

## **A New Source of Root-knot Nematode Resistance from *Arachis stenosperma* Incorporated into Allotetraploid Peanut (*Arachis hypogaea*)**

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Root-knot nematode is a very destructive pathogen, to which most peanut cultivars are highly susceptible. Strong resistance is present in the wild diploid relatives. Previously, QTL controlling nematode resistance were identified on chromosome A02, A04 and A09 of *Arachis stenosperma*. Here, to study the inheritance of these resistance alleles within the genetic background of tetraploid peanut, an F<sub>2</sub> population was developed from a cross between peanut with an induced allotetraploid that incorporated *A. stenosperma*, [*Arachis batizocoi* x *A. stenosperma*]<sup>4x</sup>. This population was genotyped using a SNP array and phenotyped for nematode resistance. QTL analysis allowed us to verify the major-effect QTL on chromosome A02, where a TIR-NBS-LRR rich region is present, and a secondary QTL on A09, each contributing to a percentage reduction in nematode multiplication up to 98.2%. In order to incorporate RKN resistance from *A. stenosperma* into peanut cultivars, F<sub>3</sub> lines (derived from the population described above) were firstly selected base on SNPs linked to the resistance and good agronomic traits; and secondly, they have been crossed and backcrossed with several peanut lines. Phenotypic screening for resistance and genotypic characterization of BC<sub>2</sub>F<sub>1</sub> lines allowed us to confirm the genomic regions that confer resistance. Currently, high-throughput genotyping of 272 advanced backcrossed lines (BC<sub>3</sub>F<sub>1</sub>) is in progress, and lines harboring the resistance alleles and that have recovered most of the recurrent genome will be selected. These lines that incorporate strong RKN resistance and the markers tightly-linked to this trait, represent a valuable tool for introgression of nematode resistance into elite peanut genetic backgrounds. I believe that this work will significantly impact peanut production in RKN affected areas.