THE PEANUT RESEARCH FOUNDATION

Annual Report
2022

Harnessing Peanut's Potential through Investment & Innovation

peanutresearchfoundation.org

A Message From Our Chair

The Peanut Research Foundation exists to promote research to help keep the U.S. peanut industry competitive. Toward this end, this past year the board evaluated 25 competitive proposals and funded 15 projects totaling more than $730,000 of industry dollars. The scientists and technologies represented in this research are outstanding.

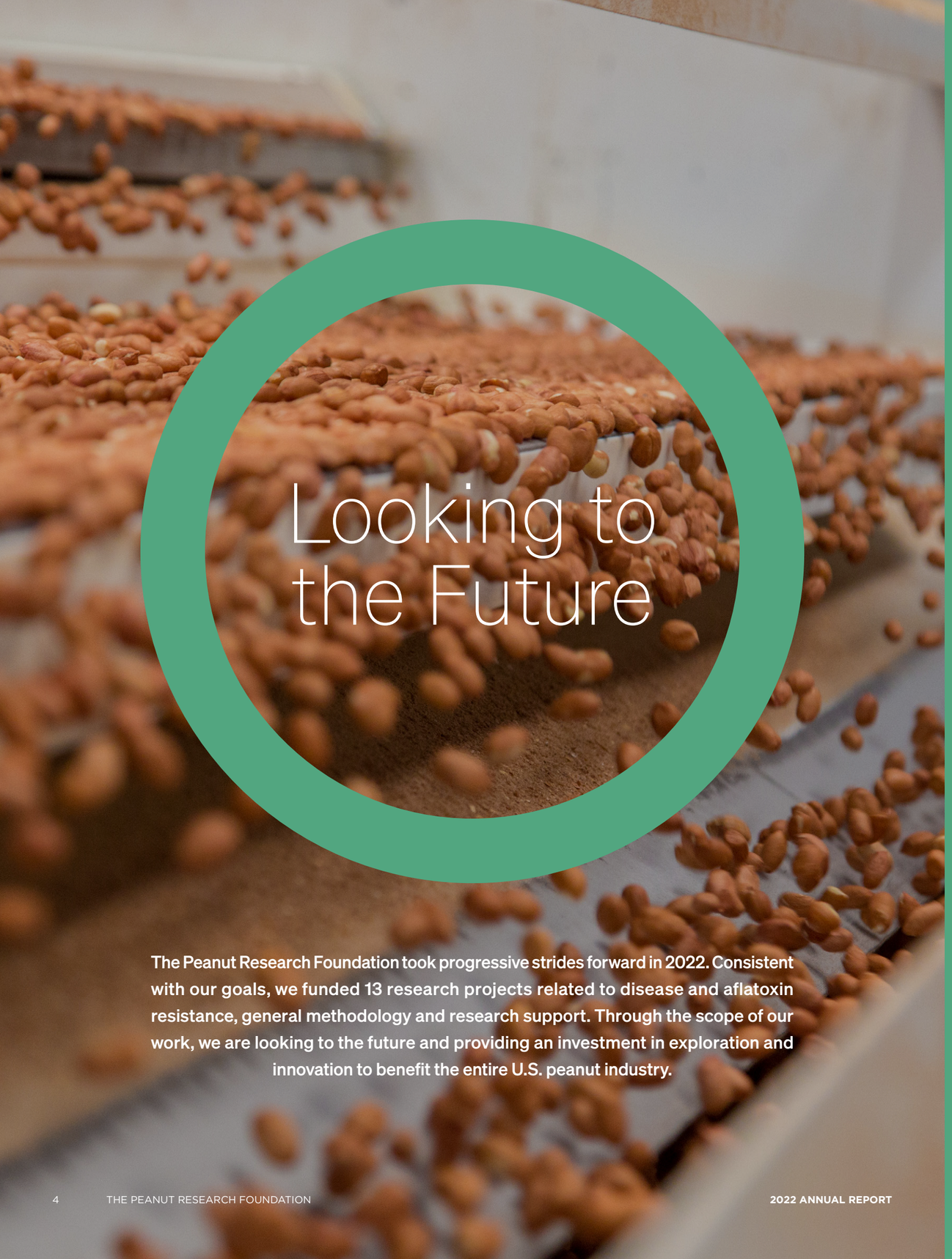
Looking ahead, the board and staff are charged with understanding industry feedback to reimagine the foundation and future research opportunities. Dr. Steve Brown, our executive director, presented a timeline at the June 2023 meeting to collect this feedback, synthesize the information and present to our stakeholders this vision for the future. Steve and the board will be interacting with all segments of the industry and the research community to accomplish this goal, but please do not hesitate to send Steve or a board member your ideas at any time. It is our goal to fund the very best research possible with precious industry funds.

