender and farmer group membership are major factors that either attract or push away youth from participating in groundnut value chains. The study also revealed the challenges in groundnut value chains which also act as disincentives for youth participation in groundnut value chains. These challenges include inadequate storage equipment, pests and diseases, cultural myths, erratic weather (drought), inadequate inputs, and drudgery. Based on the study findings, increasing access to extension services, farmer groups, inputs and mechanization is likely to drive youth to participate more in groundnut value chains.

An Efficient Means for Calling Moderate to Long Structural Variations Through Pairwise Genomic Comparison And Kmers.

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Although structure variations are less abundant than SNPs, they control many economical traits in different species. Calling valid structural variations is a computationally expensive and time-consuming process. We developed a computational approach, designated Cyclops, to compare two genomes and extract moderate to long insertions and deletions utilizing high multiple threading, which allows running each chromosomal pair in a thread in pairwise comparison of all chromosomes from the two genomes. A second round of runs is implemented to extract high quality structure variances by using Kmers extracted from Deletions/Insertions and aligned to the opposite genome, then re-stacked based on the hit results. In a case study using a novel assembled NC94022 genome against the Tifrunner genome, Cyclops recognized 309,186 deletions and 17,009 insertions, varied from 40 bp to 39 kbp in less than three hours.

The Potential Impact of Improved Peanut Varieties and Fungicide Applications on Peanut Productivity and Profitability in Haiti

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The goal of this study was to examine the marginal impact of fungicide treatments on peanut yield and quality in order to maximize farmer profit and compare the productivity of improved and local varieties. This research also sought to quantify the tangible benefits of more highly managed peanut cultivation practices in the context of a developing economy and conduct a Return on Investment Analysis (ROI). The analysis was based on trials that took place over a two-year period, spanning the course of 2015 and 2016 and in two different locations, 22 different fungicide applications, 4 peanut varieties that included both runner and Valencia varieties as well as local and improved varieties in Haiti. At one of the two locations the trials were conducted under ideal conditions including sprinkler irrigation, seed spacing, etc. Despite the differences between the two locations, it was evident that, on average, the use of fungicide significantly reduced disease severity while increasing yield and quality. The marginal impact of an additional fungicide treatment on yield was increasing until 8th treatment at the location with ideal conditions and until the 12th treatment in the other location. The average treatment effect of the fungicide treatments on peanut yield was 220kg/ha in the location with ideal conditions and 92kg/ha in the other location. Yield differences between varieties were not generally statistically significant though the results of local varieties indicate that, on average, they performed worse than their improved counterparts. In addition, the performance of an improved runner variety of peanut, the GA06G, overshadowed its local Haitian competitor.

The data were used in a Return on Investment Analysis and showed how household incomes can increase among Haitian peanut farmers given the initial investment in disease management techniques given different scenarios that mirror local conditions. The average return across the price spectrum was approximately 47% for runners and 62% for Valencia. As firms like Acceso to grow their customer base and develop training and credit packages in Haiti, inclusion of fungicide applications as well as training events on its implementation will be crucial in maintaining program loyalty and increasing the incomes of local farmers.

Measuring Peanut Sustainability Production Practices Using the Field to Market Fieldprint Calculator in Georgia

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As the world's population continues to grow, the demand for food and fiber sources has increased. With this increase, it has also led to consumer interest in purchasing food and fiber products that were grown sustainably. Peanuts are an essential row crop that are typically grown as a part of a conventional crop rotation in Georgia. Field to Market: The Alliance for Sustainable Agriculture presents a unique opportunity to quantify and measure peanut sustainability across the state with the use of their Fieldprint Calculator. This tool allows researchers and growers to manage sustainability practices of the crop and how they vary from year-to-year by providing scores to eight different sustainability metrics. These eight metrics include energy use, soil conservation, water quality, irrigation water use, land use, soil carbon, biodiversity, and greenhouse gas emissions. Researchers met with 45 South Georgia peanut growers beginning in 2014 for this on-going research. Throughout this study, trends can be identified across the various sustainability metrics. The energy use, irrigation water use, soil conservation, and soil carbon metrics had the highest scores across the growers enrolled in this project. Identifying these metric trends will lead to educational efforts focused on crop production improvements so growers may be more productive and sustainable. As data collection continues in the coming years, researchers are working with these growers and their Extension agents to help them make the appropriate changes to improve the grower's sustainability metrics for the crop.

Phenotyping and Genotyping RIL Population of Virginia-type Peanut for Drought Tolerance in Virginia Carolina Region

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Drought is one of the major constraints in peanut production in Virginia Carolina (VC) region because 90% of peanut production is under rainfed conditions (no supplemental irrigation). To mitigate drought effects, the most reliable solution for peanut growers is to adopt drought tolerant cultivars; but, for this, development of molecular and phenotypic markers to use in selection is needed. Therefore, our research focuses on phenotyping and genotyping of three populations (consisting of 722 lines) of recombinant inbred lines (RILs) for drought tolerance. Five parents for these populations were selected on the basis of previous studies showing contrasting traits for drought tolerance. The RILs were phenotyped at the Tidewater Agricultural Research and Extension Center in Suffolk, VA, and the Peanut Belt Research Station in Lewiston-Woodville, NC, in 2018, 2019 and 2020. Measurements included plant height, lateral branching, normalized difference vegetation index (NDVI), canopy temperature depression (CTD), wilting, disease rating and pod yield. Based on phenotypic data, we have identified 15% of the population (Pop 3) with contrasting characteristics when grown under rainfed conditions. This subset, which includes high and low drought tolerant lines from Pop 3 was further studied for physiological traits for drought tolerance in the field, under controlled rainfall and soil moisture using rainout shelters. In addition to NDVI, CTD, wilting, the subset was phenotyped for carbon assimilation rate and the relative chlorophyll content of the leaves (SPAD readings). The results indicated significant differences for photosynthesis, wilting and CTD among high and low drought tolerant lines. The RILs will be genotyped using a standard genotyping-by-sequencing approach. This will facilitate the identification of genomic markers associated with drought tolerance to allow generation of reliable markers to enable marker-assisted selection for drought tolerance of Virginia-type peanut breeding.

Spatial and Temporal Spread of Tomato Spotted Wilt Orthotospovirus (TSWV) in Two Runner Type TSWV-Resistant Peanut Cultivars

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Tomato spotted wilt orthotospovirus (TSWV) is a thrips-transmitted virus that causes spotted wilt disease in peanut, which is a major yield-limiting factor in peanut production in the southeastern United States. The relevance of primary and secondary spread of TSWV to peanut yield loss of TSWV-resistant cultivars was not completely understood. Replicated field experiments were conducted to characterize temporal and spatial TSWV spread in two runner type peanut cultivars with field resistance to TSWV (Georgia Green and Georgia-06G), monitor in-field thrips activity, and determine the relationship between the onset of symptom expression, symptom severity, and yield. TSWV incidence progressed continuously throughout the growing season, while thrips activity above the peanut canopy peaked only once at/before 49 days after planting (DAP). Temporal TSWV spread was best fitted by the monomolecular model and the Gompertz model when the overall incidence was low to moderate (<50%) and high (>50%), respectively. Based on the binary power law and SADIE analysis, aggregation was found and often occurred in mid- to late season, and spatiotemporal association was found as TSWV progressed throughout the season. Results of TSWV spread suggested substantial secondary spread even when using TSWV-resistant cultivars. TSWV reduced yield by 0-99.65% depending on time of symptom expression. Early-season infection had more severe symptoms and less yield when compared with late-season infection. Significant yield losses caused by TSWV were observed in plants expressing symptoms before 77 DAP. Early- and late- season infection caused 80% and 25% yield reduction, respectively. Yield reduction following TSWV infection was higher in Georgia Green than Georgia-06G, although the incidence and symptom severity were mostly not different between the two cultivars. Overall, our results suggested that secondary spread contributing to mid-to late-season infection, while early-season infection accounted for most of the yield loss.

Cost of Aflatoxin to the United States Peanut Industry.

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Aflatoxins are toxic secondary metabolites produced by *Aspergillus flavus (Link)* and *A. parasiticus (Speare)* that contaminate staple crops like peanut (groundnut), maize, sorghum, pearl millet, chilies, pistachio, cassava, etc. Aflatoxin may be found in milk from animals fed with the contaminated feed. Strict mandatory guidelines are imposed to prevent contaminated products from entering the edible food supply. In the US, the Food and Drug Administration has established an action level of 20 µg/kg for total aflatoxins in human food while industry-imposed action levels are lower than the FDA limit. Many countries have established even lower tolerances, including the European Union's limits which are 2 µg/kg for aflatoxin B1 and 4 µg/kg for total aflatoxins. While these regulations ensure a safe food supply, they impose an economic burden on various segments of the peanut industry to guarantee compliance. A study was conducted during the 1993-1996 crop years to quantify the cost of aflatoxin to the southeastern region of US. The average net cost to this region was $25.9 million per annum with a range of $10.1 to $43.8 million. An updated, nation-wide study covering the 2016-2019 crop years was conducted showing the current cost of aflatoxin is higher than the previous study. Data from the 2016-2019 study will be presented. As a result, a coordinated industry-wide aflatoxin taskforce has been established to target and support research focused on technology and systems to manage or eliminate aflatoxin in US peanuts.

Estimation of Double Reduction in Segmental Allotetraploid Peanut

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The vast majority of eukaryotes historically went through at least one polyploidization event. Polyploidy can confer evolutionary advantages and is thought to be favored during domestication and crop evolution. Such advantages of polyploidization are evident for tetraploid peanut (Arachis hypogaea L.), which is characterized by increased adaptability attributable to the fixation of the heterotic state. On the other hand, polyploidization reduced peanut genetic diversity which is one of the main limitations for crop improvement in modern peanut breeding programs. Genetic mechanisms characteristic of polyploids, such as tetrasomic recombination and double reduction spontaneously generate genetic diversity and provide a route to circumvent the genetic bottleneck associated with polyploidy. Double reduction is a special circumstance in polyploids where an individual carrying a locus in a single dosage can produce gametes disomic for this locus. In order for double reduction to manifest, three events need to occur during meiosis: multivalent pairing of chromosomes during prophase I followed by crossing-over between non-sister chromatids, and a subsequent non-disjunctional chromosomal separation during anaphase I and II. In plants, polysomic inheritance and multivalent pairing are typical of autopolyploids since high similarities are shared among the different sets of chromosomes. Conversely, allopolyploids, which were derived from the hybridization of two different species, are typically characterized by disomic inheritance and bivalent pairing. Thus, double reduction has only been inferred in autopolyploid plants. Instead, peanut is an allotetraploid species with a mostly AABB type genome ($2n = 4x = 40$), that follows a third genetic model, segmental allopolyploidy. Hence, it exhibits a mostly disomic paring, but with significant levels of multivalent pairings and tetrasomic recombination. In this study, for the first time, we estimate the rate of double reduction in an allopolyploid organism, the segmental allotetraploid peanut, by genotyping a BC_1 population of 184 individuals. This population has the neotetraploid [A. magna x A. stenosperma]^{4X} as the donor parent, and A. hypogaea as the recurrent parent. Surprisingly, about 20% of the studied individuals showed at least one clear case of double reduction in the male parent, resulting in unbalanced genomic compositions (AAAB) in the progeny. All these events occurred in chromosomes 4 and 6.

APRES presentation on COVID19

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Covid19 Biology Presentation for Virus Symposium

Spontaneous Generation of Diversity in *Arachis* neopolyploids (*A. ipaënsis* x *A. duranensis*)^{4x} as a Model for the Early Stages of Peanut Evolution

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Polyploidy is considered a driving force in plant evolution and domestication. For the genus *Arachis*, several diploid species were cultivated for their seeds. However, it was only the allotetraploid peanut, *Arachis hypogaea,* that became the successful, widely spread legume crop. This suggests that polyploidy has given a selective advantage for domestication of peanut. We studied induced allotetraploid (neopolyploid) lineages obtained from peanut's progenitor species, *A. ipaënsis* and *A. duranensis*, at earlier and later generations. We observed plant morphology, seed dimensions, chromosome makeup (by FISH and GISH) and performed analyses of genome wide SNPs. These neopolyploid lineages show more variable fertility and morphology than their progenitors and cultivated peanut. They also showed high sexual and somatic genome instability. Instability was manifest by changes of number of detectable 45S rDNA sites, mosaic chromosomal patterns and extensive homeologous recombination, that is, allele recombination between component subgenomes. Genome instability was not randomly distributed across the genome: more syntenic chromosomes had more homeologous recombination. Based on the observations of this study, we conclude that early stages of the origin and domestication of the allotetraploid peanut involved two genetic bottlenecks: the first, common to most allotetraploids, is the rare hybridization and polyploidy event, which is followed by sexual isolation between the allotetraploid and its wild diploid relatives. Here we suggest a second bottleneck: the survival of only very few lineages, which had stronger mechanisms in place for controlling genomic instability.

Integrated Weed Management Practices to Control ALS and PPO-inhibitor Resistant Palmer amaranth in Peanut

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Palmer amaranth (*Amaranthus palmeri*) is an economically damaging weed found throughout southeastern United States. Over reliance of herbicides in management has caused development of herbicide resistance in Palmer amaranth including ALS-inhibitors and PPO inhibitor herbicides. Without ALS and PPO inhibitor herbicides peanut producers are severely limited in options to control Palmer. Evaluation of alternative preemergent herbicides and cultural practices (tillage, row spacings, high residue cover crops) to control Palmer amaranth is imperative for peanut production. This project evaluates integration of high residue cover crops (CC) versus conventional tillage (CT), planting pattern (twin vs single row) and pre-emergent herbicides programs in peanut to control resistant Palmer amaranth without using PPO-inhibitor herbicides. Cereal rye was the only CC species using in CC system. Both twin and single row were used in CT system and only single row was used in CC system. Field trials were conducted under irrigation in Henry and Macon Counties Alabama in 2020. Study included a CT system and CC system that were side by side at each site. Acetochlor, fluoridone, norflurazon, pendimethalin were used as PRE-treatments in different tank mixes. Paraquat was used in CT system to clean up Palmer with 2,4-DB. Imazapic, 2,4-DB and S-metolachlor were applied in CC system to provide morning glory and residual control of Palmer amaranth.

