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

Project end

INSTITUTION: University of Georgia

PROJECT TITLE: Introgression of strong resistance to Root Knot Nematode from the wild species *A. stenosperma* into elite peanut lines

RES. AGR. NO.: 2521RC3701320 PROJECT LEADER: D. Bertioli
GACCP Budget No.: N/A

EXPIRATION DATE: December 31, 2018 NPB CONTACT: Bob Parker/Maria Mehok
NPB Budget No.: 477

REPORT OF PROGRESS:

Broader overview of introgression of the new source of nematode resistance into peanut.

The research, which begun about six years ago, has now completed the third backcross into elite southeast USA peanut genetic background. In the initial F_2 stage, plants were selected for vigor, seed size, absence of disease in field conditions and the presence of desired genome regions. Each subsequent backcross generation has been selected using DNA markers. Two introgressed chromosome regions have been confirmed to be new sources of nematode resistance (Fig. 1).

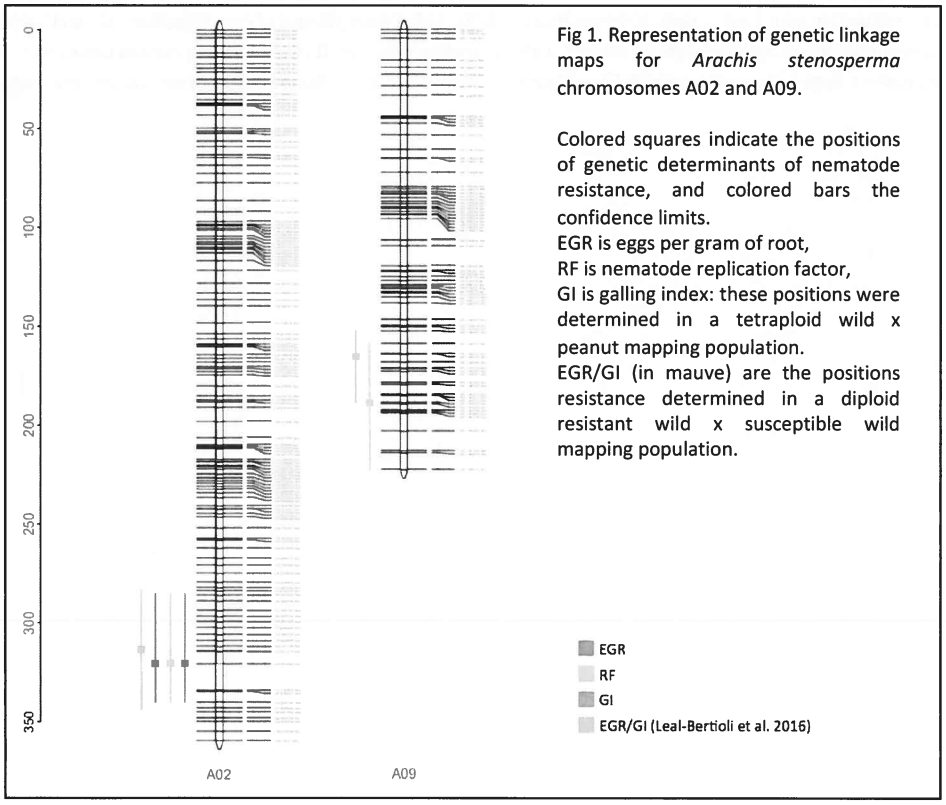

Fig 1. Representation of genetic linkage maps for *Arachis stenosperma* chromosomes A02 and A09.

Colored squares indicate the positions of genetic determinants of nematode resistance, and colored bars the confidence limits.
EGR is eggs per gram of root,
RF is nematode replication factor,
GI is galling index: these positions were determined in a tetraploid wild x peanut mapping population.
EGR/GI (in mauve) are the positions resistance determined in a diploid resistant wild x susceptible wild mapping population.

Specific project objective.

In the summer of 2018, selected BC_2F_1 plants were used as male parents for a further backcross into elite Georgia lines. Nematode assays using rooted detached leaves (Fig. 2) from these BC_2F_1 plants and controls (susceptible peanut genotypes; the resistant cultivar Tifguard; the wild species *Arachis stenosperma* and *A. batizocoi* and an induced allotetraploid derived from these two wild species) are now complete. Detached leaf assays are preferred because individual genotypes used for crossing can be assayed for nematode resistance, with biological replications, whilst, at the same time they are used as male parents for advancing backcrossing.