I am grateful to serve as chair of the foundation and work with an engaged, smart and passionate board that represents all segments of the industry. We are operating in an incredibly competitive global market. Without the best new seed varieties possible, the U.S. peanut industry cannot hope to remain global leaders. I think the research we have funded here helps provide our breeders, seed producers, growers, shellers and manufacturers with the best varieties, technologies and knowledge possible to maintain this position.

Thank you to our donors, researchers and stakeholders. Let's all work together to continue future research initiatives that help make U.S. peanuts the best a hungry world can purchase.

Jack Davis
Director of technical services, JLA International

Chair, 2022-2023, The Peanut Research Foundation Board of Directors



Looking to the Future

The Peanut Research Foundation took progressive strides forward in 2022. Consistent with our goals, we funded 13 research projects related to disease and aflatoxin resistance, general methodology and research support. Through the scope of our work, we are looking to the future and providing an investment in exploration and innovation to benefit the entire U.S. peanut industry.

HIGHLIGHTS FOR 2022 INCLUDE

01

We successfully incorporated strong leaf spot resistance from a wild species into three cultivars, setting the stage to save growers significant production costs while greatly improving the peanut industry's sustainability story.

02

We identified a marker for resistance to the soil disease Sclerotinia, which could finally give growers hope for relief from the problematic fungus.

03

We identified markers which appear to impact final aflatoxin levels and we made significant progress showing the variation in the genome's naturally occurring strains of aflatoxin-producing Aspergilus flavus, offering great promise for finally addressing this long-standing problem.

04

We are building a germplasm population that contains wild species genes in a form readily usable by breeders which could lead to further success in attaining drought tolerance, disease resistance and other desirable traits.

05

We are improving the ability to utilize complex data sets with continued investments in PeanutBase, offering search tools commonly used by genome scientists and breeders now available from a single resource.

RESEARCH SNAPSHOT

Disease Resistance

Developing multi-disease resistant runners for the southeast

Dr. Nino Brown, University of Georgia

Of the many diseases that affect cultivated peanut, late leaf spot, tomato spotted wilt virus (TSWV), and white mold (WHM) present the most economically damaging challenges to peanut production in the Southeast. The overarching objective of Dr. Nino Brown's long-term research project is to pursue genetic improvement through traditional breeding activities and map disease resistance loci in elite populations and wild species introgression lines.

In 2022, 56 F_4 progeny rows descended from TxAG-6 were grown in a plant selection nursery without fungicides. Fifty-eight individual plants were selected based on agronomic performance and late leaf spot resistance. Further selection will be made based on shelling characteristics. The F_5 progeny rows will be grown in 2023 to increase seed supply to begin replicated yield testing in sprayed and unsprayed yield trials. Once a highly resistant line with acceptable agronomic performance is identified, the line will be used to develop a mapping population. The loci conferring late leaf spot-resistance in TxAg-6 have never been identified. It is possible that this highly unique and resistant germplasm line could be a novel source of late leaf spot -resistance alleles.

Resistance to TSWV is currently being introgressed from FNC 94022 into elite pedigrees. Three-way crosses and backcrosses were made in winter 2020/2021, and F_2 populations grown in an early-planted, space-planted nursery in 2022 to maximize TSWV incidence. Resistance to the disease was apparent and quite robust in these families (***Figure 1***). Hundreds of individual plants were selected from these families and will be selected further based on shelling characteristics. The F_3 progenies will be grown in an early, space-planted nursery again in 2023 to maximize TSWV pressure and to continue selecting resistant and high-performing individuals.

Currently, Georgia-12Y is acknowledged as one of the most resistant cultivars to WHM. A recombinant inbred line (RIL) population is being developed to map WHM-resistance loci with the goal of identifying diagnostic DNA markers. Testing for WHM resistance requires a combination of high levels of replication, precise field inoculation, and a strong and uniform infestation of the disease in a test field. Thus, phenotyping for resistance cannot be done on individual plants with sufficiently high levels of precision for quantitative trait loci mapping. Thus, RILGWA populations are being developed so that genetically uniform breeding lines can be replicated for the highly accurate data needed for genetic mapping.

FIGURE 1
The result of a three-way cross between NC 94022 and elite runner breeding lines, C20019-16 (left) is pictured with a popular check cultivar (right) in 2022 early-planted, space-planted F_2 nursery plots.

Research Snapshot

Wild species introgressions show promise for improved traits in Virginia-type breeding programs

Dr. Ryan Andres, North Carolina State University

In this research by Dr. Ryan Andres, breeding lines from Arachis diogoi germplasm were tested for introgressions from the wild species. While none were found, it's important to note these lines continue to show strong resistance to leaf spot under replicated field trials. However, the lack of obvious genomic regions to target with molecular markers implies their improved resistance will be more difficult to identify and deploy. In line with the original objectives of this proposal, 11 three-way hybrids from these lines have been genetically confirmed and progeny from them are advancing through the traditional North Carolina State University cultivar development program. A genome-wide association study is currently underway to better identify underlying genetic regions contributing to leaf spot resistance in the parents.