Approximately 7000-8000 kg ha^{-1} CC residue was present at peanut planting and 2000-3000 kg ha^{-1} residue still remained on soil surface at 56 days after peanut planting (DAP) in both locations. All herbicide treatments provided effective control of Palmer amaranth with more than 90% control compared to the non-treated check (NTC) in all planting systems through 70 DAP. Twin row planting pattern did not significantly reduce Palmer amaranth counts compared to single row pattern in CT system. Single row in CC system had highest canopy width compared to twin and single row in CT system 35 DAP, possibly due to soil moisture retention by the CC residues. The CC single row NTC had 77% fewer Palmer amaranth compared to the NTC of CT twin row and 64% fewer palmer compared to NTC of CT single row at 70 DAP, respectively. Data indicated that cover crop residue allowed for quicker canopy closure and as well as effective Palmer amaranth suppression throughout the growing season. These results suggest that alternative approach of residual herbicides plus CC residue is an effective method to control ALS and PPO resistant Palmer amaranth while maintaining sufficient peanut crop growth.

QTL Mapping and QTL×Environment Interaction Analysis of Pod and Seed Related Traits in Cultivated Peanut (*Arachis hypogaea* L.)

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Pod and seed traits are important agronomy traits, which are closely related to yield in cultivated peanut (*Arachis hypogaea* L.). A RIL population, with 315 families was developed that derived from Jihua 5 with large pod and M130 with small pod, was used to identify molecular markers closely linked to pod and seed traits. A genetic linkage map containing 363 polymorphic loci was constructed using SSR, AhTE, SRAP, and TRAP markers. All polymorphic loci were mapped on 21 linkage groups, which spanned 1360.38 cM with an average distance of 3.75 cM.

A total of 97 QTLs for pod and seed traits were identified by ICIM method under five environments from 2017 to 2018, explaining the phenotypic variations of 2.36%–12.15% , and located on A02, A05, A08, A09, B02, B03, B04, B08, and B09 chromosomes. Among them, 9 QTLs were detected for pod length, 13 QTLs for pod width, 14 QTLs for pod thickness, 11 QTLs for seed length, 13 QTLs for seed width, 13 QTLs for hundred-pod weight, 10 QTLs for hundred-seed weight. Furthermore, 45 stable QTLs were repeatedly detected in more than three environments. QTL clusters were detected on A02, A08, B02, B04, and B08 chromosomes, respectively.

Risk Management Decisions from an Economic Perspective: The Case of Crop Insurance for U.S. Peanut Enterprises

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Economic viability is paramount to the future of the U.S. agricultural industry. The current state of the agricultural economy lends prudence to management decisions on U.S. agricultural operations to minimize not only costs of production but also risk and uncertainty. Crop insurance continues to be one risk management tool regarded as providing a safety net for agricultural producers. The effectiveness of crop insurance as a risk management tool, however, is impacted by a multitude of factors, including the commodity produced, the region of production, the enterprise size, farm management practices, and natural disasters. This study considers the economics of crop insurance for U.S. peanut enterprises from a multi-year and multi-region perspective. A whole-farm perspective is also examined as the economics of crop insurance for peanuts is compared to other commodities traditionally produced on a peanut operation. The study further investigates the potential relationship between crop insurance and the economic stability of peanut enterprises in the U.S.

Identifying Genomic Regions and Evaluating the Epistasis Controlling Stem Rot Resistance in Cultivated Peanut (*Arachis Hypogaea*)

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Peanut stem rot in peanut (*Arachis hypogaea*) is caused by fungal pathogen *Athelia rolfsii* (*Sclerotium rolfsii*) and can result in great economic loss during production. In this study, a recombinant inbred population with 156 lines from the cross between NC 3033 (stem rot resistant) and Tifrunner (stem rot susceptible) was genotyped by the 58 K peanut single nucleotide polymorphism (SNP) array and phenotyped for stem rot resistance at multiple locations and in multiple years. A linkage map consisting of 1451 SNPs and 73 simple sequence repeat (SSR) markers was constructed. Thirty-three additive quantitative trait loci (QTLs) for stem rot resistance were detected. Among these QTLs, six consistent major QTL regions (qSR.A01-2, qSR.A01-5, qSR.A05/B05-1, qSR.A05/B05-2, qSR.A07/B07-1 and qSR.B05-1) that explained over 10% phenotypic variance were identified. Besides, 12 pairs of QTLs with epistatic (additive × additive) interaction were identified. An additive QTL qSR.A01-2 also with an epistatic effect interacted with a novel locus qSR.B07_1-1 to affect the percentage of asymptomatic plants in a row. One hundred ninety-three candidate genes within 38 stem rot QTL intervals were annotated with functions of biotic stress resistance such as chitinase, ethylene-responsive transcription factors and pathogenesis-related proteins. The identified stem rot resistance QTLs, candidate genes, along with the associated SNP markers in this study, will benefit peanut molecular breeding programs for improving stem rot resistance.

Understanding the Genetics of Resistance to Groundnut Rosette Disease

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Groundnut Rosette Virus (GRV) causing Rosette Disease (GRD) in groundnuts, is the most destructive disease in Sub-Saharan Africa. While the development of GRD resistant varieties is the most sustainable way of managing the disease, the genetics of resistance is not well understood. In Zambia, most of the farmer-preferred groundnut varieties are susceptible to GRD and there are no genetic and genomic resources developed to enhance the selection and improve the understanding of GRD resistance. The aim of the current study was to make use of existing resources to understand the genetic control of GRD resistance in Zambian groundnut. An existing bi-parental mapping population was phenotyped in two seasons under screen house conditions for their response to GRD. The top ten most susceptible and top most resistant genotypes were selected for QTL-sequencing using Illumina technology. Phenotypic and genotypic data were analysed using Genstat v18 and in-house scripts respectively. A joint phenotypic and genotypic data analysis was done to establish marker-trait associations using SVS software Molecular markers with significant associations were selected for further development of KASP assays for future routine marker-assisted selection for GRD resistance. The new markers were validated across six bi-parental mapping populations developed between known sources of resistance and susceptible farmer-preferred genotypes in Zambia. We observed strong signals across the syntenic locations of chromosomes 4 and 14 suggesting the involvement of a major gene in the control of GRD resistance. Our results provide an immediate resource for more efficient selection for GRD resistance. We recommend the identification of more sources of resistance and pyramiding the desirable loci into farmer-preferred varieties to avoid future breakdown of the resistance observed.

Analysis of Total Fat and Total Protein Percentages from 2018-2020

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The seeds of cultivated peanut are an agronomically important crop produced for human nutrition providing protein, lipids, and complex carbohydrates. With an average of 7g of protein per serving, peanuts and peanut butter are an important plant-based protein source. Lipid (fat) content is the predominant macro component, and generally increases as the peanut matures. Given the trend of increasing fat content with maturity, questions regarding the impact of fat content as compared to other macronutrients arise. We examined the relationship between total fat and total protein over 3 different crop years. 78 samples were gathered during harvest from the SE region of the US (provided by Birdsong Co.) and analyzed for total fat by solvent extraction and total protein (Dumas Test, Medallion Laboratories). Total fat ranged from 42.6% to 50.3% and averaged 46.4%, 46.3%, and 45.6% respectively for the 2018-2020 crop years. Total protein averaged 23.9%, 24.0%, and 23.1% respectively, ranging from 21.8% to 25.9% over the three-year period. When comparing the two traits, it was noted that generally total protein decreased as total fat increased demonstrating an inverse relationship. The environmental conditions and overall crop maturity impact the significance of the relationship between fat and protein content. Guidelines for managing maturity as it impacts total protein may be a consideration going forward pending additional data across growing regions and crop years.

Proteomic Analysis of Raw and Roasted *Arachis hypogaea* Seeds

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During thermal processing, peanut storage proteins react to produce advanced glycation end products (AGEs). Three major peanut allergens (encoded by the genes *arah1*, *arah2*, and *arah3*) are extensively modified during thermal processing producing AGEs. Raw peanuts were heat treated and analyzed by bottom-up LC-MS/MS proteomics, conducted by the Proteomics Resource Center at the Rockefeller University, to determine how the time and temperature variables influenced the formation of AGEs on peanut allergens. Proteomic data revealed the relative abundance of proteins present throughout the roasting process. The results indicated the optimal roasting time for product formation. Evidence of lysine carboxymethylation, carboxyethylation, and, to a lesser extent, pyrrolation were observed to increase upon time of heat exposure. Results suggest that the storage proteins are glycated as a function of roasting time, generating reaction products which impart the characteristic roasted peanut flavor.

Evaluation of Selected Herbicide Programs for Broadleaf Weed Management in Peanut

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Palmer amaranth, sicklepod, and morning glory have characteristics that allow them to thrive in peanut production fields in South Carolina and rank among the most common and troublesome weeds in the Southern US. These attributes include rapid growth, high reproductive capabilities, drought tolerance, and extended emergence throughout the growing season. In addition, herbicide resistance is prevalent in Palmer amaranth in South Carolina. For example, Palmer amaranth biotypes resistant to Cadre are common in South Carolina peanut production, but it is still an effective option on other broadleaf weeds found in peanut production fields. To manage ALS-resistant Palmer amaranth and other problem weeds, growers rely on a series of over-lapping soil residual and postemergence herbicides to maintain weed free fields. Correct spray timing is critical for the management of these weeds. If not sprayed according to label instructions, these broadleaf weeds can be very difficult to control in peanut after exceeding a given growth stage. In addition, if these weeds are not properly controlled, the weed seed bank can increase over time making future production challenges for subsequent crops. Therefore, a total program approach is needed to manage these weeds in South Carolina peanut production. Research plots were established at Clemson University's Edisto Research and Education Center near Blackville in 2020. The study area was supplemented with Palmer amaranth, sicklepod, and annual morningglory seed scattered over the plot area. The herbicide treatments for the field study are presented in Tables 1. The experiment design was randomized complete block design with 14 treatments and 4 replications. The plot dimensions were 4 rows by 40 ft long. Conventional production practices were followed according to Extension recommendations prior to peanut planting (disking the field followed by strip till the peanut rows). Peanuts were seeded on June 2, 2020. Preemergence treatments were applied shortly after planting. Postemergence herbicides were applied on June 16 (POST1), July 1 (POST2), July 16 (POST3), and August 3, 2020 (POST4) when most of the broadleaf weeds were 2 and 4 inches in height. Adjuvants (Crop oil or NIS) were added to each herbicide program according to label requirements for optimum activity. Percent visual weed and crop injury ratings were collected 14, 28, and 42 days after each postemergence application. Disease and other in-season production practices were followed according to current Extension recommendations. Peanuts were inverted and harvest for yield on November 20, 2020. The plots received supplemental irrigation throughout the season. In terms of the preemergence treatments, All preemergence products (Brake, Valor, and Spartan Charge) provided excellent control prior to the postemergence 1 treatment (6/16/20). Peanut injury was minimal except for the Cobra and 2,4-DB treatment which showed significant injury (20-36%) 14 days after application (7-16-20). Treatments 2 and 11 were significantly lower in yield compared to the other treatments in the study. In the remaining treatments, there were no difference observed. These differences were not attributed to herbicide injury. Palmer amaranth control was very good at the 2 to 4-inch plant height with the Gramoxone + Storm, Cobra, Storm, and Basagran herbicides in the greenhouse. Palmer amaranth control did decrease as weed height increased, typically by 6 to 8-inch height Basagran and Storm alone did not adequately control Palmer amaranth. The tank mix of Gramoxone plus Storm did cause more injury to the larger Palmer amaranth sizes and regrowth was more pronounced. The overlapping residuals is key to effective herbicide programs in peanut production.

Progress in the Evaluation of Peanut Germplasm to Enable Selection for Aflatoxin Resistance

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Using single-seed analysis, we have identified novel sources of peanut germplasm that do not accumulate aflatoxin upon fungal infection. Changes in gene expression in the seed-*Aspergillus* interaction have been characterized and demonstrated that resistant and susceptible genotypes have different responses. The present study applied large-scale and small-scale SNP genotyping platforms to characterize their genetic identity, assess genetic variation within accessions, and develop diagnostic markers for pre-breeding. The analysis included wild diploid species of *Arachis* section *Arachis* and peanut landraces of *Arachis hypogaea* subsp. *fastigiata* from the U.S. peanut collection. All germplasms were genotyped with a 48K SNP peanut array. A SNP genotyping platform called RNase H2 enzyme-based amplification (rhAmp) was further implemented to validate SNPs in a larger number of individuals per accession. Informative SNPs were identified and validated using rhAmp assays. They uncovered genetic variability within accessions, confirmed F_1 hybrids, and detected spontaneous cross-pollinations. These results are discussed in the context of screening methods for detection of aflatoxin accumulation.

Evaluating the Effectiveness of Aflasafe and Agronomic Practices on Aflatoxin Contamination and Yield of Groundnut in Malawi

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During post-harvest storage, Aflasafe has been reported to have residual protective effect against aflatoxigenic fungi. Unfortunately, until now, there is limited evidence on the efficacy of single and combined agronomic practices in minimizing/reducing aflatoxin contamination and increasing groundnut productivity in Malawi.

To this end, this study seeks to:

- Further evaluate Aflasafe, both in terms of reduction of aflatoxin contamination in groundnut and relative to economic return on investment for the farmer or aggregator/marketer.
- Evaluate the effect of various single and combined agronomic practices (liming, application of inorganic fertilizers, Rhizobium inoculation and residue incorporation) in reducing aflatoxin contamination and productivity.
- Evaluate the residual effect of Aflasafe in storage

Effects of Fungicides application and Weed Management Methods on Performance of Groundnut (*Arachis hypogea)*

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Groundnut (*Arachis hypogea)* is one of the grain legumes that is widely grown in Malawi. However, productivity is constrained by a number of biotic and abiotic factors including weeds, diseases, unpredictable rainfall; and agronomic practices (eg plant density and poor weed management). Decisions on investments in weed and disease management require information on costs and benefits of the intervention. Field studies were conducted in 2019/2020 and 2020/2021 at two locations in Lilongwe, Malawi to evaluate the effects of fungicides and weed management practices on performance of two varieties (CG9- Virginia type; and Chitala-spanish variety) of groundnut at different densities. The soils are generally medium textured ranging from sandy clay to sandy clay loams; and with low to medium levels of soil organic matter.

