Project Title: Association Mapping DNA Markers to Leaf Spot Resistance in Cultivated Peanuts that can be used in Breeding Program (PID 388)

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The ongoing genome sequencing effort in peanut will result in numerous molecular markers that can be applied to mine valuable genes for peanut cultivar improvement. Association mapping based on linkage disequilibrium (LD) provides a more effective way to map trait loci since ancestral recombination events that occurred in natural populations present a potentially large number of alleles per locus to associate markers and traits. In-depth phenotyping of the diverse collection is likely to identify markers that can be employed by breeding programs to enrich the marker-trait detection. A diverse collection of 135 lines including mini-core, cultivars and advanced breeding lines was evaluated for leaf spot and TSWV in field plots for three years. A set of 192 SSR primers from peanut genetic linkage maps were utilized to genotype the population. Three markers named ‘pPGPseq2D12B’, ‘pPGSeq19B1’, and ‘TC04F12’, were confirmed to be associated with leaf spot and TSWV resistances. The marker ‘TC20B05’ can explain 15% phenotypical variation of leaf spot resistance. These markers could be applied in marker-assisted selection (MAS) for peanut cultivar improvement.

Publications:

Presentations at International Meeting:

Other presentations