Marker Development for Blanchability in Peanuts.

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A large proportion of the global peanut crop is sold as blanched (skin removed from kernel by heating followed by abrasion) product, hence it is essential that new varieties have a high level of skin removal, or blanchability. Also, many peanut products require good skin adherence and hence development of varieties with low levels of blanchability. Recent research in Australia has shown that blanchability is under strong genetic control, with development of phenotyping methods enabling rapid and accurate assessment of blanchability on fixed lines and in single segregating plants. This opens up the possibility of development of recombinant inbred populations for genetic mapping studies aimed at developing new molecular markers for blanchability, along with identification of its gene control. A genomic study was conducted for potential marker identification for blanchability using a QTL-Seq approach. Selected fixed lines having very good and very poor blanching were selected from populations that shared the same parents (i.e. iso-lines from early maturity crosses named 'P23' and 'P13'). The poor blanching parent was 'Sutherland' and a closely related selection (D147-p3-115) while the good blanching lines were derived from parental lines 'Walter' and 'Redvale'. We bulked the DNA of the selected lines and then sequenced them. We also sequenced Walter, Redvale, Sutherland and D147-p3-115 to identify parent-specific alleles. Analysis of the parental data identified about 100,000 polymorphic SNPs where 'Walter' and 'Redvale' shared an allele and Sutherland and D147-p3-115 had a different allele. These SNPs were used to analyse the "good" and "poor" blanching bulks, with the analysis showing very good evidence for the presence of 3 Quantitative Trait Loci (QTLs), with the 2 strongest located on Chromosome B01 and A06. The third QTL was on Chromosome B08, but was not as strong and may only be a minor effect QTL. These results provide good evidence for the presence of a strong QTL, which potentially may cover the exact region where the gene(s) for blanchability reside. Further research is underway to validate these QTL regions for blanchability in a related RIL population (named 'P183'). This research should soon provide peanut breeders with molecular markers for improved selection efficiency for blanchability in global breeding programs.