In the fungicide trial, the treatments included fungicide application and control (no fungicide). Results showed that application of fungicides reduced leaf spot and improved general plant health especially in Chitala variety; and also increased grain yield of the two varieties by 25-33%. For the herbicide trial, there were four weed management treatments as follows: pre emergence herbicide only, post emergence herbicide only; pre and post emergence herbicides, and untreated. In the first season, results on grain yield showed that at Horizon site, application of herbicides increased grain yield of chitala variety by 67-103% and 32-48% over the untreated (control) at low and high densities respectively; and high density only for CG9 by 44-98% compared to the untreated. Similar results were observed at Chitedze site where herbicide application increased grain yield by 14-43% in Chitala variety However, no differences were observed among the herbicide treatments. For the second season (2020/21), results on grain yield will be available in June 2021. In this paper, we also present results on costs associated with different weed management methods and implications on investments in weed management.

Economic Impact of Increased Seeding Rates in Single Row Peanut is Southeast Georgia

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The foundation for achieving maximum yield potential of peanut (*Arachis hypogaea* L.) is acquiring a uniform plant stand. Plant stands can be affected by many factors like environmental conditions, seed quality, and/or seeding rate. In the last few years, growers have experienced problems with varying environmental conditions and seed quality causing a perception that increased seeding rate is needed to get adequate stands. Growers have also adopted the idea that increased seeding rates above the UGA Extension recommendations are needed to obtain higher yield potential. On-farm trials were conducted in Jeff Davis County in 2019 and 2020 to determine the influence of seeding rates on yield potential for single row peanut. Seeding rate treatments consisted of: 6, 7, 9, and 11 seed per foot in 2019 and 7, 8, 9 and 10 seed per foot in 2020. Yields were not statistically different across treatments. Including grade and price per treatment the optimal net return above seed cost were 6 seed per foot and 9 seed per foot in 2019 and 2020 respectively. We were unable to combine both years of data because of the change in seeding rate the second year. Based on these trials, increased seeding rates above UGA recommendations may be warranted during situations where environmental conditions or seed quality are an issue but are not profitable where these factors have minimal influence.

Use of Photovoice to Assess Quality and Safety of Peanuts along the Value Chain: A case of Youth in Nwoya and Tororo districts, Uganda

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The quality and safety of peanuts in Uganda is compromised along the value chain as a result of inadequate pre and postharvest handling. There is need to put in place procedures to enhance profitability for farmers including the youth. This study aimed at assessing the feasibility of using photovoice, a community participatory research technique as an alternative for assessing peanut quality and safety along the value chain inorder to come up with appropriate recommendations.

Thirty rural-youth farmers aged 18-35 years in the Nwoya and Tororo districts of Uganda were trained in photovoice and provided with smartphones to take photographs over a six-month period about issues related to peanut value chain. Qualitative data from group discussions with the youth conducted monthly was analyzed using content analysis in Atlas ti version 6.

Preliminary findings suggest that poor produce at harvest, varietal mixtures, unsorted grains, poor processing environments, poor drying techniques, poor storage conditions, inferior packaging materials used, the safety of personnel in processing areas, and processing methods of the different products were factors associated with quality and safety along the peanut value chain.

Photovoice is a potential tool for assessing quality and safety of peanuts along the value chain.

Effect of Boron and Calcium Application, Harvesting Dates on Seed Quality and Yield Components of Groundnuts (*Arachis Hypogaea* L.)

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The experiment to study the effects of boron and calcium fertilizer, harvesting dates on groundnut seed quality, and yield components has been established for the 2020/2021 copping season at two sites, Chitedze Research Station and Horizon Farms, Lilongwe, Malawi. CG9 (ICGV-SM 08503) and Chitala (ICGV 99568) varieties were planted. Boron and calcium fertilizers were applied at 560g/ha and 200kg/ha, respectively. The pH at Chitedze site was moderately acidic (5.3), boron was very low (0.41µg B/g), calcium was very high and organic matter was also very high (5.04%). The pH at Horizon site was almost neutral (6.0), boron was low (0.64µg B/g), calcium was very high and organic matter was medium (1.73%)

The performance of groundnut plants above ground shows a variation in plant growth responses to boron and calcium application as compared to the unfertilized groundnut. There is variation in terms of plant height and canopy width of groundnut in plots applied with boron only and with those applied with boron and calcium. At Chitedze site, application of calcium increased plant growth in CG9 variety compared to boron only or a combination of boron and calcium. Results on yield and yield components as affected by fertilizer inputs and implications of the findings are presented.

Impact of Fungicide Programs and Delayed Harvest on Yield and Quality of Peanut (*Arachis Hypogaea* L.*)*.

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Peanut growers in Georgia strive to maximize yield and quality each year in order to remain profitable. Their efforts involve keeping the crop healthy by managing diseases through effective fungicide programs throughout the season, and then, harvesting peanut in a timely manner to maintain yield potential. Research was conducted in 2019 and 2020 at the University of Georgia Tifton Campus in Tifton, GA to evaluate the efficacy of different fungicide programs and their respective impact on maintaining yield and quality of peanut when harvest is delayed after digging. Treatments were arranged in a split plot design with four replications. Harvest date was the main plot effect and fungicide program was the sub-plot. Harvest date treatments were 1.) 5 days after digging, 2.) 10 days after digging, and 3.) 20 days after digging. Fungicide program treatments consisted of 1.) chlorothalonil + tebuconazole program (60, 75, 90, 110 DAP), 2.) azoxystrobin + benzovindiflupyr (60 and 90 DAP) and chlorothalonil + flutalonil (75, 110 DAP) program, and 3.) azoxystrobin + benzovindiflupyr + pydiflumetofen (60, 88 DAP). The runner market-type cultivar Georgia-09B was planted in both years. All plots received chlorothalonil at 45 and 120 DAP and were inverted at optimum maturity. Plots were rated for leafspot diseases prior to digging and southern stem rot immediately after digging to provide an assessment of plant health given the varying fungicide programs evaluated. Peanut yield declined as much as 400 lbs/A and select grade parameters (ie. sound splits) increased up to 3% as harvest date was lengthened, no matter the fungicide program. However, the more broad-spectrum fungicide programs maintained greater yields (200+ lbs/A) and quality (1+ % total sound mature kernels) compared to the chlorothalonil + tebuconozole program across all harvest dates.

Physiological Quality o~~O~~f Peanut Seeds Impacted By Drought During t~~T~~he Reproductive Development.

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Sub-optimal water availability during crop development, especially during peak flowering and pod filling, affects the quality of the seeds produced, and generally results in poor seed quality. More frequent drought periods have increased the concern of peanut (*Arachis hypogaea* L.) seed quality in the United States. Identifying the acquisition pattern of the physiological components to determine the timing peanut seeds achieve maximum physiological seed quality as well as understanding the impact of drought stress during seed development are fundamental for harvest decision making and high-quality peanut seed production. The goal of this study was to identify the acquisition of physiological quality components in peanut seed during seed development under well-watered and drought conditions. The field research was conducted in a 6.1 x 12.2 m rainout shelter in Dawson, GA using the cultivar Georgia-06G. Seeds were planted on May 21, 2020. The field was divided in two water regimes: well-watered control and drought stress. The rainout shelter was used to prevent rain/irrigation in the drought stressed plot for 30 days beginning 80 days after planting (DAP). Well-watered plots received supplemental irrigation when soil water potential reached -40 kPa. Plants were harvested at 119 DAP corresponding to 2500 growing degree days. Harvested pods were separated into eight classes using the peanut maturity profile board ('white', 'yellow 1', 'yellow 2', 'orange', 'brown 1', 'brown 2', 'black 1', and 'black 2'). Germination, vigor and desiccation tolerance tests were performed in each maturity class. In addition, to identify potential dormancy in the seeds, a sample was treated with ethephon to release dormancy and the three physiological tests were performed on the treated seeds. Dormancy was observed in peanut seeds and was likely acquired between 'orange' and 'brown 1' classes. Seeds developed under drought condition presented greater germination for classes 'yellow 2' and 'orange' than well-watered conditions, whereas germination was similar for both water regimes for the other classes. Speed of germination was higher in seeds from the drought treatment for the classes 'yellow 2', 'brown 1', 'black 1', and 'black 2', indicating superior vigor on seeds of these classes developed under stress. In general, drought stress promoted a similar or in some instances, superior physiological quality in peanut seeds than the well-watered treatment. Furthermore, the acquisition of physiological quality was accelerated in seeds under drought conditions, indicating that during development, these seeds can reach their maximum physiological quality sooner than the seeds from well-watered conditions.

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Response of Groundnuts to Rhizobia Seed Inoculation, Inorganic Fertilizer Application and Plant Density

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Plant density and nutrition are among factors that affect crop productivity. On-station experiments were conducted at two sites in Lilongwe, Malawi, during the 2019/20 and 2020/21 growing seasons to evaluate the effects of plant density, rhizobia seed inoculation and inorganic fertilizer application on yield and biological nitrogen fixation of two groundnut varieties, Chitala (Spanish) and CG-9 (Virginia).

The results showed that the varieties responded differently to density and inputs (rhizobia seed inoculant and inorganic fertilizer) and density. In both varieties, inorganic fertilizer (D-compound) increased nodule weight and total amount of N fixed by groundnut by 20 to 35%; while application of inoculant increased nodule numbers per plant. This study has also established that the Spanish variety (Chitala) is more responsive to inorganic fertilizer and rhizobia seed inoculant than Virginia variety (CG-9).

Developing Risk Management Tools to Help Farmers Minimize Risk in Peanut Production in Two Agro-ecologies in Ghana

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Profitable peanut cultivation in Ghana is beset with a number of abiotic (e.g., drought, fertilization etc.) and biotic (e.g., pests, diseases etc.) constraints that must be managed effectively to optimize yields. These constraints differ with agro-ecologies and pose significant risk to yields as well as limit financial returns to farmers. Knowledge of the interactions among key production practices such as pest management, crop rotation sequence, varietal selection, tillage systems and chemical inputs is required to mitigate these risks and to inform the quality of advice offered by Agricultural Extension Agents (AEAs) and similar advisory agencies to peanut farmers. A comprehensive, excel-based risk management tool was developed to help farmers and their advisors implement practices that minimize risk to yield while providing estimates of production costs was developed for peanut production in North Carolina (USA). This tool allowed for the development of similar ones for other countries, with Malawi being the first country in Africa to have adopted it for peanut farmers. This poster presents the first version of a similar risk tool developed to aid AEAs and farmers to make informed decisions on the right combinations of production practices that will minimize risk and increase yields in Ghana. Three risk tools were developed; one for the interior savannah zone of northern Ghana which has a unimodal rainfall pattern, and two for the forest-transition zone of southern Ghana which is characterized by a bi-modal rainfall pattern. The important differences in choices of varieties, sowing distances, fertilization and pest management between savannah and the forest-transition regions as well as the impact of their interactions on peanut yields and aflatoxin levels will be presented. Also, the differences in practices between the two different seasons (i.e., major and minor) in the Forest-transition will be highlighted. Overall, this risk management tool developed has benefits for extension service providers (government and private), breeding, agronomy, and plant protection programs as well as for teaching in higher institutions.

Evaluation of S~~s~~elected F_6 peanut progenies of BC_3-derived I~~i~~ntrogression L~~l~~ines and Spanish P~~p~~arents for R~~r~~esistance to *Aspergillus flavus* I~~i~~nfection

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Aflatoxin contamination of peanut can have serious economic and health impacts on humans and livestock. Efforts are being made to identify new sources of resistance to *Aspergillus flavus* infection. Wild species have been reported to have resistance or near immunity to *A. flavus* infection. This study seeks to identify *A. flavus* resistant genotypes from a population derived from a cross between BC_3F_6 interspecific introgression lines and Spanish peanut genotypes with susceptibility to *A. flavus* contamination. The interspecific introgression lines (BC_3F_6) originated from a cross between Florunner and TxAG-6 [*A. batizocoi* x (*A. cardenasii* x *A. diogoi*)]^{4x}. Thirty-three (33) BC_3×Spanish breeding lines selected based on resistance to leafspot disease, two *A. flavus* susceptible checks namely, Manipinta and Chinese and a resistant check, ICGV-03401 were used in this study. Ten heathy seeds with intact seed coat of each genotype were inoculated with an aqueous conidial suspension of an aflatoxigenic strain of *A. flavus in vitro* per replicate. Data were recorded on incidence and severity of *A. flavus* infection every two days. Results revealed significant ($p<0.001$) differences for both incidence and severity of *A. flavus* infection. Susceptible check cultivars Chinese and Manipinta had >70% infected seeds, and the resistant check ICGV-03401 had 38%. Genotypes, L096, L015A, L027B, L020, L030 and ICGV 03401 were found to be resistant to *A. flavus* infection and colonisation with less than 50% infection. Among these, L096, L015A and L027B had fewer than 35% infected seeds and out-performed the resistant check. The presence of resistant genotypes in this population signifies the existence of individuals within the BC_3F_6 population that may have equal or stronger levels of resistance than the Spanish parents used in developing the population under the study.

Genomic Characterization of North Carolina State University's Germplasm and Breeding Lines

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The peanut breeding program at North Carolina State University has historically utilized traditional methods, such as single seed descent, to produce cultivars for release. In the age of high-throughput and cost-effective sequencing, it is essential to integrate genomic tools into the breeding process to enhance the accuracy and productivity of the program.

