Progress report for improved markers for selection of nematode resistant lines

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Peanut root-knot nematode causes significant yield loss in infested fields. As a soilborne pest, chemical control by fumigation is costly and hazardous. Durable host resistance is the most effective and environmentally sustainable method to minimize nematode damage. Strong host resistance to root-knot nematode (*Meloidogyne arenaria*) was introgressed from the wild diploid species *A. cardenasii* to cultivated peanut. The introgressed region was previously identified as a large chromosomal region on linkage group A09, and low recombination in mapping populations has prevented further refined mapping of the disease resistance genes (Nagy et al. 2010, Mol. Breed. 26:357). In order to further define the introgressed region, additional polymorphic markers were added to the linkage group A09 using a later generation recombinant inbred line population developed from Gregory x Tifguard in which Gregory is the susceptible parent and Tifguard is the resistant parent derived through the *A. cardenasii* introgression pathway. Map distance increased to 8 cM compared to zero recombination in the earlier mapping study. Quantitative trait locus (QTL) mapping of egg mass index and gall rating detected two regions on the linkage group A09 that contribute to nematode resistance. Rare recombinants within these two regions were discovered in the population. Additional phenotyping of the recombinants demonstrated that one introgressed region represented by RIL48 confers moderate resistance while the other introgressed region represented by RIL46 confers strong resistance to nematodes. RNAseq analysis of root tissues from Gregory, Tifguard, RIL46 and 48 challenged by juvenile stage nematodes revealed differential gene regulation in response to the pathogen. A candidate nematode resistance gene *Rma* that is expressed at a low constitutive level in both Tifguard and RIL46 was discovered and is under functional analysis via genetic transformation. Nine additional SNP markers polymorphic between Tifguard and Gregory within the alien introgressed region were discovered by a single nucleotide polymorphism (SNP)-calling pipeline for peanut (Clevenger and Ozias-Akins, 2015, G3 5: 1797). Using these SNP markers, we screened 301 seeds from five C1501 RIL lines demonstrating heterozygosity in the introgressed region. Three showed additional recombination near the *Rma* candidate gene; however, seeds had low viability and plants could not be recovered. We also applied the markers to 3,570 individuals from various breeding populations. Forty individuals from five breeding populations carrying a heterozygous allele near the *Rma* candidate gene and missing the introgressed region 30 Mbp away from the candidate gene were identified. Further genotyping of progenies from these individuals will enable us to identify novel recombinants with the smallest introgressed chromosomal segment yet maintain near immunity to nematode infection. In addition, Tifguard and Gregory were genotyped on an Affymetrix SNP array consisting of 58,233 SNPs curated by Josh Clevenger. Analysis of 4,647 SNPs in the poly high resolution class revealed 54 additional polymorphic markers on the A09 chromosome spanning 150 Mbp. Using the Affymetrix array to genotype the segregating population for nematode resistance could further aid definition of the alien introgression for nematode resistance.