Marker Assisted Selection of Peanut Storage Proteins for Flavor Potential

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Roasted peanut flavor is a desirable and necessary component of economically viable cultivars in production. Currently, there are no genetic tools to allow peanut breeders to screen germplasm for flavor potential during cultivar development. Using seed samples available from the University of Georgia and the University of Florida breeding programs, and observations regarding organoleptic differences between market types, several different genotypes were selected for analysis. All seed samples were grown under similar, near optimum conditions using recommended production practices, including irrigation, to obtain high quality seed samples. The storage proteins from identified genotypes were compared by SDS-PAGE before and after roasting. Based upon protein level differences post-roasting, Arah1 and Arah2 were determined to be the most thermally reactive of the storage proteins. Primers for Arah1 and Arah2 were used to amplify DNA extracted from peanut seed for two different crop years. A separate portion, from each sample, was roasted and evaluated by expert descriptive sensory panel. The extracted PCR products were sequenced and aligned with an established control. After initial analysis of Arah1 and Arah2 sequences, it was determined that Arah1 had the greatest degree of sequence diversity with respect to the predicted flavor marker. A refined primer from Arah1 exon 4 was used to quantitatively amplify samples from a third crop year. Through, gene expression and sensory data, it was concluded that this refined primer from Arah1 exon 4 is found at a greater degree for higher scored roast peanut flavor samples.