# BREEDING FOR NEMATODE RESISTANCE IN PEANUTS FOR THE SE
## Final Report

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**Objective 1: Incorporating nematode resistance into cultivars better suited to growth conditions in the SE, and to use marker-assisted selection to facilitate this process.**

To incorporate nematode resistance into Florida germplasm, several crosses involving the nematode resistance line COAN and susceptible lines HULL, Norden and DP-2 were made and the $F_1$ plants were screened for Oleic acid content and SCAR marker Z3/265. A total of 740 $F_1$ seeds were screened for SCAR marker Z3/265, out of which 193 seeds showed its presence. All the $F_1$seeds that showed the presence of the Z3/265 marker were subsequently advanced to the $F_2$ generation. Leaves from fifty lines/genotypes that were agronomically good and disease free were collected and subjected to oleic acid and RFLP analysis with the main objective of correlation, reliability and zygosity studies, and for further advancement to the $F_3$ generation. Thirty of the 50 lines were high oleic (>70%), nine were medium in oleic acid (65-70%) and 11 (<65%) were low in oleic acid. According to the results, there is no correlation between nematode resistance and oleic acid content. The RFLP probe R2430E was used for screening the 50 $F_2$ lines. The nematode resistant and susceptible alleles were quite distinct and easy to score with this probe. Five (10%) of the lines were homozygous negative (-), five (10%) were homozygous positive (+), and the remainder (74%) were heterozygous (+-) for the marker. There was a high degree of correlation between the presence of the Z3/265 and R2430E

markers and nematode resistance to *M. arenaria* race 1 as measured by the number of galls present on peanut roots and pegs. Forty-four lines (88%) were found to be resistant and three lines (18%) were susceptible. A manuscript with all results is currently under preparation.

**Objective 2: Identification of nematode resistance gene/s (introgressed portion of wild *Arachis cardenasii*) in NemaTAM that specifically confers resistance to root knot nematodes.**

Work by several scientists to clarify the structure and mode of action of resistance genes (*R*-genes) revealed that *R*-gene resistance proteins can be characterized by the presence of LRR (Leucine rich repeat) and NB-ARC ( Nucleotide Binding, human APAF-1, Plant Resistance genes and *Caenorhabditis elegans* CED-4) domains. In our study, we used six degenerate primers designed to bind to regions encoding NBS motifs to isolate resistance genes. Degenerate PCR primers were used to amplify the nucleotide binding site (NBS) encoding regions from *Arachis hypogaea* var. NemaTAM, which is an interspecific cultivar with high levels of resistance to *M. arenaria*. This work resulted in 234 genomic clones. Analysis of clones revealed that 80 sequences belong to the section *Arachis*. Twenty-one other clones have sequences with significant homology to other genes found in *Medicago, Vigna, Pisum, Oryza, Solanum, Lycopersicum, Citrus, Cicer, Arabidopsis* and *Vitis*. Of the remaining clones, eight have sequences related to genes found in animals. Interestingly, one peanut clone showed significant homology to *Arachis cardenasii* (C8_V_504) resistance protein (93% at nucleotide level and 89% at protein level). Further characterization of this clone for its linkage to nematode resistance is currently underway.