Progress report for High Resolution Phenotyping of Diverse Peanut Lines

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Technological advances and cost reductions in DNA sequencing are accelerating genome sequencing in plant species. Peanut, as the world's fifth most important oil crop, lags behind soybean and rapeseed whose whole genome sequences are publicly available. Peanut genome sequence information is much needed not only for advancement of basic biological science but also for cultivar improvement. As of Jan 2013, a rough draft of the peanut genome sequence from cultivar Tifrunner has been generated, although considerable refinement and quality control of the assembly must be done before the sequence is released. Nevertheless, a useable version of the sequence is anticipated within the next few months. This reference sequence will facilitate the identification of sequence variation among peanut genotypes.

Allelic variation in the genome determines heritable phenotypic changes. Strong association between phenotypic change and genetic variation enables the application of genetic markers in breeding, thereby accelerating the pyramiding of desirable traits in elite cultivars and reducing the time and cost of selection. For example, converting Tifguard to a high oleic variety through marker assisted selection took only 26 months (Chu et al., 2011. The Plant Genome 4:110), approximately 1/3 the time of conventional breeding. The present bottleneck for translating genomic information to breeding will be phenotyping of parents and segregating populations. With the initiation of the Peanut Genome Project, it has become even more critical to conduct phenotypic evaluation of peanut genotypes and populations so that molecular markers can be associated with complex traits. These significant associations will enable selection for and against traits of importance to cultivar development.

An association mapping panel was generated by collaborators at USDA-ARS (Tifton), UGA, NCSU, and UF using two common (Tifrunner and Florida-07) and eight unique (NC3033, SPT 06-06, N08082olJCT, C76-16, SSD 6, Florunner, OLin, New Mexico Valencia A) parents representing the spectrum of diversity in cultivated peanut. Trait evaluation has not been systematically conducted across these parental lines, yet doing so would allow an efficient and comprehensive plan for population mapping to be developed. All ten parents were planted in the field as randomized blocks with three replicates of each line.

Field TSWV incidence was surveyed at 111 DAP (days after planting). Tifrunner, SSD 6, and N08082olJCT had significantly less disease incidence than New Mexico Valencia A, NC 3033, or C76-16. Growth habit was measured at 120 DAP. Mainstem height and lateral stem length of SSD 6 were greatest among tested genotypes in 2013, as also observed in 2012. The architecture of SSD 6 is not conducive for high yield. The greater height of the plant demands peanut pegs to travel a longer distance before reaching the soil. Yet this var. *hirsuta* genotype has been reported to have a high level of TSWV resistance. Interspecific-derived SPT 06-06 had the shortest mainstem, consistent with 2012 results, but it was not significantly shorter than Tifrunner, Florida-07, Florunner, or NC3033. There was no significant difference among genotypes for internode length.

Pod maturity tests by the hull-scrape method and image analysis revealed significant differences among genotypes and the two methods showed a good correlation with one another. Not surprisingly, New Mexico Valencia A was the earliest maturing line, showing over 70% brown/black pods at 120 DAP, followed by N08082olJCT, OLin, and C76-16. These four lines plus Florunner were not significantly different from one another in maturity by 138 DAP. SSD 6 and New Mexico Valencia A showed a significant percentage of triple-seeded pods even though total pod weight was similar to Tifrunner. Kernel weight was significantly less for SSD 6, OLin, and SPT 06-06 than Tifrunner or Florida-07. Pod fill was less for SSD 6, thus this genotype also had the lowest pod density.

Genotyping of four parents used to produce two recombinant inbred line (RIL) populations (C1799 (Tifrunner x NC3033) and C1801 (Florida 07 xSPT 06-06), on which population-scale phenotyping has been initiated) has been performed with a set of simple sequence repeat (SSR) primer pairs. For C1799, and C1801, respectively, the RIL population size is 286 and 192; polymorphic SSR primer sets: 136 and 79; primer sets used to genotype the RIL populations to date: 98 and 79. Single nucleotide polymorphism (SNP) markers are under development.