

Characterizing a Peanut Chromosome Segment Substitution Line Population Using High Throughput Phenotyping

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Currently, high throughput genomics aided breeding is being tested in peanut research. This has been facilitated by the recent development of high quality genomic resources, a phenomenal feat considering the genetic heritage of cultivated peanut. Its recent polyploidization, self-pollinating breeding system, and domestication bottleneck have resulted in a crop with reduced diversity. To harness polymorphism from its wild relatives, a chromosome segment substitution line (CSSL) population was created via the tetraploid route to interspecific hybridization. The 58K and 48K peanut Affymetrix SNP chips were used to characterize the genetic makeup of the population. To associate the genotypic differences with specific traits, phenotype data was manually collected in 2017. In 2018, field based high throughput phenotyping (HTP) techniques were deployed to alleviate some of the drawbacks of manual phenotyping such as labor and time intensiveness. Sensors mounted on an unmanned aerial vehicle (UAV) were used to acquire data on various vegetative indices as well as canopy temperature. A combination of aerial imaging and manual scoring showed that CSSL 100, CSSL 84, CSSL 111 and CSSL 15 had remarkably low *tomato spotted wilt virus* (TSWV) incidence, a devastating disease in South Georgia. CSSL 100, CSSL 84, and CSSL 111 also performed well under early leaf spot (ELS) pressure. The vegetative indices strongly correlated with the disease scores, indicating that aerial phenotyping is a reliable way of selecting under disease pressure. In addition to being potentially resistant to foliar diseases, the latter three lines also had high plot pod yields comparable to the cultivated check Tifguard. Using a CSSL population, this study has enabled us to propose that chromosome segments from peanut wild relatives may be a potential source of valuable agronomic traits.