SPT 10-12 has been identified as the only line in our program that carries the three major leaf spot resistance introgressions from A. *cardenasii* on chromosomes 02, 08 and 13. In addition, this line is high oleic; carries a fourth, previously unknown introgression at the beginning of chromosome 07; and possesses a significantly larger version of the chromosome 08 introgression that was also previously unknown. SPT 10-12 will be released as the germplasm line GP-NC WS 18 following the completion of replicated field trials. SPT 10-12 has been crossed with Bailey II (the leading Virginia-type variety for the Virginia-Carolinas (VC) production region), in order to transfer this additional leaf spot resistance into an elite Virginia-type background. Progeny from this cross are progressing through a marker assisted backcross-breeding program with Bailey II as the recurrent parent and an F2-derived marker assisted selection program in two separate pathways to accomplish this objective.

The A. *cardenasii*-derived breeding line GP-NC WS 6 was found to contain a unique introgression on chromosome 09 containing the same alleles as a previously published root knot nematode (RKN) candidate gene region. Furthermore, GP-NC WS 6 was released as a RKN resistant line. Thus, GP-NC WS 6 is the most adapted Virginia-type to the VC region with the RKN resistance gene. As such, GP-NC WS 6 has been crossed with Bailey II to confirm this RKN resistance and transfer it to an elite Virginia-type cultivar via an F2-derived marker assisted selection program.

Promising results point toward development of a Sclerotinia resistance marker

Dr. Kelly Chamberlin, USDA ARS

Sclerotinia is a soil disease that plaques many of our production regions, particularly the Virginias/Carolinas and the far western regions. Dr. Kelly Chamberlin, in collaboration with the HudsonAlpha Institute's Dr. Josh Clevenger and others, has identified a marker for resistance to this disease. The marker is currently in validation trials, but hopefully will soon be used in breeding programs to finally give growers hope for relief from this disease.

Previously, TPRF funded the phenotyping and genotyping of two recombinant inbred line populations developed specifically to identify quantitative trait loci (QTL) directly involved in Sclerotinia blight resistance. The results from that work identified three QTL strongly associated with resistance. Using whole genome sequencing and the Khufu platform (HudsonAlpha Institute) and phenotypic data from 2018-2020, 65,000 single nucleotide polymorphisms were scored in Dr. Kelly Chamberlin's research. Results identified significant QTL on chromosomes 5 and 15 which are associated with Sclerotinia resistance. A minor QTL was found on chromosome 18. Phenotyping experiments to validate these QTL will be conducted in the 2023 and 2024 growing seasons. If validated, markers will be developed which can be used in breeding programs.

Developing genomic tools for Virginia-type breeding programs

Dr. Jeff Dunne,
North Carolina State University

In this research by Dr. Jeff Dunne, information from the completion of the Bailey II genome assembly is helping drive further exploration into the development of genomic tools for Virginia-type breeding programs. The completion of the Baily II genome provided a Virginia-type specific reference for improved germplasm evaluation and marker development for materials in the North Carolina State University peanut breeding program. Using the Bailey II genome, whole-genome sequencing of peanut lines selected to represent a large portion of the genetic diversity present in Virginia-type peanuts were aligned for single nucleotide polymorphism identification. A total of 14,523 high-quality markers evenly spaced across the genome were identified for use in the peanut breeding program.

> Results identified significant QTL on chromosomes 5 and 15 which are associated with Sclerotinia resistance

In 2021 and 2022, 265 lines, including novel breeding lines and germplasm material coming through the breeding pipeline, were grown at the Peanut Belt Research Station (Lewiston-Woodville, N.C.) and the Upper Coastal Plains Research Station (Rocky Mount, N.C.) for the characterization of leaf spot pressure and differentiation in the resistance among genotypes. In both years, plots were rated for leaf spot severity, both visually and with multi-spectral cameras, for a high-throughput approach. Data is currently being compiled across both years and locations for mapping QTL for improved leaf spot resistance among the 265 breeding lines.

Research Snapshot

High level of late leaf spot resistance in three new USDA/ UGA cultivar releases

Dr. Corley Holbrook, USDA ARS

This year, the first cultivars that were a direct result of the TPRF-funded Peanut Genome Initiative were released by Dr. Corley Holbrook's USDA breeding program in Tifton, Ga. Benefitting from a long-standing collaboration with Dr. Peggy Ozias-Akins at the University of Georgia, Dr. Holbrook and numerous collaborators successfully incorporated strong leaf spot resistance from a wild species into three cultivars with various other desirable traits. It will take a few years to build an adequate seed supply, but when fully deployed, these cultivars stand to save growers significant production costs and greatly improve the peanut industry's sustainability story.

