

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

PI: David Bertoli, University of Georgia, bertoli@uga.edu

Overview

The cost of controlling pests and diseases and the loss of yield they cause is 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

So far twenty-six wild species derived tetraploids have been made. The wild species accessions have been chosen from an unprecedentedly detailed tree of relationships of the wild species accessions that we have constructed. Accession choice was designed to incorporate the greatest possible range of wild species diversity possible into the hybrids. Currently twelve new diploid hybrids, confirmed with DNA markers, are being created with colchicine to double their chromosomes and make them cross compatible with cultivated peanut:

New Diploid hybrids being treated with colchicine
<i>A. batizocoi</i> PI 666081 x <i>A. cardenasii</i> PI 475996
<i>A. batizocoi</i> PI 666081 x <i>A. hertzogii</i> PI 476008
<i>A. batizocoi</i> PI 666081 x <i>A. kuhlmannii</i> PI 666089
<i>A. batizocoi</i> PI 666081 x <i>A. schinini</i> V9923
<i>A. batizocoi</i> PI 666081 x <i>A. stenosperma</i> PI 599186
<i>A. magna</i> PI 599183 x <i>A. cardenasii</i> PI 476993
<i>A. magna</i> PI 599183 x <i>A. herzogii</i> PI 476008
<i>A. magna</i> PI 599183 x <i>A. kuhlmannii</i> V 9214
<i>A. magna</i> PI 599183 x <i>A. stenosperma</i> PI 599186
<i>A. williamsii</i> Grif 14229 x <i>A. cardenasii</i> PI 475996
<i>A. williamsii</i> Grif 14229 x <i>A. kuhlmannii</i> V9214
<i>A. williamsii</i> PI 688988 x <i>A. hertzogii</i> PI 476008

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. We are creating 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.