As the foundation for genomic work in the NCSU program, cultivar 'Bailey II' (*Arachis hypogaea* subsp. *hypogaea* var. *hypogaea*) was assembled as the reference genome for Virginia-type peanut. The assembly quality and utility of the Bailey II reference genome will be discussed. Subsequently, whole genome sequencing (WGS) was conducted for ninety six lines that represent the diversity relevant to the NCSU breeding program. WGS data were used to identify variants throughout the entire length of the Bailey II genome. This data, along with known pedigree information allowed introgression blocks to be identified. The composition of variants in this data along with confirmed introgression blocks will be presented. The findings in this study will inform the future development of markers for use in marker assisted selection and a genotyping strategy suitable for genomic selection.

Successful Implementation of Speed Breeding Techniques in a Peanut Breeding Program

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Traditional peanut breeding strategies used in Australia have been based on a pedigree breeding system after initial glasshouse hybridisation. Utilising this strategy, new peanuts varieties are commercially released to industry in around 12 years after initial hybridisation. Over the past decade the Australian Peanut Genetic Improvement Program (APGIP) and now the Future Peanut Breeding Program (FPBP) have developed new strategies to reduce the time taken to release new varieties and improve the efficiency of the breeding program. Speed breeding, the growing of plants under controlled environment conditions, in conjunction with marker-assisted backcrossing provides an opportunity to not only reduce generation time but also to simultaneously incorporate genetic marker selection tools. A speed breeding facility (SPF) has been established in a 40 foot insulated shipping container on site at the Kingaroy Research Station in Queensland, Australia. Lighting is provided by 12 light emitting diode (LED) units with two reverse cycle air conditioners installed to ensure temperature remains at optimum levels. Preliminary trials, run through the 2020 winter, indicated viable seed could be achieved harvested at 85 days after planting (DAP). A follow up study will assess if growing time can be further reduced, in order to turn-around and entire generation, including post-harvest processing in around 90 DAP. This will enable four generations to be grown in a calendar year, significantly reducing generation time. In order to facilitate a marker assisted backcrossing program, cuttings were taken from F1 plants grown in a North Queensland winter nursery in August 2020. These cuttings were transported to and successfully established in the SBF the following day. The F1 cuttings continued to grow and flower successfully in the SBF and the flowers from these males were subsequently used for crossing in the facility. Crossing was generally successful, however more research is required to improve the success rate. In summary, peanuts have been shown to grow successfully from seed and cuttings in the SPF, as well as being able to be crossed. This is a critical step in rapid generation of a marker assisted backcrossing program to the BC3F3 generation, before plants are then grown out in the field for further assessment of yield and quality traits.

Enhancing the Efficiency in Data Collection in Peanut Through Whole-Plot Data Capture: The Case of Above Ground Biomass and Foliar Diseases

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Peanut is an important grain legume worldwide famed for its oil, food and feed qualities. The crop is grown on nearly 29.6 million ha with a production of 48.76 million metric tons worldwide. In Ghana, total peanut production stands at 535,685 metric tons on an area of 403,447 ha. The major constraints facing the peanut industry in Ghana is the use of old varieties with inherently low yielding potential and foliar diseases. There is therefore the need to develop new improved varieties with tolerance to foliar disease. These efforts require the development and accurately phenotyping of large populations within short time with minimal resources. This work presents the preliminary findings from the use of an UAV (DJI Mavic Pro) carrying an RGB camera to estimate biomass yield and foliar diseases in peanut with the aid of open-source software (WebODM and FieldImageR). WebODM is a photogrammetry software that can be used to generate orthomosaics, point clouds, elevation models, 3D models, measure plant traits and health, it accepts any camera and can process multispectral images from UAV. FieldImageR on the other hand is a package developed to run on the open access R software for the extraction and calculation of spectral indices. Results show a strong relationship between digitally estimated canopy area (CanArea), variable atmospheric resistance index (VARI), normalized green red difference index (NGRDI), and early leaf spot (ELS, caused by *Cercospora arachidicola* S. Hori) and late leaf spot (LLS, caused by *Cercosporidium personatum* Berk. and Curt.) AUDPC. While VARI and NGRDI had a consistently negative relationship with ELS and LLS throughout the study period from growth stage R1 (beginning flowering) to R7 (physiological maturity), CanArea had a positive relationship with ELS and LLS at R1 although not statistically significant ($p>0.05$). CanArea had a positive correlation with biomass yield at R7 ($r = 0.88$, $p<0.001$). The estimated rate curve suggested that the strength of correlation between UAV estimated parameters with ELS and LLS AUDPC increases with crop maturity. The UAV estimated parameters could therefore provide an inexpensive whole-plot data for selection for ELS and LLS tolerance and higher biomass in peanut.

Survey, Isolate and Apply Calcite Dissolving Bacteria as a New Form of Calcium Source.

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Calcium is a critical nutrient for proper peanut (*Arachis hypogeae*) pod development and an effective agent in enhancing resistance to fungal pathogens. Insufficient calcium within the peanut pegging zone during flowering can lead to embryo abortion, plant stress and reduction in seed quality. The current practice is to apply hundreds of pounds of gypsum or lime to fields during the start of peanut flowering. The application of this fertilizer is a large expense for farmers, which is expected to increase due to the current rise in transportation and manufacturing costs. To alleviate the need to apply gypsum, a group of calcite dissolving bacteria (CDB) have been isolated based on their ability to produce soluble calcium through the dissolution of calcite (mineral for of calcium). Native CDB have been identified in Tifton, GA. We also observed a negative correlation between soil calcium level and the abundance of CDB. Preliminary results showed that application of CDB in field soil increased the soluble calcium level and promoted seed germination. We aim to engineer these bacteria into a cost effective biofertilizer and fungicide through its innate ability to increase calcium levels.

Marker Analysis of Breeding Lines for High Oleic Oil and Nematode Resistance

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Breeding line accessions were grown in replicated trials in Texas in 2019, 2020, and 2021. Seeds of the accessions were screened for high oleic trait using a Thermo Scientific Nicolet iS10 spectrometer (Thermo Fisher Scientific, Waltham, MA). High oleic seed chips were extracted. DNA was quantified using the Quantifluor dsDNA System (Promega, Inc, Madison WI) kit on a Tecan Infinite F200 plate fluorometer. Genotyping for the *Ma-1* locus (Burow *et al.*, 1996) was performed using Kasp markers for the POA_A9:5,944,580 locus (Clevenger *et al.*, 2017). PCR reactions were run on a Roche LightCycler 480 II. Accessions were grouped using the LightCycler software. Susceptible checks (Tamrun OL07 and CC270) were scored as susceptible (XX). Resistant checks (NemaTAM and Tx071304) were scored as resistant (YY). Accessions were scored as belonging to one of these groups. Resistant, susceptible, and segregating breeding lines for root knot nematode were observed, and lines with high oleic and nematode resistance were selected.

Water Management Strategy in Peanut for Improved Seed Physiological Quality

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Irrigation is critical to peanut seed production as drought episodes have become more frequent and intense in recent years in Georgia. Too much water applied during seed development delays acquisition of physiological components of seed quality such as germination and vigor. A comprehensive understanding of water management for the different growth stages of peanut plants is critical to achieve greatest yield potential and produce seeds with improved quality. The objective of this research is to determine more accurately the optimum irrigation trigger points in the different plant developmental stages of peanut to achieve greatest yields and physiological quality of seeds. The field experiment was carried out at the University of Georgia C.M. Stripling Irrigation Research Park in 2020 season under a variable rate lateral irrigation system capable of independently controlling water applications within eight-row wide by 40 ft long plots. Irrigation management included eight combinations of three soil water tensions (SWT) levels (20 kPa, 45 kPa, and 70 kPa) and a dryland using three replications of each treatment for a total of 27 plots. Peanut cultivar Georgia-06G was planted on May 6. SWT sensors were installed in the plots approximately 2 to 4 weeks after emergence and data were collected hourly and utilized to make decisions on irrigation scheduling triggers. Yield was determined at harvest. A pod subsample was taken to the laboratory, separated into six maturity classes (white, yellow 1, yellow 2, orange, brown, and black) according to the maturity profile board. Pods were shelled for evaluation of seed germination and vigor. No significant differences were observed among water treatments. However, irrigation water use efficiency (IWUE) was greatest for the water treatment 20/45/45 kPa and lowest for 70/20/45 kPa. Over-applying water during seed development did not reflect in greater yield or water use efficiency. In addition, seed germination in some of the maturity classes was impacted by water management. For the ‘brown’ class, the water treatment exposing plants to a moderate drought stress early season followed by optimum water supply during seed development (70/45/45 kPa) resulted in germination 37% higher than the dryland and 42% higher than the treatment over-irrigating the plants early season followed by a moderate drought during seed development (20/70/45 kPa). Seeds from ‘yellow 1’ followed a similar trend of ‘brown’, with greater germination for 70/45/45 kPa compared with 20/70/45 kPa and dryland. In conclusion, water can be managed more efficiently to improve IWUE and physiological quality of peanut seeds without negatively affecting yield.

2020 Peanut White Mold Fungicide Program Comparison in Cook County, Georgia

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White Mold (WM), (*Sclerotium rolfsii*) is the most destructive disease in peanut production in Georgia. This disease's capacity to reduce yield and quality makes its control a priority among Georgia peanut producers. Growers have many peanut fungicide options available, each with varying costs and WM efficacy. UGA Extension in Cook County, Georgia collaborated with UGA Extension Peanut Disease Specialist, agriculture industry and a local grower to install and evaluate nine peanut white molds fungicide programs in a 15 acre replicated trial. WM ratings showed tebuconazole alone as the least effective treatment program for WM (33% WM incidence). The three block Elatus program showed the greatest WM control in this trial (8% WM incidence). The three block Excalia program (2oz, 3X); the two block Umbra; and the Lucento (2X)/Convoy/Elatus/Muscle ADV program were similar but not equal for WM efficacy (11%, 11.1% and 11.3% WM incidence respectively). The three block Excalia program (3,3, 2 oz) and two block Convoy programs were also similar but not equal in WM efficacy (13.1% and 13.3% WM incidence respectively). The four block Fontelis program showed 18.5% WM incidence while the two block Elatus program showed 19.5% WM incidence. Profit comparisons showed the least expensive program (Muscle ADV 4X) allowed for the highest incidence of WM while the most expensive program (Priaxor 2X; Convoy 2X) did not result in highest profits. In this trial, Excalia applied at 2 ounces per acre, 3 X, produced the highest yields and profits compared to the treatments in this trial.

Peanut Response to Soil-Applied Liberty® (Glufosinate)

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Liberty® (glufosinate) is registered for preplant burndown and postemergence weed control programs in numerous row crops but not peanut. Additionally, current labels prohibit peanut planting for 180 days after application. Therefore, the objective of this research was to evaluate the response of peanut to soil applications of Liberty. In 2020, small-plot field trials were conducted in Arkansas (Newport), Georgia (Ty Ty), South Carolina (Blackville), and Texas (Yoakum) to evaluate the effects of Liberty 2.34SL applied at 0, 32, and 64 oz/A, either 1 day before planting (DBP) or 1 day after planting (DAP), on peanut growth and yield. In Georgia, treatments were applied either 7 DBP + 1 DAP or 1 DAP. Treatments were arranged in a randomized complete block design with a 2 (timing) X 3 (rate) factorial arrangement with 3-4 replications. All plot areas were maintained weed-free using a combination of labeled herbicides and hand-weeding. Data collected included peanut plant density (21 DAP) and peanut yield. All data were subjected to ANOVA and means separated using Fisher's Protected LSD Test ($P<0.10$) when appropriate. No significant interactions between Liberty timing and rate were observed for any response variable ($P\geq0.1209$). Generally, peanut tolerance to soil-applications of Liberty was adequate. In Georgia, peanut density was reduced 6% with 64 oz/A of Liberty (averaged over timing). In South Carolina, peanut density was reduced 3% when Liberty was applied 1 DAP (averaged over rate). At all locations, peanut yield was not reduced by any timing or rate of Liberty. Based upon these results, Liberty can be used for preplant burndown weed control programs in peanut without concern for undesirable crop injury.

Unmanned Aerial System (UAS) Phenotyping for Organic Peanuts

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The use of Unmanned Aerial System (UAS) can accelerate peanut breeding by generating high-throughput data for analysis. The demand for organic peanut is on the rise, implying the need for organic peanut cultivars. The aim of this study will be to evaluate the feasibility of UAS phenotyping for agronomic traits in organic peanut breeding lines. UAS data will be collected from a total of twenty peanut breeding lines and cultivars from the peanut breeding program and genetics from Texas A&M AgriLife in Stephenville. Peanut lines will be established on organic plot at Texas A&M AgriLife at Vernon in the summer of 2021. UAS data will be collected from a SlatRange 4P+ sensor that will collect six different spectral bands. UAS flights will be conducted at 7, 14, 21, and 28 days after sowing to estimate stand count. During the reproductive stage, UAS flights will also be conducted once a week. The UAS data for each individual plot will be extracted using the QGIS software program. The UAS data will be used to derive the Normalized Difference Vegetation Index, Normalized Difference Red Edge Index, Canopy Chlorophyll Content Index, Chlorophyll Index Green, etc. for each peanut line using the Pix4Dmapper software program. Data analysis will be conducted at the UAS data analysis station at Texas A&M AgriLife in Vernon. We expect to identify statistically significant differences in the UAS data and a significant correlation between the UAS data and agronomic traits. The results from this study can accelerate breeding for organic peanuts adapted to North Texas.

Field Evaluation for Organic Peanuts in North Texas

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A large portion of the U.S. organic peanut production comes from West Texas. In order to meet the increasing demand in organic peanut, exploring various areas for organic peanut cultivation will be of interest. In this view, we aim to evaluate the agronomics of some peanut breeding lines on an organic plot in North Texas. Twenty peanut breeding lines and released cultivars, obtained from the peanut breeding program and genetics from Texas A&M AgriLife in Stephenville, will be planted on organic plot at Texas A&M AgriLife at Vernon in the summer of 2021. The entries will be planted on a two-row plot of fifteen-foot long with a three-foot alley between plots. For each row, about seventy-five peanut seeds will be sown. The experiment design will be a randomized complete design with four blocks. Stand count will be evaluated at 7, 14, 21, and 28 days after sowing. Canopy coverage, time to lap, and days to maturity as well as yield and grade data will be collected. Diseases such as leaf spot, sclerotinia, and pod rot will be evaluated on a scale ranging from 0 to 10 (0: no disease and 10: plant death or 100% infection). We expect to identify statistically significant differences in the evaluated traits among the peanut breeding lines. The results from this study will help develop organic peanuts adapted to North Texas.