Through his research, Dr. Corley Holbrook identified three new cultivars with high levels of resistance to late leaf spot. His research found that an A. *hypogaea* breeding line has three well-defined segments of the wild A. *cardenasii* chromosomes, conferring excellent resistance to late leaf spot. Molecular markers associated with these chromosomal segments are also available. Numerous hybridizations have already been made and marker assisted selection (MAS) is being used in an accelerated backcross breeding scheme to introgress resistance to leaf spot in high yielding genetic backgrounds adapted to U.S. peanut growing regions.

Increased donor funding also enabled us to simultaneously increase seed using summer and winter nurseries. This will speed the usual time necessary for seed increase so that these cultivars will more rapidly be available to peanut farmers. We anticipate releasing cultivars in 2023.

Based on results from 2021 and 2020, three lines (***CB 1, CB 2, and CB 7***) have been selected for release and are already being increased by Georgia Seed Development in Plains, Ga. (see photo below). Growing these three lines with no fungicide sprays produced the highest net revenue per acre in our 2021 tests (***Table 1***).


CB 1


CB 2


CB 7

Entry	Net Revenue Per Acre		
	MAX	MIN	NON-SPRAYED
CB 1	$606	$1014 (9)	$1146 (2)
CB 2	$607	$1018 (7)	$1068 (3)
CB 7	$942	$1064 (4)	$1173 (1)
CB 20	$911	$1031 (6)	$1063 (5)
CB 24	$906	$971 (13)	$997 (11)
GA-06G	$672	$728	$841
GA-13M	$1016 (8)	$1013 (10)	$882
GA-16HO	$868	$641	$823
TifNV-High O/L	$648	$959 (14)	$983 (12)
TifNV-HG	$773	$761	$958 (15)

MAX = *Full fungicide regime;*
Min = *One application of Convoy for white mold control.*
Non-Sprayed = *No fungicides.*
Numbers in parentheses are rankings for the top 15 genotype/production system combinations.

TABLE 1
2021 net revenue per acre under different productions systems

Exploring new sources of fungal disease resistances in wild species

Unsprayed plots of 'GA-06G' (left) and IAC-321 (right) in October 2021 field trials in Midville, Ga. Main disease pressure is Late Leaf Spot. IAC-321 has three chromosome segments from the wild species A. cardenasii. These segments are being combined with the resistances of 'Bailey' which are also derived from A. cardensaii.

Dr. David Bertioli, University of Georgia

In this research by Dr. David Bertioli, several wild species, including Arachis cardenasii, A. stenosperma, A. batizacoi and A. magna, are being evaluated for valuable fungal disease resistances. In 2015, the Bertioli lab (working with an international team of collaborators, with funding from TPRF and others) clearly identified leaf spot resistance in existing introgression segments from A. cardenasii. Markers were then developed to identify the presence of these critical segments. These advances led to the release of highly resistant cultivars in Brazil and, now, to the release of additional cultivars from the U.S. Agriculture Department-University of Georgia.

Efforts are now underway to combine leaf spot-resistant segments with segments known to confer resistance and apply to other key diseases. Segregating progeny from well-designed crosses were tested in the field in Midville, Ga., and in controlled detached leaf assays. Genetic markers were able to help in the prediction of the most resistant plants, which combine the

Research Snapshot

resistances against late leaf spot, early leaf spot, rust and root-knot nematode in an unprecedented way. The resistances against rust and root-knot nematode are as good as the best of the controls and the resistances against the leaf spots are better than the best of the resistant controls.

In collaboration with the Agronomic Institute of São Paulo, Dr. Bertioli has developed highly productive lineages with very strong resistance to foliar diseases from the species A. *stenosperma* and A. *magna*. By correlating field disease scores with genotyping data, we have identified the genetic determinants for these resistances. This source of resistance is an alternative to the newly released A. cardenasii derived resistance.

Highly productive lineages of peanut with very strong resistances against foliar diseases from the wild species A. stenosperma and A. magna in São Paulo grown under no sprays. The "burnt up" row on the bottom right is IAC OL4, the most popular cultivar in São Paulo State

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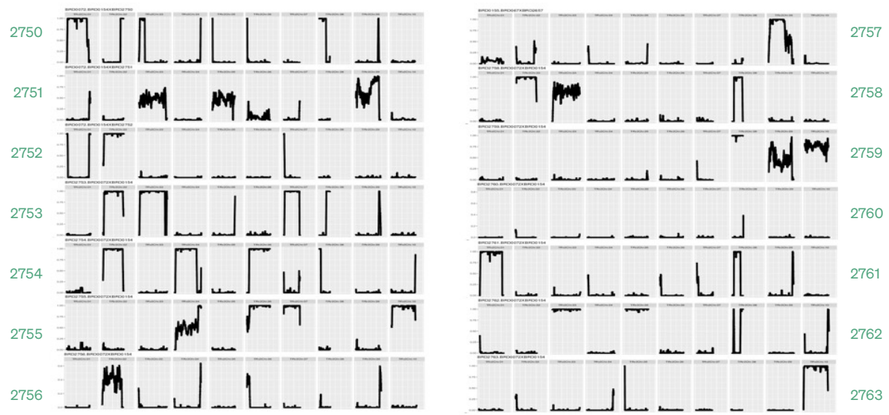

