

**Introgression of disease and pest resistance traits from wild species
For sustainable peanut improvement**

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Overview

The cost of controlling pests and diseases and the loss of yield they cause has been estimated at more than \$160 million per year for peanut farmers in Georgia. Plant Protection Products are vital for peanut disease and pest management. However, their application not only increases the cost of peanut production but is under increasing regulatory pressure, is time consuming, and damaging to the environment. Development of disease and pest resistant cultivars is one of the most economical ways to control pests and diseases. This project utilizes the genetic diversity of wild peanut species, converting them into a tetraploid form that can be directly used in breeding programs. These wild species tetraploids are then used to develop new germplasm lines with much stronger resistances than available when breeding with cultivated peanuts of pure pedigree. This work makes full use of the advances in genetics made possible by the Peanut Genome project and, via germplasm release, will create a legacy resource for breeders consisting of new tetraploids and peanut lines with new wild species traits

Results

Twenty-four unique crosses were made with diploid wild peanuts in 2020. The diploid hybrids were confirmed with molecular markers and morphological traits, and thousands of cuttings were treated to induce chromosome doubling. So far [sixteen](#) distinct synthetic tetraploid wild peanuts were developed from these crosses, we are currently multiplying them and characterizing their pest and disease resistances, chromosome characteristics, DNA content and phenotypic traits, for germplasm release. In 2021, five new tetraploids were deposited in the USDA National Plant Germplasm System making them freely available to breeders and researchers. [In 2022, six new tetraploids were approved for subsequent germplasm release. Also 2022, using 8 new diploid species accessions strategically chosen from a tree of relationships, fifteen new cross combinations were made.](#)

New diploid species accessions used for crosses in 2022	
B genome females	A genome males
<i>A. williamsii</i> PI688988	<i>A. cardenasii</i> PI 475996
<i>A. magna</i> PI 599183	<i>A. stenosperma</i> PI599186
<i>A. batizocoi</i> PI666081	<i>A. hertzogii</i> PI 476008
	<i>A. schininii</i> V9923
	<i>A. kuhlmannii</i> PI666089

Perspectives

By strategically choosing initial wild species accessions from a tree of relationships, we are incorporating structured wild diversity in a tetraploid form, which is directly crossable with peanut. This will allow us to create a new Core Germplasm Collection of representative wild diversity. This Core Collection will be hosted by USDA and other seed banks, free to access for researchers and breeders.