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NATIONAL PEANUT BOARD/SOUTHEAST PEANUT
RESEARCH INITIATIVE
REPORT FOR WORK
DONE UNDER RESEARCH AGREEMENT

Quarter Ending
Dec 31, 2015 FINAL + Summary

INSTITUTION: University of Georgia

PROJECT TITLE: **GENE-BASED MARKERS FOR BREEDING OF NEMATODE
AND LEAF SPOT RESISTANCE**

RES. AGR. NO.: PROJECT LEADER: P. Ozias-Akins
GACCP Control NO.:

EXPIRATION DATE: Jun. 30, 2015 NPB CONTACT:
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REPORT OF PROGRESS:

Sequence to expand marker discovery ability was generated using RNA-Seq, which is a high-throughput, deep-sequencing method that can capture most transcribed sequences from the tissue(s) under study. In addition to gene annotation, comparative evaluation of gene expression can lead to identification of candidate genes for functional processes. Indeed, we have used RNA-Seq of nematode-infested roots of Tifguard, Gregory, and recombinant susceptible and resistant inbred lines (RILs) to characterize the chromosomal region that confers nematode resistance. This effort has resulted in localization of recombination breakpoints and identification of a novel candidate resistance gene in Tifguard and the resistant RIL. The gene is absent from the susceptible RIL and Gregory. The recombinant line with the candidate gene remains strongly resistant while the second RIL still shows partial resistance. Markers spanning both of the introgressed regions conferring strong or partial resistance to the root-knot nematode and based on single nucleotide polymorphisms have been developed. The marker type (KASP) enables rapid screening of thousands of progeny in a field season using crude DNA extractions and gel-free marker analysis. The markers near the candidate gene are ideal for marker-assisted selection since there is low probability for recombination between marker and trait. They also have resulted in detection of additional recombinants with a smaller introgressed chromosomal segment and therefore less linkage drag. The markers have now been used for screening thousands of individuals in the breeding program. Materials for studying gene expression during late leaf spot infections also were generated and are being analyzed as part of the ongoing research.