

Genetic Mapping of Yield-related Traits in Three Bi-parental Recombinant Inbred Line Populations

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Crop yield is a complex trait influenced by multiple genes. Each gene has a small quantitative effect on yield and the effect has environmental influences. Yield component traits contributing to peanut production include not only commonly measured traits such as pod/seed size, weight, maturity, seed per pod, shelling percent and harvest index but also traits describing plant architecture and phenology such as mainstem height, growth habit, canopy size, branching pattern, peg-to-pod ratio, vegetative and reproductive node numbers, time-to-flower, etc. Three recombinant inbred line populations advanced from Florida-07 x NC 3033, Tifrunner and GT-C20 reciprocal crosses, Florida-07 and ICG1471 reciprocal crosses were utilized to dissect the genetic controls of these yield component traits. Polymorphic SNP markers detected by the Axiom_*Arachis*2 SNP array were used to construct linkage maps. Total map distances were 5683 cM, 3362 cM and 4594 cM for the respective populations, and the linkage maps consisted of 27, 20 and 30 linkage groups for the three populations, respectively. These three populations were planted in the field in 2020 and 2021 to be utilized for phenotypic data collection. Multiple interval mapping of the 2020 data set identified 80 QTL regions for thirty traits from the three populations. Additional QTL mapping will be performed for 2021 data to determine stable QTL across environments.