IpaSten (45 lines) Introgression on the A genome

Building genetic resources to support resistance to multiple diseases

Dr. Peggy Ozias-Akins, University of Georgia

Breeders need sources of resistance to incorporate into their breeding programs. A National Science Foundation project is supporting the development and release of pre-breeding germplasm which provides those sources. This TPRF project helps characterize the products of that project with the goal of germplasm release and integration of useful traits into the joint USDA-UGA peanut breeding program. Four synthetic tetraploids were crossed with cultivated peanut lines progeny and were genotyped to identify introgressions. Advanced lines are derived from three released and one unreleased (due to insufficient seed yield) allotetraploid lines. All allotetraploids were crossed and backcrossed with a nematode resistant and a nematode susceptible line of cultivated peanut and regions of introgression were identified. An example of the power of this genotyping approach is shown in the figure above, where the peaks indicate introgression from the wild species and the troughs represent the cultivated peanut background.

Research Snapshot

Aflatoxin Resistance

Understanding diversity in Aspergillus flavus

Dr. Baozhu Guo, USDA ARS

Dr. Baozhu Guo has made progress showing the variation in the genomes' naturally occurring strains of *Aspergilus flavus* which produce aflatoxin. In this research, he references genomes for two Aspergillus flavus isolates, AF13 (high aflatoxin producer) and NRRL3357 (moderate producer), revealing distinct differences. Dr. Gao found a large 310kb insertion on chromosome 1 was only present in AF13, but absent in NRRL3357. It contains 60 genes, including a new bZIP transcription factor gene, named *atfC*, which may be involved in environmental/oxidative stress tolerance and aflatoxin production.

A single reference genome does not represent the gene content of a species due to the many variations which occur within a species. The pan-genome of a species is subdivided into two components, the 'core' genome, containing genes conserved across all observed genomes from a species, and the 'accessory' genome, containing genes specific to some fungal isolate genomes or individual isolates within a species. The core genes are usually essential for the viability of an individual organism, whereas the accessory genes could influence phenotypic differences between isolates. The pan-genome is the union of core conserved genes and all accessory non-conserved genes across all isolates/strains of a species. A pangenome can be used as a reference genome for single nucleotide polymorphism identification and to identify novel aflatoxin regulator genes. Using 347 A. *flavus* isolates, we constructed AflaPan, the first pangenome and a comparative whole-genome sequence-based method for A. *flavus*. We found a total of 17,855 genes, 7,315 as the core with 10,540 accessory genes. The 310Kb insertion has been detected in only three toxigenic isolates.

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Research Snapshot

Using wild species to search for aflatoxin resistance

Dr. Alicia Massa, USDA ARS

Genetic variants in the peanut transcriptome of A-genome species (A. duranensis and A. cardenasii) in response to Aspergillus infection were identified in a previous TPRF project. These variants were validated and a set of single nucleotide polymorphism markers (SNPs) associated with aflatoxin-resistant germplasm were developed. In the 2022 project by Dr. Alicia Massa, these SNPs were used to detect novel alleles, as compared to non-A genome species. Only novel alleles are candidate for marker development.

Overall, markers developed during this study will assist in the selection process, including verification of genotype identity, evaluation of intra- and interspecific genetic variability, and tracing candidate alleles and quantitative trait locus in advanced pre-breeding and breeding generations.

Recent transcriptome analysis of the peanut-Aspergillus interaction has indicated that peanut seeds of certain genotypes down regulate a gene cluster in A. flavus, which controls the synthesis of aflatoxin at early stages of the infection and, consequently, prevents aflatoxin accumulation. The studies have also revealed the biological variability that accounts for gene expression differences between resistant and susceptible peanuts. To further leverage these research findings, work is currently in progress to generate genetic resources, including mapping populations and interspecific crosses for the development and release of peanut germplasm that is less susceptible to pre-harvest aflatoxin contamination. The goal of the research is to develop molecular markers and evaluate non-A genome species of Arachis for aflatoxin resistance.

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Exploring genetic controls for aflatoxin contamination

Dr. Peggy Ozias-Akins, University of Georgia

Most would agree that aflatoxin contamination remains the biggest quality issue affecting marketing and exporting of peanuts. Aflatoxin is an incredibly complex problem, but genetics play an important role in the development of a lasting solution. Dr. Peggy Ozias-Akins has identified markers which appear to impact final aflatoxin levels. These markers are being validated but offer great promise for finally addressing this long-standing problem.

