

Mapping of Resistance to Root-knot Nematode from the Wild Species *A. stenosperma* and Introgression into Peanut *Arachis hypogaea* L.

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The cultivated peanut (*Arachis hypogaea* L.) is a very important crop worldwide. It is an allotetraploid species with very low genetic diversity and high susceptibility to root-knot nematode (RKN) *Meloidogyne arenaria*, which reduces yield and quality, and increases the production costs. Although, single source of RKN resistance (derived from the wild species *A. cardenasii*) is available in cultivars widely grown in US, the nematode could eventually breakdown the resistance and cause devastating consequences for the peanut industry. Among other wild diploid species that can be utilized to enrich peanut's genetic diversity, we find the species *A. stenosperma* accession V10309 that has been described as very resistant to the root-knot nematode. Candidate genomic regions that control nematode resistance have been mapped on linkage groups A02, A04 and A09. To confirm these chromosome segments in a tetraploid background, an F₂ population was developed from a cross of *A. hypogaea* RunnerIAC886 with an induced allotetraploid (*A. batizocoi* K9484 x *A. stenosperma* V10309)^{4x} and genotyped using the 'Axiom_Arachis v01' 58K high-density SNP array. A framework map, comprising 1499 polymorphic SNP markers, in combination with phenotyping of three different components of resistance, allowed us to verify previously described QTL. F₂-derived F₃ (F_{2:3}) lines harboring these chromosome segments have been selected using RKN resistance-linked SNP makers, crossed and backcrossed with peanut elite breeding lines from Tifton, GA. Unexpected genetic events were observed, such as tetrasomic recombination, gene conversion and unusual marker. Further characterization of BC₃F₂ lines will be done (phenotyping, genotyping and skim sequencing), in order to validate markers, understand the chromosome segments and select the best individuals to continue with the backcrossing process. This work will contribute to the production of advanced peanut lines that incorporate wild-derived genomic regions with strong and durable resistance to RKN, and to the further understanding of the complex genetics of peanut.