

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

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Certain roasted peanut quality sensory attributes are very important breeding objectives for peanut manufacturers and consumers. Currently the only means of measuring these traits is the use of a trained sensory panel. This is a costly and time-consuming process. It is desirable, from a cost, time and sample size perspective, to find DNA- marker and trait associations for the implementation of marker-assisted selection (MAS) in breeding programs. One hundred and thirty accessions including the U.S. mini core collection were used for sweet, bitter and roasted peanut sensory attributes analysis including tocopherols, fatty acids and sugars. A total of 17,224 high-quality single nucleotide polymorphisms (SNPs) in the whole peanut genome were revealed. Genome-wide association studies (GWAS) analysis indicated some of the markers are associated with sensory attributes, tocopherols, fatty acids and sugars. Candidate genes responsible for corresponding traits will be further analyzed in genomic regions surrounding the peak SNPs based on genomic data available on PeanutBase. These findings provide a promising insight into the complicated genetic architecture of quality attributes in peanut, and reveal whole-genome SNP markers of beneficial candidate genes for marker-assisted selection (MAS) in future breeding programs.