Development and Phenotyping of Recombinant Inbred Line (RIL) Populations.

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Development and phenotypic evaluation of recombinant inbred line (RIL) populations, along with molecular genotyping, will be essential for marker development. The primary objective of this research is to develop 16 structured RIL populations that can be used by the peanut research community, and to begin high-resolution phenotyping of these populations. Crosses were made using a 2 x 8 (common x unique) factorial nested association mapping design. Parents were selected to attempt to maximize genetic diversity while meeting practical breeding objectives. First, two modern runner cultivars (Tifrunner and Florida 07) were selected as common parents because runner cultivars account for about 80% of the production in the US. Second, the eight unique parents were selected to supply diversity across market classes and botanical varieties and are donor of favorable alleles for enhancing drought tolerance and resistance to most important diseases of peanut in the US. The eight unique parents are a Bailey derived high O/L breeding line, C76-16, NC 3033, SPT06-6, SSD 6, Olin, New Mexico Valencia A, and Florunner. The 16 populations were advanced using summer and winter nurseries. An update on the current status of these populations will be presented. A plan for phenotyping, including some preliminary data, will also be discussed.