A Comparative Analysis of Peanut Seed Systems: Searching for Innovation to Sustainably Unlock Improved Genetics

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Improved varieties hold great promise for improving yield and resilience across the all peanut producing areas. However, in many countries and particularly in Sub-Saharan Africa, the predominant varieties are often decades old and sub-optimal despite efforts to introduce and scale improved varieties. There are several potential reasons for limited adoption, but the predominant limitation lies in the structure and function of the seed systems. Using data collected from primary sources and key informant interviews across several countries, we have developed a comparative analysis of peanut seed systems and identified common economic, social and environmental challenges using a sustainability lens. Through key case studies, we have also proposed potential interventions and strategies for resource limited environments and identified future potential bottlenecks for scaling improved varieties.

Photosynthetic Efficiency and Yield of Peanut Plants Treated with Dodine

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Peanut plants are generally susceptible to leaf spot, which can reduce considerably the final yield. The most widely used fungicide in the control of this disease is chlorothalonil. However, Europe is anticipating a ban of this chemistry due to its high risk to amphibians and fish. Dodine is an alternative fungicide with a similar range of activity. But this chemistry was reported to suppress photosynthesis in pecan. Therefore, studies on photosynthetic activity in peanut plants treated with dodine are needed before recommending its application. The objectives of this research were to evaluate the effects of dodine on leaf photosynthesis of peanuts and validate the potential of dodine as a replacement of chlorothalonil. The experiment was conducted at the University of Georgia Lang Farm in Tifton using the cultivar Georgia-06G. The experimental design was a randomized complete block. Treatments consisted of four fungicides, 1) chlorothalonil (Bravo 720 g/L) at 1.2 L/ha (full rate), 2) chlorothalonil at 0.6 L/ha (half rate), 3) dodine (Elast 400 g/L) at 1.7 L/ha ml (full rate), and 4) dodine at 0.8 L/ha (half rate). Total chlorophyll and total carotenoid were collected from 37 days after planting (DAP) until 135 DAP. A LI-6800 portable photosynthesis system with a fluorometer chamber was used to obtain weekly net photosynthesis rate. Final yield was collected at harvest. Pod maturity profile was also assessed at harvest by using the Peanut Profile Board. Significant differences were not observed in net photosynthesis among the four treatments over the season. Total chlorophyll and total carotenoids as well as maturity profile and yield were not significantly different between the treatments, indicating that these parameters were not affected by the fungicides and rates. In summary, results demonstrated that the use of full and half rate of chlorothalonil or dodine did not impact the photosynthetic activity of peanut plants, pod maturity profile, and final yield. Hence, dodine could be considered as a potential replacement of chlorothalonil in the control of leaf spot in peanut. This study will be replicated in 2021 season to validate the results obtained in 2020.

Plant Growth and Leaf Spot Control of Peanut Plants Treated with Different Fungicide Programs

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One of the most spread disease in peanut crop is leaf spot, which can decrease plant growth and yield. To control this disease and reduce its severity, many fungicide programs have been developed and used in recent years. However, studies relating the effect of fungicides on the physiology and growth of peanut plants are still needed. Therefore, the aim of this study was to evaluate the effect of different fungicide programs on the control of leaf spot (caused by *Nothopassalora personata* and *Passalora arachidicola*) and plant physiology and growth in peanut. This experiment was conducted at the University of Georgia Attapulgus Research and Education Center. Treatments consisted of three cultivars, 1) Georgia-06G, 2) Georgia-18RU and 3) TifNV-High O/L and four fungicides programs, 1) Non-treated Control (NTC), 2) chlorothalonil applied five times (30, 45, 60, 90, and 120 days after planting [DAP]; RED), 3) chlorothalonil applied seven times (30, 45, 60, 75, 90, 105, and 120 DAP; CL), and 4) chlorothalonil applied three times (30, 45, and 120 DAP) plus Miravis applied two times (60 and 90 DAP; CLM). The experimental design was a randomized complete block with five replications. Measurements included leaf area index (LAI), disease severity and yield. Results showed lower severity of leaf spot in plots planted with TifNV-High O/L and in plots treated with CL and CLM. Therefore, LAI was greater in plots planted with the cultivar TifNV-High O/L and treated with CL and CLM. A negative correlation between leaf spot and LAI was observed, suggesting that greater leaf spot intensity corresponded to lower LAI. Plots treated with CL and planted with TifNV-High O/L yielded more compared to the other fungicides and cultivars. Overall, results demonstrated that the use of CL and TifNV-High O/L increased the control of leaf spot incidence without negatively affecting plant growth (LAI) and yield.

Thrips and Peanut Response to Imidacloprid and Fluopyram Applied At Planting

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Tobacco thrips (*Frankliniella fusca* Hinds) can reduce peanut (*Arachis hypogaea* L.) yield if not controlled in many instances in North Carolina and Virginia. Systemic insecticides are often applied in the seed furrow at planting to suppress tobacco thrips and protect peanut yield. Foliar sprays of acephate are often made regardless of the insecticide applied at planting. Imidacloprid plus fluopyram is registered for use in peanut but information in the peer-reviewed literature is limited relative to effectiveness in suppressing tobacco thrips and whether or not a foliar application of acephate is needed when this product is used. Peanut injury caused by tobacco thrips was lower when phorate or imidacloprid were applied alone compared with imidacloprid plus fluopyram in 16 trials conducted in North Carolina and Virginia from 2014 through 2020. However, all insecticides applied at planting protected peanut from injury caused by tobacco thrips well enough to prevent yield loss compared with non-treated peanut. While acephate decreased visible injury caused by tobacco thrips, yield was not affected by acephate regardless of the systemic insecticide applied at planting. Results from these trials indicate that that imidacloprid plus fluopyram offers adequate suppression of tobacco thrips to protect yield. Although acephate suppressed tobacco thrips, yield was not affected by acephate.

Evaluation of Fifteen Peanut Varieties under Dry Conditions on Summer 2019, in State of Morelos, Mexico.

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During summer 2019 in Cuauchichinola, State of Morelos, Mexico, 15 peanut lines and commercial varieties, were planted. It was a very dry rainy season, only 15 inches of precipitation were recorded. Main objective was to understand what was the best yielding peanut variety, growing during a very dry growth season. Peanut materials (bredlines and others) were planted on June 20, 2019, in rows of 80 cm coming apart. A randomized blocks design, and four replications were used. Pod number, pod weight per plot (2.16 m^2) and 100 pod weight were measured. Statistical analysis indicated that significative differences, among varieties, were found. Arbol (A18), Rio Balsas 93 and Cech, ranked in pod high yielding per plot, varying between 611 (2.8 t ha^{-1}), and 514 g $plot^{-1}$. The most low pod yield was recorded in Ixcatlan, (176 g), Rojo de Cuauchi (230 g) and Huazulqueño (243 g per $plot^{-1}$), respectively. These varieties are being planted by small farmers of States of Hidalgo and Morelos, in southern Mexico.

Pod yield was correlated with pod number per plot. Cech, and others lines, are being characterized, throughout phenotypic traits, for future official registration, at SNICS-SADER, a Federal Office, for this concern.

Evaluation of Alternatives to Chlorothalonil for Peanut Disease Control in Southeast Alabama

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Alternatives to chlorothalonil were evaluated for their efficacy in controlling early leaf spot (*Passalora arachidicola*), late leaf spot (*Novopassalora personatum*), rust (*Puccinia arachidis*), and white mold (*Athelia rolfsii*) in southeast Alabama at the Wiregrass Research and Extension Center (WGREC) in Headland, AL on 'Georgia-16HO' peanuts. Leaf spot intensity was evaluated using the Florida leaf spot 1-10 scoring system then converted to percent defoliation. Rust was evaluated using the ICRISAT 1-9 rating scale. White mold incidence was assessed immediately after plot inversion by counting the number of disease loci per row. Yields were reported at <10% moisture.

Leaf spot intensity was significantly lower for all fungicide programs than for the nontreated control, which suffered considerable premature defoliation. Among the fungicide programs, the full-season Elast treatment program and Elast+/Fontelis had greater defoliation than did the Oranil 6L only full-season standard. Lowest defoliation was observed with Elast+/Provost Silver. Rust severity was significantly lower for all treatment programs when compared to the nontreated control. Rust severity was highest with the CuproFix Ultra + Topsin program and the CuproFix Ultra full-season treatment. White mold incidence was significantly lower for all fungicide programs when compared to the nontreated control. Peanuts treated with Alto + Oranil+/Oranil+/Elast + Miravis had the lowest white mold incidence in this trial. Among the remaining treatment programs, white mold incidence was statistically similar when compared with the Oranil 6L only full-season standard. All treatment programs had significantly higher yields when compared to the nontreated control. Yield among all fungicide programs was statistically similar to that observed with the Oranil 6L only full-season standard.

Influence of Geographical Location and Time of Planting on Pest Densities and Yield of Peanut Varieties in Ghana

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Peanut (*Arachis hypogaea* L.) has received international attention as food and cash crop. The high oil and protein content in the peanut make it an important food and cash crop. However, in Ghana, potential yields of most peanut varieties are usually not attained on farmers' field due to damage caused by soil arthropod pests. Hence, the objective of this study was to determine the effect of variety × planting time × location on pest density and yield of peanuts in Ghana. A 3 × 3 × 2 factorial study laid in split-split plot design was used. Location (Nyankpala, Wa and Kumasi) was the main plot, time of planting (early may, mid-May, early June) as sub-plot and variety (Chinese and Sarinut 2) as the sub-sub-plot. The results showed that white grubs (*Lachnosterna serrata*), millipedes (*Aphistogoniulus corallipes*), wire worms (*Gonocephalum* spp.), termites (*Macrotermes* spp., *Microtermes* spp.), plant hoppers (*Empoasca* spp.) and aphids (*Aphis craccivora*) were the major pests of peanut in all 3 locations. Generally, pest numbers were highest at Nyankpala and lowest at Fumesua. Across locations, pest numbers were highest in June planting and lowest in May planting. Also, infestation in Chinese was higher than Sarinut 2. In terms of damage, Chinese planted at Fumesua recorded the highest damage, irrespective of the location. Pod damage decreased with delayed planting at Fumesua. In contrast, this variable decreased with delayed planting up to May and increased afterwards, at Nyankpala and Tanina. There were significant location × variety interactions for pod yield, with Chinese planted at Tanina recording the lowest yield while Sarinut 2 sown at Fumesua was highest. Irrespective of the location and variety, delayed planting of peanut resulted in decreased pod yield. In conclusion, early planting of improved varieties minimizes pest damage and increases pod yield, irrespective of geographical locations in Ghana.

Potential Use of RAMAN Spectroscopy for Trait Identification in Peanut (*Arachis hypogaea* L.)

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In the past, trait identification of peanut germplasm for breeding was performed by expensive, time and labor-intensive and in some cases destructive hand sampling techniques as well as field trials and hand selection. These constraints often lead to under-representative trait identification due to limited sampling and limited time, as well as the introduction of possible human errors. There is a significant need for time saving non-destructive and non-invasive methods to identify traits in peanut breeding lines. With the introduction of Raman spectroscopy (RS), these hurdles can be overcome. Studies show that this chemometric analysis can be used to evaluate levels of protein, starches, oils, and nutrients in peanuts. Preliminary data shows that RS can also be used to identify value added traits such as nematode, leaf spot and drought resistance, and has been used to identify NPK deficiencies. Trait identification data was collected on peanut by the Texas A&M AgriLife Research peanut breeding program located in Stephenville, TX. Raman spectra were collected with a hand-held Resolve Agilent spectrometer equipped with an 830-nm laser source. PLS_Toolbox (Eigenvector Research Inc.) was used for statistical analyses of the collected Raman spectra. Initial results are encouraging and demonstrates the potential for Raman spectroscopy to become a valuable tool for peanut research. These attributes will be presented and discussed in a poster seminar presentation.

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Photogrammetry Enables Indirect Selection and Increase Genetic Gains for Leaf Spot Tolerance in Peanut Breeding Program in Ghana.

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Early and late leaf spot diseases are part of the major destructive peanut diseases. Peanut genotypes that are tolerant or resistant to leaf spot diseases are important to increase peanut production. A comprehensive breeding approach along with accurate phenotyping and genotyping are needed to increase yield and crop tolerance to biotic and abiotic factors in order to guarantee sustainable food production and security. This work reports on the effectiveness of photogrammetry as a high-throughput phenotyping tool to increase precision in the assessment of peanut for leaf spot tolerance in a breeding program in Ghana. A replicated experiment arranged in a lattice design was conducted during the 2020 rainy season using a set of 60 genotypes as the training population and 192 genotypes as the validation population for the development of indirect selection models for leaf spot tolerance using red-green-blue (RGB) color space indices. Florida 1 to 10 visual rating scale where 1 indicate no disease (0% defoliation) and 10 indicate plants killed by leaf spot disease (100% defoliation) was used to assess early leaf spot (ELS) disease caused by *Cercospora arahidicola* and late leaf spot (LLS) disease caused by *Cercosporidium personatum.* Visual ratings were done at 70, 80, 85 and 95 days after planting (DAP). Samsung Galaxy NX300 RGB camera that captures 20.3 million effective pixels was used to take plot pictures at the same time with the visual disease evaluations. The indices derived from the RGB image were green area (GA), greener area (GGA), Hue and crop senescence index (CSI). ANOVA was performed on the raw data using R statistical package version 4.0.2. Adjusted means from the ANOVA were used for Multiple linear regression, Principal component analysis and Pearson correlation. The highest scores for ELS for the training population were seen at 85 DAP and ranged from 3 to 6. However, the highest scores for LLS for the training population was at 95 DAP and ranged from 3 to 7. In particular, green area (GA), greener area (GGA) and Hue exhibited negative significant associations ($p < 0.000$) with both ELS and LLS. Crop senescence index (CSI) on the other hand showed significant positive association ($p < 0.001$) with both ELS and LLS. The eleven important traits were grouped into two principal components and explained 73.7 % of the total variation. The principal component analysis shows that GA, GGA, Hue, Pods/plant and pod weight/plant are important key traits for the exploitation of genetic variability in the peanut breeding program in Ghana. Biplot of the genotype groupings from the PCA further indicates that geographical origin did not influence the principal components demonstrating it is not a measure of genetic diversity in this study. The RGB indices exhibited comparable or better broad sense heritability to the visual score indicating that they can be used in the breeding programs to increase genetic gain in selecting for leaf spot tolerance.