The degree of aflatoxin contamination in peanuts is dependent upon many complex factors. Peanut genetics is but one of those factors and has only recently been evaluated to understand how it works and how strong of an influence it can be. One objective of Dr. Peggy Ozias-Akins' project has been to determine the usefulness of a new method of assessing the amount of contamination in a single seed. Raman/FTIR spectroscopy was used to quantify aflatoxin in inoculated seed, then the seed were tested using the standard High-performance liquid chromatography method. Correlation was a disappointing 0.4862. Several modifications of the protocol and model are being tested. Since the rapid FTIR-based assay cannot yet be deployed, we have continued to test selected lines with standard methodology.

Previous work with two populations recognized for reduced aflatoxin accumulation has identified four quantitative trait loci for resistance on chromosomes A01, A02, B03 and B10. Markers have been used to identify homozygous resistant individuals. The resulting population has been advanced in Tifton, Ga., but is very non-adapted to the environment and does not yield well. A resistant line (CS229) from this population has been used as a parent to develop a structured population designed to segregate traits (known as MAGIC). This MAGIC population holds the promise of developing, for the first time, genetic resources to mitigate aflatoxin contamination in peanuts. All parents were selected as having reduced aflatoxin contamination either because of drought tolerance, reduced fungal growth or reduced aflatoxin production. The eight-way crosses are in progress and should be harvested in the spring of 2023.

All parents from the MAGIC population described above, as well as a separate 18-parent, 16-way MAGIC population and some additional controls, were both increased and grown in rainout shelters during the 2022 field season. The shelters were inoculated at 60 days with cracked corn infected with *Aspergillus flavus*, and were drought stressed during the last 40 days of growth. Drought tolerance was evaluated with canopy temperature measurements and visual ratings for which there were clear differences among genotypes. Aflatoxin analysis is currently in progress. Seeds from the increased plots have also been used for in vitro inoculation and aflatoxin contamination screening.

Research Snapshot

General Methodology

Developing a resource for inexpensive genotyping for QTLS in peanut breeding programs

Dr. Mark Burow, Texas A&M University

Genetic probes for relevant traits would offer an inexpensive method of genotyping high volumes of individuals in large breeding programs. With this goal in mind, Dr. Mark Burow developed probes for 2,770 highly polymorphic targets. These probes were screened against DNA from 48 peanut accessions, including individuals from the U.S. minicore collection, closely related breeding lines from all four market classes of peanut, wild species and introgression lines.

So far, 3,411 additional single nucleotide polymorphism targets have been identified. Depending on the results of the original 48 and additional 144 accessions, we may replace some targets or add many or all of the additional set of targets. These targets were derived from minicore single nucleotide polymorphisms (SNPs) associated with yield and grade under water deficit stress and quantitative trait loci-associated SNPs for resistance to leaf spots and rust in a wild-species derived population.

A structured wild tetraploid germplasm collection for use in peanut breeding

Dr. Soraya Leal-Bertioli, University of Georgia

It is commonly recognized that a variety of wild peanut species harbor a wealth of genes imparting desirable traits. Many of those wild species are difficult to work with and don't readily cross with cultivated peanut. To alleviate that problem, Dr. Soraya Leal-Bertioli and her collaborators are building a germplasm population which contains wild species genes in a form readily usable by breeders. Most breeding programs are now utilizing wild species genes for efforts to attain drought tolerance, disease resistance and other traits.

The genus Arachis contains 86 described species divided into nine botanical sections. The botanical section Arachis is of particular interest because it includes cultivated peanut, and closely related wild species, most of which are diploids. The main collections of wild Arachis species in the U.S. are at

Research Snapshot

Progress managing large volumes of peanut genome data

Dr. Sudhansu Dash, National Center for Genome Resources

Peanut genomes are large and data sets can be difficult to work with, but through Dr. Sudhansu Dash's work sourcing large volumes of peanut data has been made easier to navigate. A modern multimodal genome browser has successfully been installed in PeanutBase (peanutbase.org) and is currently being tested. Simultaneous visualization of multiple genomes has been successfully tested with dot plots pointing to the regions with structural differences in the genomes. An updated tool has been deployed and provides capability to easily visualize variations. This is a convenient way to compare breeding parents, derived lines or cultivars for various decision-making steps in a breeding program.

The genotyping data from African lines have been incorporated with updates. The catalogs of U.S. core and minicore germplasm collections are now served on PeanutBase.

Almost all genomic and genetic data are now in Data Store (data.legumeinfo.org/Arachis/) where the community can openly access and download data along with preservation of many previous versions. More importantly, multiple software in both PeanutBase and the Legume Information System access the data from the same source, thus making the entire process easy to maintain and avoid unnecessary duplication. Now, all the search tools (genotype/variant, phenotype, genome-wide association study, quantitative trait loci, data visualization, along with PeanutMine for integrated searching of genetic and genomic data) commonly used by genome scientists and breeders are sourced from a single resource.

the Plant Genetic Resources Conservation Unit, the U.S. Agriculture Department, Texas A&M and North Carolina State University. Together, these collections hold around 75 Arachis species. Diploid species of the Arachis section have traits of agronomic interest (eg. resistance to pests and diseases, larger seed, productivity, drought tolerance, etc.) that can be transferred to cultivated peanut through hybridization methods. Several cultivars derived from wild relatives have been released (Webb, TifNV H/O, Bailey, Georgia 14N, etc.), with higher disease resistance, thus saving farmers resources.

