First Insight into Population Structure and Linkage Disequilibrium in Peanut, and
Association Mapping of Drought Tolerance-Related Traits in the US Peanut Minicore Collection.

V. BELAMKAR, Department of Plant and Soil Science and Center for Biotechnology and Genomics, Texas Tech University, Lubbock, TX 79409; M. GOMEZ and J.L. AYERS, Texas AgriLife Research, Texas A&M System, Lubbock, TX 79403; P.R. PAYTON, Plant Stress Germplasm Development Unit, USDA-ARS, Lubbock, TX 79415; N. PUPPALA, Agricultural Sciences Center, New Mexico State University, Clovis, NM 88001; and M.D. BUROW*, Texas AgriLife Research, Texas A&M System, Lubbock, TX 79403 and Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409.

Ninety-six genotypes comprising 92 accessions of the US peanut minicore collection, diploid progenitors A. duranensis (AA) and A. ipaënsis (BB), and a component line of the cultivar Florunner and the synthetic amphidiploid accession TxAG-6 were investigated with 392 SSR marker bands amplified with 32 highly-polymorphic SSR markers. Both distance and model-based (Bayesian) cluster analysis revealed the presence of structured diversity. UPGMA analysis divided the population into four subgroups, two major subgroups representing subspecies fastigiata and hypogaea, a third containing mixed individuals, and the last containing diploid progenitors and TxAG-6. Similarly, model-based clustering identified four subgroups - fastigiata and hypogaea subspecies, a third consisting of diploid progenitors and TxAG-6, and a fourth being mixed. At the significance threshold of p≤0.01, marker loci pairs with distance <50cM, beyond 50cM, and unlinked were found in strong LD. Linkage disequilibrium stretched to a longer distance within the fastigiata subspecies, in accord with LD extending to great distances in self pollinated crops. Minicore accessions were screened for six drought tolerance-associated traits namely, SPAD chlorophyll, canopy temperature, flower count, leaf closure, plant height and width, in two environments, over two growing seasons (2007 and 2008). Unified mixed linear model (MLM) analysis incorporating population structure and kinship identified several SSR loci associated with drought tolerant traits. The current findings imply LD mapping could be an excellent tool to exploit the natural variation present in cultivated peanut.