High Throughput Functional Traits to Screen Peanut Productivity and Adaptation in Senegal

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Groundnuts is the main source of income for agricultural households in Senegal, especially in the groundnut basin. Since the 1970s, this crop has experienced a yield decrease mainly due to climate change. In this context, varietal selection must deliver to farmers genotypes more adapted to climate change. Thus, in this study, our objective is to identify for peanut breeding programs high throughput functional traits for adaptation to climate change. Thus, a collection of 21 varieties with a 90-day cycle was tested in two environments with contrasted rainfall, i.e Nioro and Bambey. The experimental set-up was in completely randomized blocks with 4 replicates in each of the environments. Physiological measurements at different dates of the plant development cycle were performed with easy-to-handle equipment for measurement of NDVI, chlorophyll level, chlorophyll fluorescence and LAI. At Bambey, the test received rain for 73 days with a cumulative 475.8 mm. At Nioro, the test received rain for 85 days with a cumulative 739.3 mm.

In each of the sites, physiological traits correlated significantly with the yield components. NDVI, chlorophyll content, chlorophyll fluorescence and LAI would therefore be high throughput phenotypic traits that can be used to screen collections or breeding lines for peanut productivity and adaptation in Senegal and Sub-Saharan Africa.

Evaluating Sampling Methods for Two Rootworm Pests, *Diabrotica undecimpunctata* and *Diabrotica balteata*, and Determining Their Relative Abundance in Georgia Peanut Fields

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The Southern Corn Rootworm, *Diabrotica undecimpunctata*, is native to the US where it is a serious pest of peanut. The banded cucumber beetle, *D. balteata*, is native to the tropics, but it has expanded its range to include most of the US peanut production area. A recent increase in reports of rootworm injury to peanut in Georgia coincided with anecdotal accounts of large populations of *D. balteata*. This study examined the relative abundance of adult rootworms in commercial peanut fields in Georgia using sweep nets and two different plant volatile lures attached to yellow sticky traps. Banded cucumber beetle adults greatly outnumbered southern corn rootworm adults in sweep net collections and sticky traps at all locations on all sample dates in 2020. The implications of this result on rootworm management in peanut are unknown and require additional investigation. Traps baited with Spotted Cucumber Beetle lure had a higher overall catch rate of both species than traps baited with Banded Cucumber Beetle lure. Compared to the ratio of species abundance observed in sweep nets, Spotted Cucumber Beetle baited traps were biased towards *D. undecimpunctata*. The relative proportion of species collected on Banded Cucumber Beetle baited traps did not differ from that of sweep net samples.

Valuing Disease Resistance: A Comparison of the Florunner and GA16HO Cultivars

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The Florunner cultivar was released by the University of Florida in 1969 and became one of the most widely used runner-market type varieties for years; primarily known for producing high yields and excellent grades. However, more disease resistant cultivars eventually took over the runner-market. Fifty years after its initial release, a comparison of Florunner and Georgia-16HO was designed to come up with an estimate of the value of disease resistance with and without the use of pesticides to treat thrips. The study was conducted via a randomized complete block design with three treatments per cultivar (non-treated control, Thimet treated, and Admire Pro treated) and replicated six times. The study was conducted in 2019 and repeated in 2020. Disease ratings, yield and quality data were collected. The revenue was based on the loan rate and adjusted by grade. Treatment costs were also collected. A partial budget approach was used to determine the relative value of the disease resistant cultivar (Georgia 16HO) over Florunner by comparing the average adjusted revenue per acre. Average adjusted revenue is defined as revenue adjusted for yield, grade, seed and insecticide treatment costs. Results indicate the average difference in value of the Georgia 16HO was greater than Florunner by at least $540/acre in 2019 across all treatments and by at least $320/ac in 2020 across all treatments. It should be noted that disease pressure was higher in 2019. Disease resistance is even more valuable in a situation or environment where disease pressure is expected to be higher.

Simple Non-Destructive Method for Quantification of Aflatoxins in Individual Peanut (*Arachis* spp.) Seeds

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Two high-throughput purification procedures for quantification of aflatoxins in individual peanut seeds using UPLC have been developed. Aflatoxins were extracted from a pulverized sample, and after a single cleanup step on a minicolumn packed with Florisil or C_{18}-Al_2O_3 mixture, were determined by UPLC equipped with a C_{18} column and a fluorescence detector. A gradient mobile phase composed of H_2O, MeOH, and MeCN provided baseline separation of aflatoxins B_1, B_2, G_1, and G_2; recoveries of these toxins from peanuts spiked at 1 - 50 ng/g exceeded 80%. The methods have been used for the exploration of wild *Arachis* germplasm to identify accessions resistant to *Aspergillus* and to determine and characterize novel sources of genetic resistance to this fungus. Both methods are non-destructive since they use only half of the seed, and leave the other half containing the embryonic axis intact. Such a technique allows germination and growth of the peanut plant to full maturity from the same seeds used for the aflatoxin analysis.

Identifying Alternative Host(S) Of Groundnut Rosette Disease Virus Complex

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Groundnut crop losses due to Groundnut rosette disease (GRD) are endemic across Sub-Saharan Africa. The disease causes significant economic losses, jeopardizing food security and the livelihoods of groundnut farmers. To date, no alternative host plants have been identified that could act as a source of inoculum. subsequently, the epidemiology of the disease is poorly understood, creating gaps in disease management options. GRD is caused by an interaction of 3 agents; groundnut rosette assistor virus (GRAV), groundnut rosette virus (GRV) and the satellite RNA (satRNA) of GRV. The disease is transmitted persistently by the aphid, *Aphis craccivora* Koch.

In this study, we have surveyed 3 GRD hotspots and 1 major growing district in the different agro ecological zones of Uganda for GRD. In each zone, plants showing GRD symptoms and/or having colonies of *Aphis craccivora* were identified and samples were collected.

Using RT-PCR, we have tentatively identified two alternative hosts that have all the 3 GRD agents. Two additional plants tested positive for both GRAV and either satRNA or GRV, suggesting they could also be alternative hosts. The list could grow bigger as more analyses are ongoing. Vector transmission studies are in progress and will confirm if the alternative host can act as sources of inoculum for groundnut.

Genome-Wide Association Study on Peanut Water Deficit Stress Tolerance Using the U.S. Minicore to Develop Improvement for Breeding

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Global climate change has resulted in large variations in weather, exacerbating the drought situation around the world. This can result in decreased crop yield, which may lead to severe outcomes such as food crisis. Peanut is one of the most important crops in the world and has been widely planted in many semi-arid areas. Therefore, it is important to develop peanut varieties that are tolerant to water deficit stress. Genetic studies can assist by identifying specific genes or markers for selection. In this research, we included 104 minicore accessions. We extracted 125 DNA samples from peanut seeds harvested in 2017 and sent them for SNP chip analysis on the Affymetrix platform for genotyping. A total of 8,189 SNPs were included in this analysis. Data related to water deficit stress tolerance were collected from the field in TX, OK, and VA in 2017. We used STRUCTURE to perform the linkage disequilibrium analysis and estimate the population structure (Q matrix) with a putative number of populations. GWAS was performed first using SPAGeDi to estimate kinship (K matrix), then association mapping was performed using TASSEL using a mixed linear model (GLM+Q+K). We have identified 120 SNPs (P-value = 10^{-4}) and 558 SNPs (P-value = 10^{-3}) significantly associated with the phenotypic data. Of these, 71 SNPs are significantly associated with more than one trait (44 SNPs associated with 2 traits, 26 SNPs associated with 3 traits, and 1 SNP associated with 4 traits). Overall, 163 SNPs are considered the most reliable SNPs, significantly associated with traits over different locations, or associated with multiple traits, or both. We will validate these significant SNPs again by using phenotypic data collected in 2018 and 2019. These SNP markers are important for future use such as marker-assisted selection (MAS) in peanut breeding. The SNP data can be used for identifying marker trait associations (MTAs) including water deficit stress tolerance and other important traits.

Peanut Germplasm Resources and Genetic Vulnerability Considerations

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The USDA-ARS managed National Plant Germplasm System (NPGS) maintains and distributes peanut germplasm resources for research and educational purposes. The germplasm resources represent most of the peanut global genetic diversity and serve as a primary resource for domestic as well as global research community for peanut improvement. The germplasm resources provide desirable traits for peanut improvement and have been used to develop high yielding, climate resilient cultivars for domestic producers. The germplasm collection contains approximately 9,500 accessions of both cultivated and wild species, preserved as seeds in cold storage at the Plant Genetic Resources Conservation Unit, Griffin, GA. All germplasm is also backed up at the National Laboratory for Genetic Resources Preservation, Fort Collins, CO. Several active genetics, genomics and breeding programs exist at state universities, the USDA-ARS facilities in GA and OK and two private seed companies. Although the 2019 certified seed acreage included 21 cultivars developed by these programs for commercial seed production, only a few cultivars dominated in each of the peanut production regions. Further, the cultivars within a breeding program tend to have some common genetic background. Thus, the dominance of a narrow list of cultivars with related pedigrees may make the crop vulnerable to pests and pathogens. Currently, the vulnerabilities, threats and limitations facing peanut include i) evolving and emerging pathogens and pests, especially seed borne viruses and the peanut smut fungus, *Thecaphora frezii*; ii) lack of efficient diagnostic tools and resources for detection of these pathogens and pests; iii) insufficient knowledge of genetic diversity within the US peanut germplasm collection and commercial cultivars for evolving/emerging pathogens and pests leading to unknown degree of genetic vulnerability; iv) inconsistent international pest/pathogen monitoring systems; v) threat to *in situ* conservation of landraces and wild species due to global climate change and urbanization; vi) international treaty restrictions for germplasm access and exchange; and vii) reduced operational capacity for public breeding and plant genetic resource management.

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Effect of Mixing Elemental Sulfur with Demethylation Inhibitors (DMI) And Quinone Outside Inhibitors (Qoi) on the Management of Late Leaf Spot (*Nothopassalora Personta)* and Rust (*Puccinia Arachidis*) Of Peanut (*Arachis Hypogaea*)

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Peanut (*Arachis hypogaea)* has many foliar diseases that decrease pod yield. Some of the most devastating diseases are caused by fungal pathogens such as late leaf spot (LLS) caused by *Nothopassalora personta* and peanut rust caused by the fungus *Puccinia archidis.* Some demethylation inhibitor (DMI) and quinone outside inhibitor (QoI) fungicides have lost efficacy due to resistance development within these fungal populations. A recent study found that adding elemental sulfur to a DMI with poor efficacy significantly improved control of LLS in the field. The purpose of this study was to see if adding elemental sulfur to a QoI with poor leaf spot control would show the same effect, and to see if sulfur mixtures enhance DMI and QoI efficacies for rust. A field study was conducted in Tifton, Ga in 2020 with four replications of the following treatments: 1) nontreated control, 2) elemental sulfur, 3) Tebuzol 4) sulfur mixed with Tebuzol, 5) Abound and 6) sulfur mixed with Abound. Late leaf spot severity was assessed using the Florida 1-10 scale and rust severity was assessed using a modified ICRISAT 1-9 scale. Assessments were made weekly following the onset of disease. Results showed that adding sulfur to both fungicide classes significantly decreased LLS, but did not reduce rust.

Honeybee Foraging in a Mixed Crop Landscape

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Row crop production, largely corn and soybean grown for grain and silage, represents the dominant use of arable land in the United States and worldwide. There is a large body of literature on the risk, and consequences, to pollinators of pesticide use in these systems. Additionally, the contribution of row crops, self-pollinating plants traditionally considered not to feed pollinators, to honey bee colony nutrition is an important consideration. Cotton, corn, soybean, and peanut flower during months where alternate forage may be lacking in the environment. We used the honey bee waggle dance, which allows us to map where bees have foraged, and high-throughput sequencing and visual identification of returned pollen samples to determine when, and in what amount, bees prefer to forage in crop production fields. We also characterized insecticide exposure by quantifying residues in the pollen. Our two-year study took place in a largely agricultural landscape containing multiple crops. We will specifically address foraging in peanut across the growing season (April-October).

