Genome-Wide Association Study of Sweet, Bitter and Roasted Sensory Attributes in Cultivated Peanut

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As more consumers are paying attention to food quality and nutrients, obtaining desirable roasted sensory attributes becomes an important breeding objective for peanut. In order to find DNA- marker and the trait association for the implementation of marker-assisted selection (MAS) in breeding programs we used 120 accessions of the U.S. mini core collection for sweet, bitter and roasted peanut sensory attributes analysis and genotyped with the Affymetrix version 2.0 SNP array. A total of 90 quantitative trait loci (QTLs) were identified with phenotypic variation explained (PVE) from 9.9% to 16.7%, in which 33 QTLs are for sweet, 23 QTLs for SA, 17 QTLs for bitter, 13 QTLs for RB, 3 QTLs for WHS and 1 QTLs for DR. Of the 90 QTLs, 45 were on the A sub-genome and 45 were on the B sub-genome, which suggested that both sub-genomes played an important role in sensory attributes. In the surrounding of genomic regions of the QTLs, 16 significantly associated and 85 suggestively associated genes were found within 1 Mb windows. Most of them are known to be involved in synthesis and metabolism of carbohydrates, fats and proteins. These findings provided a promising insight into the complicated genetic architecture of quality attributes in peanut, and revealed whole-genome SNP markers of beneficial candidate genes for marker-assisted selection (MAS) in future breeding programs.