Sixteen structured RIL populations from a 2 x 8 (common x unique) factorial nested association mapping design have been developed, and four have been advanced to F6:7 or F6:8 generations. The two common female parents are Tifrunner and Florida-07 and the unique male parents include N08082olJCT (a Bailey derived high oleic breeding line), C76-16, NC 3033, SPT 06-06, SSD 6 (PI 576638), OLin, New Mexico Valencia A, and Florunner. Twenty-four simple sequence repeat (SSR) primer pairs were applied to all parental lines, and we observed that New Mexico Valencia A was genetically most distant from the female runner-type cultivars. A group of 310 SSR primer pairs was screened against parents of Tifrunner x NC3033 and Florida 07 x SPT06-06 populations of which 129 (42%) and 87 (28%) detected polymorphism, respectively. Genotyping of both populations with SSR markers is underway. Phenotyping of late leaf spot was performed with the Florida 07 x SPT06-06 population and the disease resistance was found to be quantitatively inherited among the RIL lines. The population, Florida 07 x NC3033, has the potential to segregate for resistance to CBR according to the result of a greenhouse inoculation study. Parental lines of all populations were phenotyped for growth habit, maturity, seed germination and seed and pod traits. Significant phenotypic variation was documented among these parental lines indicating which RIL populations might be most useful for QTL mapping of these traits.