The Effects Plant Type and Seeding Density on Plant Growth and Pod Yield

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Peanut genotypes vary widely in their plant architecture, in this case meaning the width and height of their canopies. This study aimed to determine if two experimental runner market type genotypes with very small plant architecture (i.e. shorter main stem and lateral length) would produce increased pod yield (as compared to two runner types with large vines) when planted in greater density (6 seeds/row ft. vs. 12 seeds/row ft.) in 9 inch twin rows. Results showed that the seeding density resulted in different plant stands at harvest (7.6 plants/ft for the 12 seeds/row ft. vs. 4.4 plants/ft for the 6 seeds/row ft.; LSD=0.62 plants/row ft.). Genotypes differed in their final plant stand (LSD 0.33 plants/row ft.) with FloRun^{TM} '331' (7.0 plants/row ft) > TUFRunner^{TM} '297' (6.1 plants/row ft) > 12x23-4 (5.7 plants/row ft) = 12x23-1 (5.4 plants/row ft). In addition to the main effects, there was genotype x seeding density for final plant stand whereby there was no difference in final plant stand among the genotypes when seeding density was 6 seeds/row ft. but when planted at 12 seeds/row ft., each genotype had different final plant stand (LSD=0.47 with the smallest difference among means of 0.51 plants/row ft.). Plant height was greater in the 12 seeds/row ft. compared to 6 seeds/row ft. (16.9 inches vs. 15.2 inches). Genotypes differed in plant height with FloRun^{TM} '331' (19.4 inches) > TUFRunner^{TM} '297' (16.9 inchs) > 12x23-4 (14.1 inches) = 12x23-1 (13.8 inches). Pod yield was largely unaffected by seeding density or genotype with less than 186 pounds/acre pod yield difference on average between the 6 and 12 seeds/row ft. seeding densities. FloRun^{TM} '331' had higher yield (6017 lbs./A) than the other three genotypes (<5676 lbs./A) but there was no difference among the other three (LSD=212 lbs./A). It appears that genotypes with larger vines may not offer higher yield potential than those with much smaller vines. This would indicate that the harvest index of peanut, at least as measured by above-ground biomass is mailable. Even though we did not measure the biomass directly, the main stem length of the largest genotype was 5 inches greater than the two smallest genotypes which is likely to translate into significantly more above-ground biomass in FloRun^{TM} '331' and TUFRunner^{TM} '297'. Peanut genotypes with smaller canopies and competitive pod yield could be beneficial for mechanized agriculture since there is less vine mass to interfere with digging and picking processes. Smaller plant architecture might even speed the digging and harvest processes resulting in a net increase in efficiency of harvesting operations.

Anthem Flex Use in Peanut (*Arachis hypogaea*)

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Weed management is vital for the success of any crop. Producers must utilize herbicide programs to maintain a growing environment that lends itself to high yields. The use of Anthem Flex herbicide (pyroxasulfone + carfentrazone-ethyl) is an option available to peanut producers to control troublesome weeds. Trials were conducted to evaluate weed control in peanut with the use of Anthem Flex based herbicide programs.

Research was conducted across 6 years at the Oklahoma State University Caddo Research Station near Ft. Cobb, OK to evaluate the effectiveness of Anthem Flex when used as a PRE, early POST, or late POST in multiple herbicide programs. Peanuts were planted in 36-inch rows in May of each year. Visual injury and weed control were evaluated throughout the growing season. Visual injury was 10% or less across all years with applications of Anthem Flex PRE and POST. The exception was 2015 when peanut was planted late due to weather and injury occurred with all PRE treatments which included Valor and Anthem Flex. Control of Palmer amaranth (*Amaranthus palmeri*) was at least 99% 14 days after cracking with a preemergence treatment of Anthem Flex (2 fl oz/a) + Prowl H_2O (32 fl oz/A), except for 2020, when control was 94%. Texas Panicum (*Panicum texanum*) control was at least 88%, 14 days after cracking, with the same PRE application of Anthem Flex + Prowl H_2O, with the exception of 2017, when control was 84%. Palmer amaranth control was 87%, 14 days after treatment (DAT), with an early POST application of Anthem Flex (3 fl oz/A) + Gramoxone (16 fl oz/A) in 2019, but in 2020, an early POST application of Anthem Flex (3 fl oz/A) + Gramoxone (8 fl oz/A) + Storm (16 fl oz/A) only provided 55% control of Palmer amaranth 14 DAT. This low control was likely due to the size (2-14 inches) and population (2-10 per foot). Ivyleaf morningglory (Ipomoea hederacea) control was at least 99%, 14 DAT, with a late POST application of Anthem Flex (3 fl oz/A) + Cobra (12.5 fl oz/A) + 2,4-DB (18-20 fl oz/A). Yellow nutsedge control never exceeded 34%, 14 DAT, with the same treatment. These trials highlighted the effectiveness of Anthem Flex herbicide for use in peanut for specific weed species. They also proved the need for the use of an effective preemergence program to allow the crop to get a head start on troublesome weeds. Research will need to be continued to better understand the optimal timing of applications for Anthem Flex herbicide in peanut.

A Novel Source of Resistance to Peanut Stem Rot from Wild-derived Allotetraploid ValSten1 Identified by Greenhouse and Field Evaluation Methods

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Peanut stem rot (white mold), caused by the fungus *Athelia rolfsii* (*Sclerotium rolfsii*), is one of the most severe soil borne pathogens in US peanut production. Cultivated peanut has limited sources of resistance. Therefore, it is essential to seek stem rot resistance in wild relatives since they can be a potential resistance resource for peanut. Greenhouse bioassays and field evaluations were conducted to characterize resistance among wild-derived allotetraploid peanuts. In a greenhouse bioassay, twelve allotetraploids and two cultivated cultivars, resistant controls Georgia-12Y (GA-12Y), and susceptible control Georgia-09B (GA-09B), were evaluated three times in 2020. Disease was introduced by *A. rolfsii* mycelial plugs (0.7-cm-diameter) on sixty-day-old stem cuttings. The resulting lesion lengths were measured at 3, 5, 7, and 9 days after inoculation (DAI) and the area under the disease progress curve (AUDPC) was calculated. For 2019 and 2020 field evaluations, seven allotetraploids were evaluated with the same controls, GA-12Y, and GA-09B. Testing genotypes were transplanted under the canopy of GA-12Y as interspersed individuals with a similar microclimate. Each plant was inoculated midseason as described above, and the disease was rated during midseason and at harvest. Four allotetraploids, BatSten1 (*A. batizocoi* K9484 x *A. stenosperma* V10309)^{4x}, GregSten1 (*A. gregoryi* V6389 x *A. stenosperma* V10309)^{4x}, ValSten1 (*A. valida* PI 468154 x *A. stenosperma* V10309)^{4x}, and IpaDur3 (*A. ipaensis* KG30076 x *A. duranensis* 30060)^{4x} showed similar disease levels as the resistant control, GA-12Y, and significantly smaller lesions than the susceptible control, GA-09B. ValSten1 consistently has a similar disease level as GA-12Y and statistically lower disease rating than GA-09B. In conclusion, Valsten1 provides a new source of resistance for peanut stem rot breeding.

Replanting of Gaps in Peanut Rows.

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Peanut (*Arachis hypogaea* L.) producers in Georgia every year are faced with whether seedling emergence is adequate to produce optimal yields. Producers may replant fields when unnecessary. An experiment was conducted to determine the most optimum method of replanting stands with varying lengths of gaps in the row to maximize yield and grade (total sound mature kernels) of peanut. Tomato spotted wilt virus (*Tospovirus*; TSWV) incidence was also assessed. The trial took place in Tifton, Georgia in 2017, 2018, and 2019. Plots were planted, then thinned to 6.6 plants/m except for one standard 13.1 plants/m check plot. Plants were removed from random sections of the initial row to establish 61, 122, or 183 cm of consecutive row length where no plants would grow. Each length was pulled either once or twice per 10.4 m row, as separate treatments. All gap scenarios were factorially replicated with replant treatments: 1) none (“no-replant”), 2) replant only in the length of gaps (“gap-only”), and 3) replant the entire length of the row (“full-row”). All replant treatments were made at a rate of 13.1 seed/m approximately 19 days after the initial planting and 8 cm to the side of the initial row. Pod yield for the “full-row” replant was greater than “no-replant” (16 to 33%) and “gap-only” (14 to 17%) as gap length increased. There was no difference in grade between “no-replant” (73%) and “gap-only” (73%), but “full-row” replant (75%) was greater. The “full-row” replant treatment (26%) had less TSWV compared to “no-replant” (35%) and “gap-only” (33%). The “full-row” supplemental replanting was beneficial in increasing yield and grade while decreasing TSWV incidence. The “full-row” replant could be a viable alternative planting method to maximize outputs and minimize risks when conditions allow.

Comparison of Peanut White Mold Fungicide Programs in Bulloch County, Georgia

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White mold is a critical problem for peanut producers in Bulloch County and must be addressed with additional on-farm research to establish “best management” practices. The producers’ current best line of defense to combat the problem involves selection of more-resistant varieties and judicious use of fungicides. Further research is needed to provide recommendations to growers with regard to use of newer fungicides and application strategies for the management of white mold. In this demonstration conducted in 2020, the effectiveness of eight different fungicide programs was evaluated. The experimental design was a complete block design with three replications. Data collected throughout this study included severity of leaf spot and incidence of white mold. Means were separated using Fisher’s protected LSD. From this research, the effectiveness of the fungicide treatments in reducing the incidence of white mold was evaluated as part of a disease management program to improve yield and quality. This data will play an important role in recommendations for future use of peanut fungicide selection to reduce white mold in Bulloch County and the Southeast.

On-Farm Evaluation of Nozzle Types for Peanut Pest Management Using Commercial Sprayers

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More growers are adopting auxin-resistant technologies each year and adding auxin resistant crops to their production systems. In Georgia, growers who plant auxin-resistant cotton are required to utilize nozzles that produce coarser droplets when spraying auxin herbicides to minimize potential off-target movement of pesticides. Consequently, these nozzles are also being used in peanuts (an important rotational crop with cotton) since changing nozzles between crops is uncommon for growers. However, larger droplets can result in reduced spray coverage leading to less effective pest control. Therefore, seven on-farm trials were conducted in commercial peanut fields using commercial sprayers from 2018 to 2020 across four different locations in Georgia to compare the spray performance of air-induction (AI) nozzles that produce very coarse to ultra-coarse droplets with non-AI (conventional flat fan) nozzles that produce medium to coarse droplets for pest management in peanuts. For each trial, test treatments were implemented in replicated strips where each strip represented a nozzle type. For nozzle comparison, XR and XRC represented non-AI nozzles while TADF, TDXL, TTI, and TTI60 represented the commonly used AI nozzles in these trials. Spray deposition data for each nozzle along with disease ratings, weed and insect counts were collected in all on-farm trials. Peanut yield was collected at harvest. Results indicated that the AI nozzles produced larger droplets than the non-AI nozzles in all nozzle tests; however, spray coverage varied among the nozzle types. Nozzle type did not influence pest (weed, disease and insect) control, or peanut yield in any of the on-farm trials, which suggested that peanut growers can utilize these coarser droplet nozzles for pest management without any noticeable reduction in pest control or peanut yield. Future research on nozzle evaluation needs to investigate the influence of droplet size, carrier volume, and pressure on coverage and canopy penetration.

Using CRISPR/Cas9 in Hairy Roots System to Explore the Gene Functions during Peanut Nodulation

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With the available allotetraploid peanut genomes, further functional genomics studies of the genes in peanut are very critical for peanut crop improvement. As an important legume crop, peanut plant forms root nodules to fix nitrogen through a symbiotic relationship with rhizobia. However, the nitrogen fixation efficiency in peanut is relatively low comparing with many other legume crops. In addition, rhizobia infect the peanut plants via an intercellular crack entry, which is a very different invasion path from the well-studied root hair invasion path as showing in model legume species and many other legume crops. Whether there is any connection between the crack entry or non-root hair invasion in peanut and low nitrogen fixation efficiency remains as a big question. Understanding the non-root hair rhizobial invasion process in peanut will not only reveal novel molecular mechanisms of an antecedent invasion process in legume symbiosis, but also will provide knowledge to enhance crop production while to reduce fertilizer input and promote sustainable agriculture.

CRISPR/Cas9 system is emerged as a robust tool for gene functional study and crop improvement, which haven’t been extensively utilized in peanut yet. We have established a system to transfer the CRISPR-Cas9 constructs targeting genes involved in peanut symbiosis and nodulation to peanut hairy roots for gene function validation. As an example, we have applied the CRISPR/Cas9 in peanut hairy root transformation system to explore the function of Nod factor receptors (*NFR*) genes, which play an important role in initiating the rhizobia symbiosis in model legume species. Through gene sequence retrieval, qRT-PCR, making CRISPR construct, hairy root transformation, phenotypical evaluation of transformants, and target gene sequencing of transformants, we found that targeted genes were successfully edited by the CRISPR system though chimeric events existed. The mutants with editing in the two *AhNFR5* genes showed non-nodulating phenotype, thus validated the function of *AhNFR5* genes in nodule formation in peanut. The results demonstrated the efficacy of the genome editing tool established for targeted mutation in allotetraploid peanut, which can be used in peanut hairy root transformation system for peanut functional genomic studies, specifically on genes functioning in roots.

Construction Pan-genome Graph for Peanut species

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For roughly three decades, bioinformatics has operated under a single-reference genomic paradigm. This approach was appropriate for individuals that are closely related to that single reference. As individuals diverge at the sequence level, fewer and fewer sequencing reads align correctly or at all to this reference, severely limiting modern genetic methods. In plant breeding, divergent material is often a major source of novel traits. Such exotic material can even belong to other genera. Indeed, the usage of exotic material may have been curtailed within the last few decades *not* because its agronomic value has lessened but because such germplasm confounds the ability to develop markers and understand their segregation patterns within a single-reference genomic paradigm.

Our recent work with peanut illustrates this point.

Biological sequence alignment seeks to create a data object that pairs every base in two sequences that were the same base in a common ancestor sequence. Chromosome-scale sequence alignments have a comparable goal, but this goal is often complicated by structural rearrangements and duplications. Duplications create ambiguous alignments because a base in one sequence should be matched to two bases in the other. Linear alignment methods must choose one match over another, and they do this based on gross collinearity with the surrounding sequence. In the final alignment, this ambiguity is lost.

Emerging graph data objects can represent these relationships without having to “choose” one representational over another. In this way, these graphs allow all ancestor relationships to be presented and all reads from any individual in the graph to be mapped entirely. While conceptually useful, such a representation is often difficult to adapt to genetic methods using meiotic recombination to associate subsequences in the genome with phenotypes of interest. Within a trait-associated locus, the evolutionary relationship between repeat elements that have expanded to hundreds of copies is fairly irrelevant, but the presence of such a repeat in a gene might be critical. By carrying such evolutionary relationships along in the graph structure, many current approaches are operational intractable and difficult to interpret genetically.

