Analysis of a BC_3F_6 Interspecific Peanut Introgression Population Using Genome-specific SNP Markers

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Cultivated peanut is reproductively isolated from its ancestral wild species parents because of differences in ploidy and genomes, and the self pollinating nature of the peanut. There is considerably less polymorphism among cultivated peanuts than among wild species. One way of introducing genetic diversity into cultivated peanut is through hybridization with wild species. A BC_3F_6 population developed from a cross with the synthetic amphidiploid TxAG-6 [*A. batizocoi* x (*A. cardenasii* x *A. diogoi*)]^{4x} as donor and Florunner as recurrent parent has lines having high oil contents, resistance to leaf spot disease, root-knot nematodes, and rust. The aim of this study is to perform a marker analysis of the BC_3F_6 population. Genome-specific SNP-based markers were designed and used to genotype 317 BC_3F_6 individuals from this population on the Fluidigm Biomark system. Results showed that 82 out of 127 A-genome SNPs (65 %) and 64 out of the 128 B-genome SNPs (50 %), altogether averaging 58%, gave the expected theoretical Florunner to TxAG-6 segregation ratio of 15:1. Population structure analysis revealed that the population can be divided into two sub-populations (Q1 and Q2). Q2 had a higher average genetic distance and a lower F_{ST} value whilst Q1 had a lower average genetic distance and higher F_{ST} value. Neighbor joining grouped individuals into three clusters (1, 2 and 3) and showed that individuals with a higher percentage of TxAG-6 allele had longer branch length suggesting a higher level of diversity. Principal coordinate analysis produced clusters similar to neighbor joining. Comparative analysis between individuals in NJ and structure, and NJ and principal coordinates analysis explained the two-sub-populations obtained by population structure analysis.