Through research by Dr. Soraya Leal-Bertioli, five new allotetraploids were produced: CruziSimp2, MagHoehnei1, MagHoehnei2, MagHoehnei3 and MagKuhlma1 (***Figure 1***). After 601 crosses, four new diploid hybrids were produced. Eight allotetraploids were tested for resistance to early leaf spot, with several showing semi-immunity (***Figure 2***). Six allotraploids were released as germplasm. These will be valuable germplasm resources for peanut breeding programs.

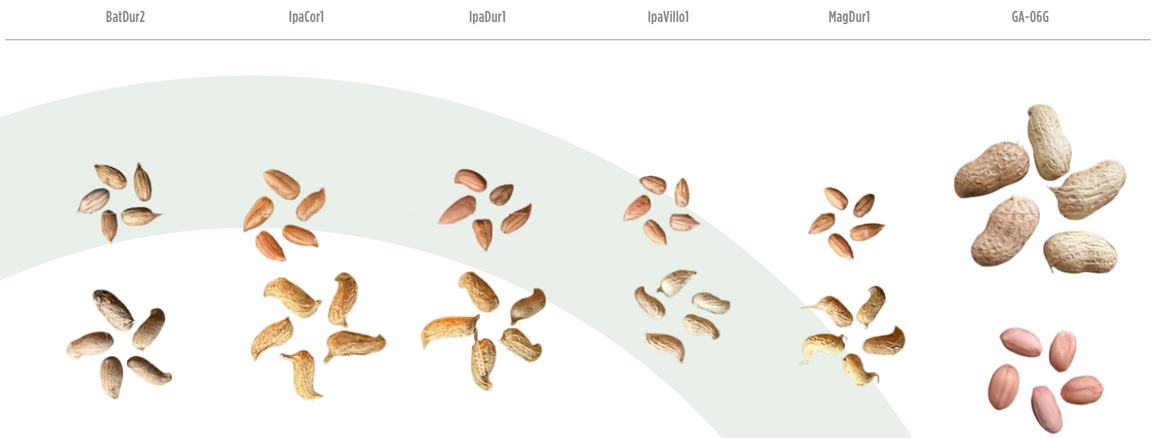


FIGURE 1
Seeds and pods of neotetraploids released in 2022: BatDur1, IpaDur1, IpaCor1, IpaVillo1 and MagDur1. GA-06G is added for comparison of pod and seed size.

Simultaneous visualization of multiple genomes has been successfully tested with dot plots pointing to the regions with structural differences in the genomes.

