

Proteomic Analysis of *Arachis hypogaea* Seeds from Different Maturity Classes

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Physiological maturity impacts seed quality through a variety of mechanisms including vigor, desiccation tolerance, dormancy induction, synthesis of raw materials including seed storage proteins, and reorganization of metabolism. Peanut seed development can be classified into seven classes with four incremental stages in each class. Based on the color of the mesocarp, the final three stages are commonly referred to as “orange”, “brown”, and “black”, respectively. In 2017, freshly harvested pods from one specific genotype of runner market-type peanuts grown under conventional cultural practices were obtained from the University of Georgia research facility. Pods were removed from the plant material, and ‘pod blasted’ to reveal the mesocarp. The blasted pods were separated by color into three different maturity classes, orange, brown, and black. After separation, the remainder of the pod outer layer was removed, and the seeds segregated for proteomic analysis. Raw peanuts were analyzed by bottom-up LC-MS/MS proteomics, conducted by the Proteomics Resource Center at The Rockefeller University, to identify significant protein composition differences in each maturity class. MS Data was queried against a peanut gene model (November 17, 2015) FASTA protein database with 78,603 entries using Proteome Discoverer™ Software 1.4, ThermoFisher Scientific™ / Mascot 2.4. Proteomic data revealed differentially expressed proteins as a function of maturity class. The differentially expressed proteins were classified according to function including heat shock proteins (HSPs), late embryogenesis abundant (LEA) proteins, seed storage proteins, transporter proteins, and transcriptional regulation proteins. Analysis of the proteomic data identified proteins which displayed large magnitude fold changes as well as high statistical significance changes across maturity classes.