

Identification and Validation of Wild Introgressions Affecting Pod Constriction in Peanut

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Pod constriction is considered an undesired agronomic trait affecting peanut acceptability, especially for the in-shell industry. Deep pod constriction is a trait of wild peanut species which can be observed in the progeny from cultivated x wild crosses in peanut breeding programs. The use of wild peanut relatives enables the introgression of new traits such as pest and disease resistance into elite lines, however deep pod constriction can also be incorporated due to linkage drag. Because of its agronomic undesirability, selection against this trait is crucial. The identification of wild genome segments that confer pod constriction can enable DNA marker selection to aid this process. For this, we used a BC₃F₂ backcross population (n=72) derived from a cross between cultivated peanut (*Arachis hypogaea*) and the synthetic allotetraploid BatSten1 ([*A. batizocoi* K9484 x *A. stenosperma* V10309]^(2n=4x=40)). This population was genotyped with the Axiom_Arachis v02 SNP array and was scored for pod constriction with a scale of 1-5, being 1 - very deep constriction, 2 - deep, 3 - moderate, 4 - no constriction and 5 - single pods. The association analysis performed using 419 SNPs and the phenotypic analyses done with GAPIT (v.3), allowed us to identify a significant QTL on the top of chromosome 18, derived from *A. batizocoi*. The lines with the wild segment were found to have a deeper pod constriction in comparison with lines carrying the *A. hypogaea* allele. We also identified two BC₃F₂ backcross families harboring this wild allele in a homozygous state and four with the heterozygous allele. For validation of the QTL, BC₃F₃ progenies from these families were planted in the field and the harvested seeds (BC₃F₄) were evaluated for pod constriction. We found that all progenies from the two backcross families having the wild allele in homozygous state had severely constricted pods (average pod constriction= 2.25 and 2.26 respectively) and the families did not segregate for pod constriction. In contrast, the progenies from other four backcross families which had the allele in a heterozygous state segregated for pod constriction, validating the QTL and its effect on pod constriction. KASP assays are in progress to further validate the QTL in other segregating families. These markers will be useful to accelerate the breeding process by allowing marker selection against this allele whilst maintaining other traits of interest.