Utilizing Qtlseq Pipeline to Identify Genetic Regions Linked To The Black Pod Trait.

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The peanut black pod trait has been studied at the University of Florida peanut breeding program in the recent years. Its relationship with maturity has been confirmed, nevertheless, other reasons to include the trait into commercial lines is continuously being explored. There is a need to understand more about the genetics of the trait at a molecular level. Bulk segregant analysis aided by QTLseq analysis has been used extensively to identify genomic regions controlling traits in a vast number of crops in the recent years. A population of peanuts segregating for the BP trait has been developed by crossing the BP line and FloRun '331' in 2016. After, F_1, F_2 and F_3 populations were grown in Marianna FL. DNA of F2 plants was extracted and same plants were sowed the following year in a plant to plot setting. F3 plots were evaluated as only black, white or segregating for pod coloration to confirm F2 plant's identity. Bulked DNA of F2 plants and parental DNA was sent for sequencing at RAPiD genomics. From these sequences it was possible to identify 220,714 single nucleotide polymorphisms (SNP) between the plants expressing the black pod traits and the ones expressing normal pod coloration. Using the QTLseq pipeline the SNP-index for both the black pod bulk and normal pod bulk samples was calculated. Delta SNP-index was calculating by comparing the previously calculated SNP-index of both samples. Based on delta SNP-index the analysis identified three possible regions controlling the black pod trait at a 95% confidence. G-statistics were used to improve the results, this yielded a region of 5.36 mega bases on Chromosome 20 as the responsible of the black pod trait. Effects of the SNPs within this region were analyzed, and four genes were identified as candidates for the black pod trait.