We feel the central utility of a graph is not that it elegantly reflects and compresses all structural variability but that it can support 100% full-length short-read alignments (ignoring contamination and chimeras). This is opposed to a linear reference, which can often support >90% read alignment but only by splitting reads. Such splits are difficult to interpret and often lead to false variation calls. Moreover, a single reference inevitably contains single-copy regions that have duplicated or triplicated in an unrelated sample. Short-read coverage of these regions is often very difficult to threshold given the general variability of true single-copy coverages. Such scenarios conspire to generate more false variation.

With this is mind, our goals were: 1) Find an optimum between breaking a chromosome-scale alignment into sub-alignments at positions of major structural change, 2) Retain positional stringency within those sub-alignments, 3) Retain coordinates of the underlying sequences, 4)

Maximize high-quality short-read mapping, 5) Visualize results relative to original sequence coordinates and multi-chromosome alignments. To achieve these goals, we first used a positional homology method for large-scale alignment that allows for rearrangement. These alignments are then hierarchically sorted based on underlying sequences in the alignment: sequences that are either community standards and/or have the highest quality can be prioritized by the user. Graph data objects are then generated from these alignments. In this way, we are able to account for effectively all structural variation when aligning reads, while still organizing the result in a manner that is applicable to further genetic interrogation.

Epigenetic Gene Expression Regulation of NSP2, a GRAS Family Transcriptional Factor Controlling Peanut Nodulation

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Cultivated peanut (*Arachis hypogaea L.*) is an allotetraploid species (2n = 4x = 40, AABB) derived from two wild diploid ancestors *A. duranensis* (AA genome, 2n = 2x = 20) and A. *ipaensis* (BB genome, 2n = 2x = 20). As a member of the legume family, peanut has the capacity of nodule formation to perform biological nitrogen fixation through a symbiotic association with rhizobia. Through a map-based cloning approach, we have identified that *Nodulation Signaling Pathway 2 (AhNSP2-A08* or N_a and *AhNSP2-B07* or N_b) encodes a GRAS family transcriptional factor controlling peanut nodulation. Interestingly, we identified that only the N_b allele can express in the $n_a n_a N_b n_b$ Nod+ plant and only the n_b expressed in the $n_a n_a N_b n_b$ Nod- plant. The results of backcross indicated that the $n_a n_a N_b n_b$ plant derived from the combination with $n_a N_b$ from female gametes and $n_a n_b$ from male gametes appeared Nod- phenotype. The $n_a n_a N_b n_b$ plant derived from the combination with $n_a n_b$ from female gametes and $n_a N_b$ from male gametes exhibited Nod+ phenotype. Therefore, we hypothesize that the non-Mendelian inheritance pattern of N_b is under epigenetic control, where DNA methylation alters parental-origin alleles expression. Allele-specific expression of *AhNSP2-B07* in female gametes is suppressed by maternal imprinting. To test the hypothesis, we implemented bisulfite PCR and sequencing to identify the differentially methylated sites between female and male gametes. Specifically, the whole gene sequences including upstream 2000 bp of CDS as potential promoter and the full length CDS (1551bp) of *AhNSP2-B07* were amplified from bisulfite converted ovary and pollen DNA samples from heterozygote plants. The sequencing comparison between the male and female gametes will reveal the epigenetic control of the *AhNSP2-B07* gene expression during peanut nodulation. The results will illustrate the epigenetic mechanism of peanut nodulation, which will provide fundamental knowledge of gene expression regulation in tetraploid peanut with two closely related sub-genomes.

Comparison of Standard and Newly Registered Peanut Fungicides against *Athelia rolfsii* Through a Laboratory Bioassay using Detached Plant Tissues

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Stem rot of peanut, caused by *Athelia rolfsii*, is one of the most important fungal diseases impacting peanut production worldwide. Foliar applied fungicides can be used to manage the disease, and several new fungicide products have been labeled for stem rot control in peanuts over the past several years. The objective of this study was to compare the fungicidal, residual, and potential systemic activity of standard and new stem rot fungicides using a laboratory bioassay of detached plant tissues inoculated with *A. rolfsii*. Peanut plants grown in the field were treated with eight different fungicides approximately 90 days after planting. Plant tissues were sampled weekly for five weeks following fungicide treatment so that the fungicidal activity of the different fungicides could be assessed at 1, 2, 3, 4, and 5 weeks after application. For the laboratory bioassay, peanut plants were separated into the second newest fully mature leaf present at the time of fungicide application, the newest fully mature leaf present at the time of sample collection, upper stem, and crown. Each tissue type was inoculated with *A. rolfsii* and then incubated at 30°C. Lesion length was measured two days after inoculation, and percent inhibition of fungal growth by each fungicide relative to the control was calculated. Differences in fungal inhibition were compared among fungicides, plant tissues, and over time. All fungicides provided the greatest inhibition of *A. rolfsii* on the leaf tissues that were present at the time of fungicide application, followed by the newly grown leaf and upper stem. Little inhibition of fungal growth occurred on the crown. Inhibition of *A. rolfsii* decreased at a similar rate over time across all fungicides tested. Among the fungicides evaluated, succinate dehydrogenase inhibitors provided less basipetal protection of the upper stems than quinone outside inhibitor or demethylation inhibitor fungicides. The properties of different fungicides characterized in this study, which included several newly registered products, are useful in developing fungicide application recommendations that maximize fungicide efficacy for control of both foliar and soilborne peanut diseases.

Effects of In-Furrow Fertilizer on Peanut Germination

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In-furrow applications of inoculants and select pesticides have grown in importance in peanut production in Georgia over the last decade. With the ease of application, industry has also begun to recommend in-furrow fertilizers to help with emergence and yield. Evaluations of Riser 7-17-3 (Loveland Products) applied in-furrow on emergence of peanut seed were conducted in a bare ground greenhouse in Tifton, Georgia in 2021. The soil type used in the greenhouse was a Tifton loamy sand. ~~Plot sizes were .3048m wide by .6096m in length.~~ 'Georgia-07W' ~~seed~~ was seeded 5.1 cm deep at a rate of 19.7 ~~6~~ seed/m in plots 0.6 m long with a row spacing of 0.3 m between plots. ~~per meter.~~ Fertilizer treatments consisted of 4.7 L/Ha~~0.5 g/A~~, 9.3 L/Ha~~1 g/A~~, 18.7 L/Ha~~2 g/A~~, and 28.0 L/Ha~~3 g/A~~ with a total carrier volume of 65.4 L/Ha~~7g/A~~. A non-treated check was also tested. Treatments in each of the two trials were arranged in a randomized complete block design with 8 replications. Treatment response was evaluated based on stand counts over a 14-day period. Peanut seed emerged 1 to 4 days quicker and at a higher rate until 8 days after planting in the untreated check plots than plots treated with the fertilizer in-furrow at all rates. Final emergence at 14 days after planting was significantly greater for the untreated check compared 18.7~~2~~-L and 28.0~~3~~-L ~~gallon~~ rates. Overall, ~~I~~in-furrow fertilizer delayed and/or reduced emergence in this bare ground greenhouse trial. Larger scale, replicated field trials should be conducted at several locations in the future to validate these findings.

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Using Remote Sensing to Predict Peanut Pod Maturity

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The standard method of measuring peanut pod maturity is removing the exocarp and sorting the pods based on mesocarp color onto a maturity profile board. Growing Degree Days (GDD) are accurate in predicting digging dates. However, the relationship of GDD with peanut pod color progression over time is unclear. Additionally, late-season daily temperatures impacting peanut maturity may be different at latitudes further north than the Lower Coastal Plain, where the peanut profile board was developed. There has also been no established method of estimating peanut pod maturity through remotely sensed methods that could predict peanut maturity. Therefore, these studies' overall objectives are 1) evaluate peanut pod color progression using the maturity profile board and GDD models; 2) evaluate the relationship between peanut canopy reflectance and pod maturity. Remote sensing imagery was collected before each digging timing. It is expected harvest timing prediction tools may need to be adjusted for climate and cultivar differences. The ability to assess whole field maturity using remote sensing may optimize harvest timing for improving seed quality and yield.

Impact of Adoption of Improved Varieties on Household Share of Peanut Income in Northern Ghana

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Peanut cultivation is one of the farming activities with the potential to reducing rural poverty among small holder farmers. A current survey show majority of farmers still use their local varieties in peanut cultivation resulting in reduced yields and low financial returns. There has been very little information on the adoption of improved varieties and its impact on household income in Ghana. This paper therefore is to measure the adoption of improved varieties of peanut and the impact on household share of peanut income. Using a survey data of 108 farm households in the Upper West, Savanna and Norther regions in 2020, an endogenous treatment effect model (ETEM) was used to model the impact of adoption of improved varieties on household share of peanut income. The model allows for correlation structure between non-observables affecting the household adoption of improved varieties and those affecting the household share of peanut income. The model allows for the correction of sample bias. The study revealed a 23% adoption rate of improved varieties. Among the adopters, a 52% adoption rate for improved varieties was observed among households participating in the peanut innovation lab project. Household average income from peanut production was found to GHS 2,726.00 ($478.25). The study found that, the average treatment effect of the treated is about GHS 2,175.85 ($381.60). The implication is that, adopters of improved peanut varieties had significant positive increases on household share of peanut income by GHS 2,175.85($381.60) additional income on the average. The use of improved varieties by household had significant impact on household share of peanut income. Hence, extension should be geared towards the need for improved variety use by farm households in the peanut production in Ghana. This can effectively improve the general farm household income and potentially reduce poverty.

Are Calcite Dissolving Bacteria a new player in the soil calcium cycle?

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Microbial communities play critical roles in mobilizing soil nutrition and, consequentially, shaping plant growth. Soluble calcium in the pegging zone is essential for peanut yield. Calcium starvation may lead to seed abortion and increased incidence of disease, such as pod rot. Currently, gypsum or lime are often used to supplement calcium in the pegging zone. Calcite dissolving bacteria isolated from lime mine or animal wastes can dissolve insoluble calcite into calcium. Here, we report the isolation and characterization of calcite dissolving bacteria from a peanut field in Tifton, Georgia. We identified 65 CDB isolates, representing 17 unique strains belonging to 10 different genera. Six CDB strains increased soluble calcium levels ranging from 11% to 91% when applied to soil. Some of the CDB strains when coated on seeds promoted germination rate. In a survey of CDB in soils with different crop histories, we found that CDB abundancy was negatively associated with a soluble calcium level. In summary, we conclude that CDB has the capacity to influence calcium availability in soil, and the abundance of CDB in a bacterial community may respond to calcium levels.

Physiological Responses of Peanut Varieties to Mid Season Drought Stress

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Peanut is an economic cash crop mainly planted in arid and semi-arid regions where the drought causes around 20% loss of peanut production every year. Researches suggested that crops have various physiological mechanisms against drought stress, such as reduction of photosynthetic rate, closure of stomatal, amelioration of water use efficiency (WUE), and differences in the partitioning of dry matter to pods. There are few field studies about which physiological characteristics are responsible to drought tolerant traits in the Southeast United States due to the fact that severe rain events can happen during the season. To study the physiological effects of drought stress on peanuts, a 2-year experiment carried out in rain-out shelters in which planted different peanut varieties with different drought resistant performances. Plants were grown under irrigated conditions until 60 days after plant (DAP), moment at which the drought treatment started and lasted until 100 DAP, later re-irrigated until harvested. Photosynthetic rate, leaf relative water content, and specific leaf area were measured 4 times at different development stages in 2019 but measured 7 times in 2020. After harvest, leaf area, pod yield, pod number, and HI were collected. 13C and 15N isotope discrimination and N content measured for pods and aboveground biomass. Different varieties have significant differences in photosynthetic rate, pod yield and carbon isotope discrimination. In order to increase and stabilize peanut yield under drought conditions, integrated application of physiology-genetic methods is needed to be further explored.

Allele Specific Expression of a Gene Encoding a GRAS Transcription Factor in Controlling Peanut Nodulation

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Legumes are well known for establishing a symbiotic relationship with rhizobia to fix nitrogen from the atmosphere. Multiple genes are involved in symbiosis. The nodulation signaling pathway 2 gene (NSP2), encoding a GRAS transcription factor, plays a critical role in this process.

Through map-based cloning, we identified a NSP2 gene on the peanut chromosome 17.exhibiting a non-Mendelian segregation ratio in the field. The distorted ratio is mainly because that the plants with a heterozygous genotype at the chromosome 17 NSP2 locus were either nodulating or non-nodulating. By genotyping the expressed alleles of the heterozygous plants, we found that only one allele was expressed in the roots of the heterozygous plants. When the recessive allele expressed in heterozygous plant roots, the plants do not produce nodule, while when the dominant allele expressed in the heterozygous plant roots,the plant produce nodule normally. However, the expressed allele in the heterozygous plant leaves didn’t correlated with the phenotype. The results of this study provided the genetic basis and unique regulation of a key gene involved in peanut nodulation, which can be potentially used for nitrogen fixation improvement in peanut.

Peanut Cultivar Response to Residual Soil Test Potassium Amounts in North Mississippi

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The average U.S. peanut (*Arachis hypogaea* L.) yield has increased by approximately 25% with the adoption of Georgia-06G. Since this adoption, many new runner cultivars have been released with similar yield potential and possibly greater soil nutrient requirements to achieve high yields. The objective of this study was to evaluate the growth and yield response of recently released peanut cultivars to soil test potassium (STK) amounts. Cultivars Georgia-06G, Georgia-16HO, Georgia-18RU, FloRun^{TM} '331', and AU-NPL-17 were planted across Mississippi State Soil Test Potassium ranges of low, medium, and high based on a soil cation exchange capacity (CEC) ≥ 14 . A positive pod yield response occurred in both site-years when average STK increased from 143 kg K ha^{-1} to 187 kg K ha$^{-1.}$ No additional yield was gained when STK amounts were greater than 187 kg K ha^{-1}. These results demonstrate the need to adjust peanut soil potassium sufficiency levels for CEC. The positive yield response to STK was similar among all peanut cultivars indicating that soil potassium management does not need to be altered for specific runner cultivars. Further evaluation of peanut soil test K sufficiency levels is needed for soils with a more moderate CEC range.