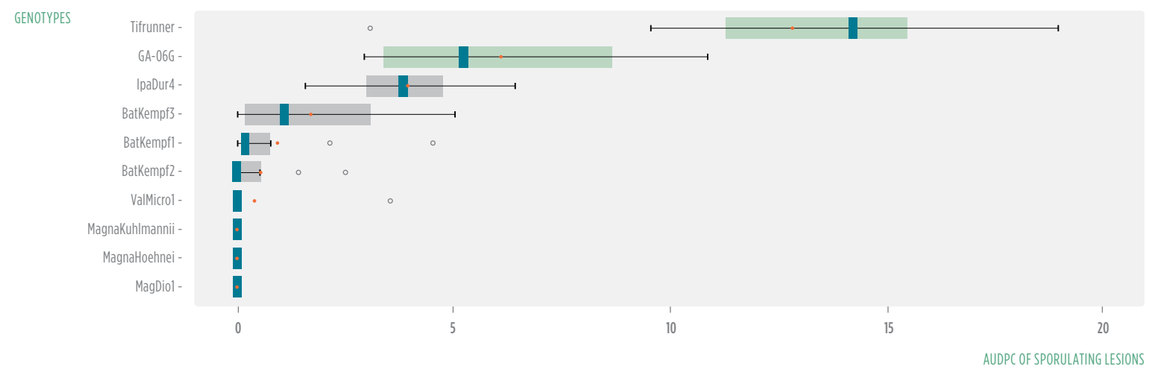
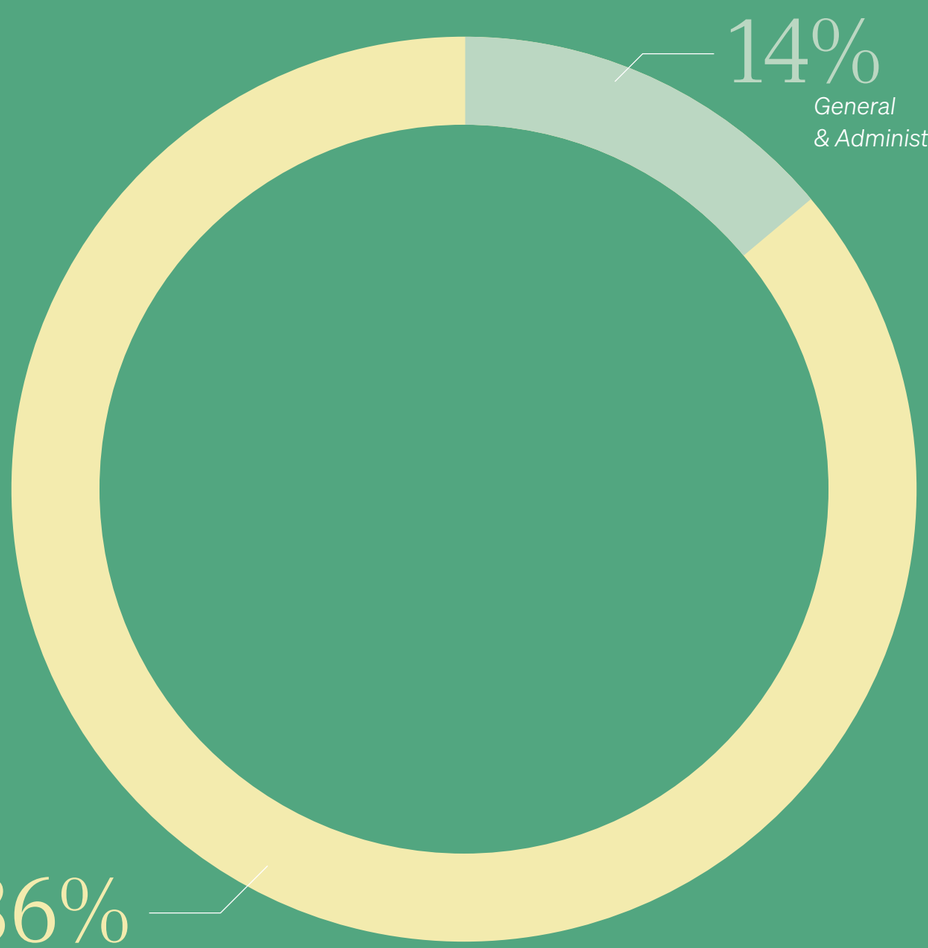


FIGURE 2
Area under the disease progression curve of Sporulating Lesions per Leaf Area of allotetraploids inoculated with ELS causing fungus, Passalora personata.

2022 Expenses



DONOR / FUNDING STATS

Shellers

$385,500

Growers

$238,000

Manufacturers

$186,500

Allied

$24,800

HOW WE ARE FUNDED

The Peanut Research Foundation is funded entirely by the U.S. peanut industry. The vast majority of those funds are spent to sponsor research and on programs to transmit key learnings. To learn how to support our research, contact TPRF Executive Director Steve Brown at sbrown@peanutsusa.com.

HOW WE INVEST OUR FUNDS

The Peanut Research Foundation's Board of Directors selects which peanut-specific production and processing research proposals to fund each year. TPRF transmits learnings from completed research projects to industry and other stakeholders through a range of programs, including presentations to industry segments, this annual report and sponsorship of scientific conferences. TPRF's general & administrative expenses, which include staffing, are minimal.

Growers, shellers and manufacturers pledged $200,000 per year for the four-year Phase II initiative. Numbers sometimes vary from that level depending on when payments are made during the fiscal year. These numbers reflect actual receipts for fiscal year 2022.

Thank you to our 2022 Donors

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OUR MISSON

The Peanut Research Foundation is the research arm of American Peanut Council. Our mission is to lead funding, coordination and promotion of an organized science research and knowledge-transfer plan that results in a more resilient and competitive U.S. peanut industry. We are the only funder of peanut production and processing research that represents the entire industry. Our Board of Directors represents the diversity of the U.S. peanut industry, including growers, shellers, manufacturers and allied industries. In addition to financially supporting relevant peanut-specific research, we also interact with government, university research institutions and other peanut industry organizations to coordinate research needs and to leverage research funding opportunities. TPRF focuses on production and processing research, while The Peanut Institute concentrates on human nutrition research; the two groups may occasionally have areas of overlapping interest.

MEET OUR BOARD OF DIRECTORS

The Peanut Research Foundation's work is led by our Board of Directors, whose 17 members represent all segments of the U.S. peanut industry. The operations of the foundation are managed by the American Peanut Council.

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Jennifer Bencz, Algood Food Company, manufacturer representative
Jon Moore, J.R. James Brokerage Co., allied industry representative
Collins McNeill, MC McNeill & Co., APC board chair

TPRF

Richard Owen, American Peanut Council president & CEO and TPRF ex officio
Dr. Steve Brown, TPRF executive director

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