

Summary

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Root-knot nematodes and late leaf spot are a very damaging to the peanut crop. Resistance to late leaf in peanut cultivars is limited, and currently only a single source of resistance to root-knot is available (originating from the wild species *A. cardenasii*, and available in cultivars like Webb, and H/O Tifguard). There are serious concerns that this root-knot resistance could be broken. In this project we investigated new sources of resistance to root-knot nematode and late leaf spot from the wild species *A. stenosperma*. This was done by studying plants derived from a cross involving peanut (*A. hypogaea*) and *A. stenosperma*.

Peanut has two sets of chromosomes that originally derived from two wild species, one contributing "A-chromosomes" and the other "B-chromosomes". *A. stenosperma* has only A-chromosomes, therefore to be able to cross with peanut, it needed to first be crossed with a B-chromosome species (in this case a species called *A. batizocoi* was used). These hybridizations were carried out before the beginning of the project.

In this project, a population of 230 plants specially structured for genetic analysis, from the cross *A. hypogaea* x (*A. batizocoi* x *A. stenosperma*) was tested for resistance to root-knot nematode and late leaf spot using controlled quantifiable methods. This information will be used together with DNA-typing information and genetic mapping to identify chromosomal regions that confer resistance and to develop molecular markers to aid in the production of new resistant peanut varieties.