

## Towards a new source of late leaf spot resistance

### - Introgression of *A. stenosperma* wild species chromosome segments into elite peanut lines.

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#### Overview

Control of late leaf spot infection in peanut is expensive. Breeding for resistance using cultivated peanut of pure pedigree is limited by a lack of strong sources of resistance. In contrast, wild peanut species have very strong resistances. This project used a backcrossed population which genetically is predominantly of elite breeding material, with a small proportion of DNA from the highly late leaf spot resistant wild species *Arachis stenosperma* and *A. batizocoi* incorporated into each line. Using new genetic tools that have been developed after the sequencing of the peanut genomes, we genetically characterized the population at high resolution and correlated the results with late leaf spot resistance. These results will guide the selection and advancement of peanut plants that incorporate strong late leaf spot resistance from the wild species *Arachis stenosperma* and *A. batizocoi*.

#### Results

More than 300 putative third backcrossed plants derived from the elite breeding line 5-646-10 and a tetraploid hybrid of *A. stenosperma* V10309 and *A. batizocoi* K9484 were genotyped with 48,000 DNA markers distributed over the peanut genome. Analysis of the results confirmed that more than 250 of the plants did indeed harbor genetic contributions from the wild species, varying from only about 1% to almost 20%. Wild genetic contributions were in discrete fragments (segments). The plants were scored for late leaf spot resistance, and the genetic results correlated with late leaf spot resistance. Genetic regions indicated in strong late leaf spot resistance are on *A. stenosperma* chromosome A06, and *A. batizocoi* chromosome B02 (Fig. 1). This information will be used to aid in the selection of plants to be taken forward for the creation of improved peanut lines.

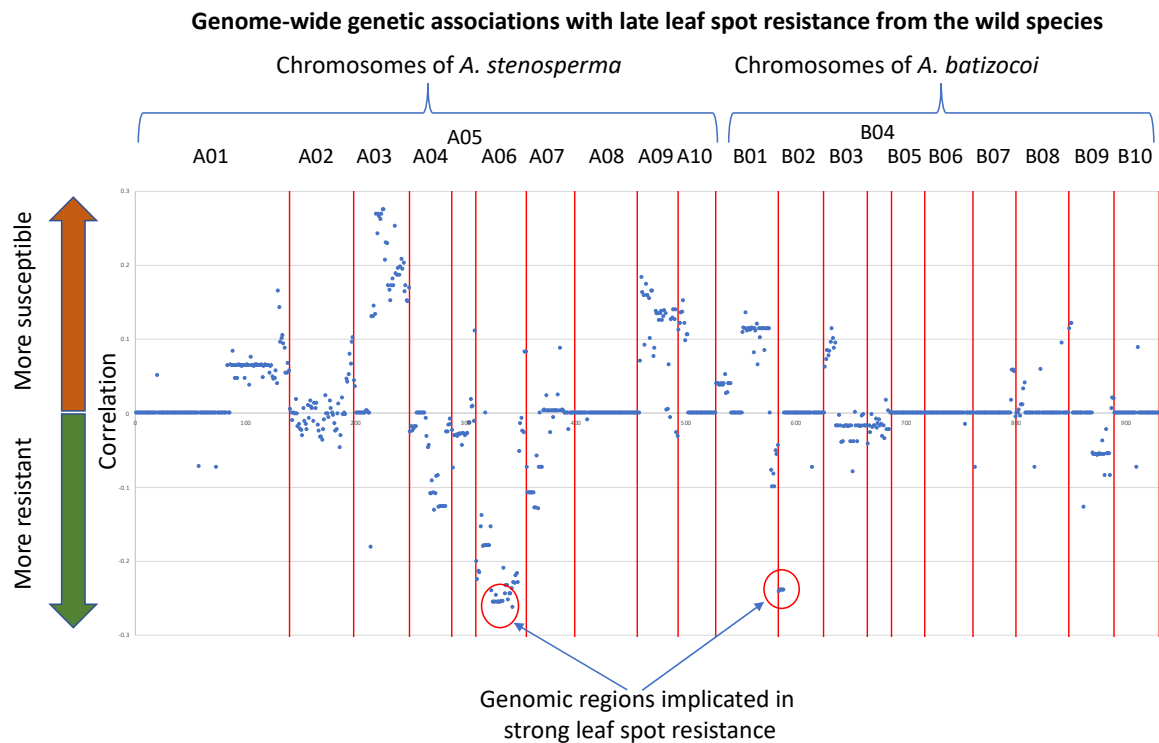


Figure 1. Correlations between resistance to late leaf spot and genetic contribution from the wild species *Arachis stenosperma* (chromosomes A01-A10) and *A. batizocoi* (chromosomes B01-B10), in a highly backcrossed population. Genetic regions on chromosomes A06 and B02 are strongly correlated with resistance. Markers for these genetic regions will be used to help select the next generation of plants of plants, helping insure they are highly disease resistance, and perform well in field conditions.