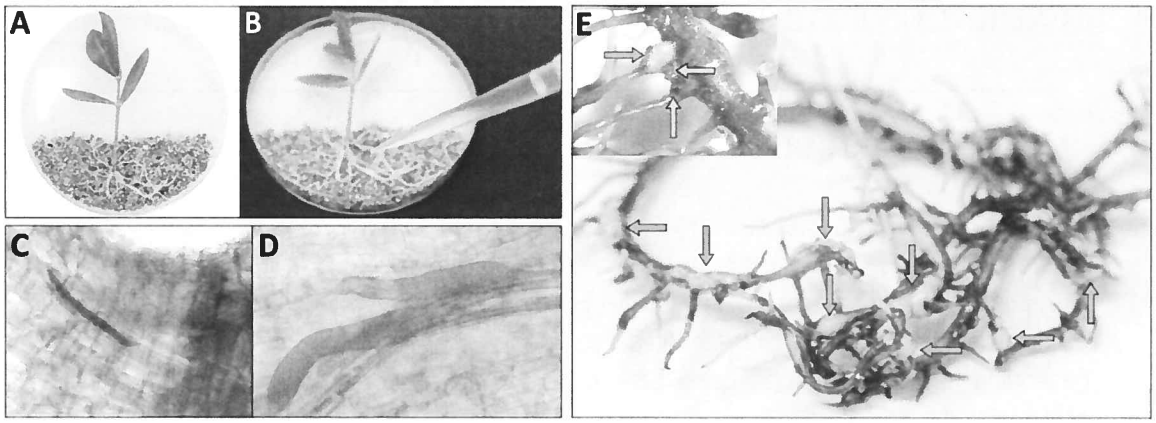

Fig 2: Overview of assay for root-knot nematode resistanceusing detached leaf bioassays. (A) Emerged roots in the detached leaves; (B) Inoculation with 1 ml of nematode solution at ~3,000 J2/ml after 30 days of root induction; (C) and (D) juvenile nematodes developing on susceptible controls, stained with cotton blue solution; (E) Galls and egg masses observed on the susceptible *A. hypogaea*. Eggs masses stained with Erioglaucine solution. Galls are indicated by green arrows and egg masses by blue arrows.

Eight, second backcross male parents, selected by DNA markers, were used as male parents in a third round of backcrossing. Seven of these male parents were completely resistant to nematodes (Fig 3).

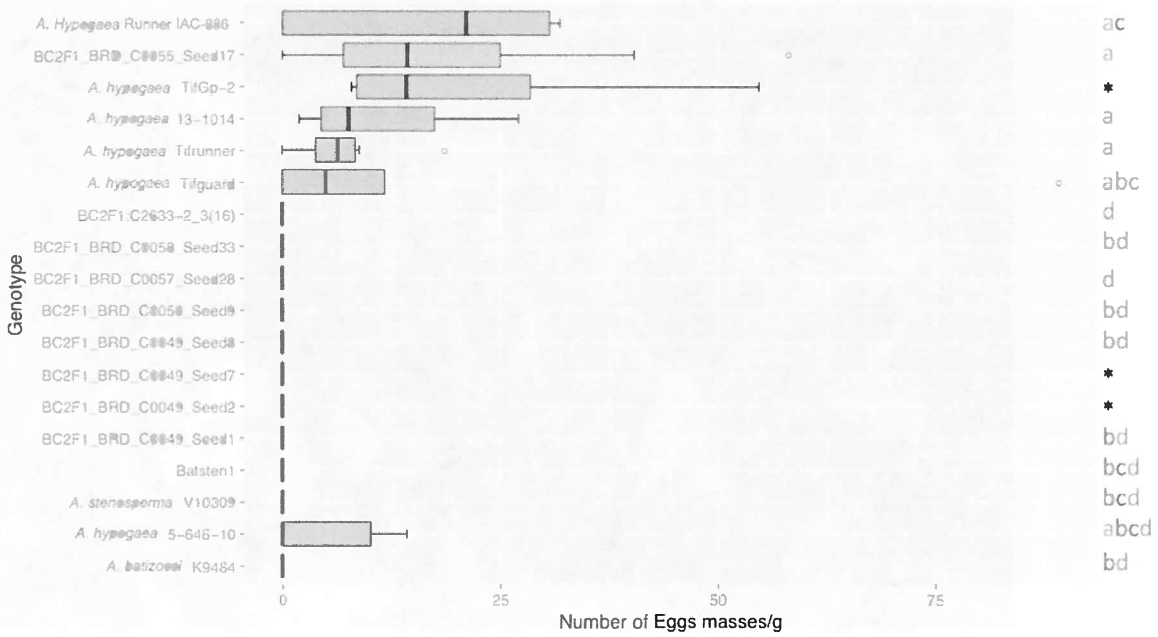

Fig 3. Egg masses per gram of root produced in assays by controls and second backcross male parents used in this year's third backcrosses (names beginning BC2F1). Black bars across boxes indicate median values. The tops and bottoms of the boxes represent the highest values recorded, and the lines are confidence limits. Genotypes with the same letter, on right hand side, do not differ significantly ($P<0.05$) (Lines with "*" were not included in statistical analysis due to incomplete data)

Over 300 potential third backcross plants are now in the greenhouse (Fig. 4). On average, they harbor about 94% elite cultivated genetic material and 6% wild. Currently we are doing DNA marker analysis, preliminary results indicate at least 200 plants are real backcrosses (and harbor wild chromosome segments). We anticipate that the plants with resistant loci on A02 and/or bottom of A09 are nematode resistant. Thus two new sources of nematode resistance will have been introduced into cultivated peanut. Since the genomic locations of these resistances are different to the resistance of Tifguard (which is at the top of A09), pyramiding resistances is possible. Further backcrossing, selection and breeding will be probably needed for cultivar release.

Fig 4. Population of BC3F1 plants in greenhouse (Spring 2019). Plants have agronomically adapted growth habits, and market-standard seed size and pod conformation. Their genetic material is about 94% USA southeastern adapted elite. Carolina Ballen, who did the genetic mapping of the resistance loci, is standing in the photo. Her PhD. stipend was partially supported from this project.