

Profiling of differentially expressed genes critical to storage root development in hydroponically and in-vitro grown sweetpotato for space farming

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Environment is known to have significant effects on the nutrient content and quality of crop plants especially through its impact on the temporal and spatial expression of genes. Little is known about the molecular changes and harvest index in plants in response to microgravity. Sweetpotato (*Ipomoea batatas* L., Lam) is one of the most important root crops and an excellent NASA crop for space farming to provide essential nutrients to sustain human life on long-term space missions. The initiation and development of storage root formation is one of the most critical processes determining yield of sweetpotato. The molecular mechanism of storage root initiation and development in sweetpotato is poorly understood. To this end, knowledge of gravity perception, the genetic and molecular nature of the induction process of storage root, will tremendously help improve on sweetpotato harvest index for space farming. cDNA-AFLP techniques were employed to investigate temporal and spatial expressions to gain molecular insights and identify transcripts differentially expressed during early stages of sweetpotato storage root development. Two hydroponically grown cultivars using Nutrient Film Technology (NFT) and microstorage roots were evaluated. TU-82-155, an early maturing (90 DAP) with orange flesh and tinge red skin, and PI318846-3, a late maturing (135 DAP) with white flesh and off-yellow skin, were compared for differential genes expression during storage root development at 14, 21, 28, 35 and 45 DAP. Total RNA was isolated from developing storage roots from five sequential harvests of each cultivar and used to generate cDNA subjected to cDNA-AFLP techniques. Sixty-seven primer pairs were screened, of which eleven have been identified for producing Transcript Derived Fragments (TDFs) in developing storage root specific to initiation, root color change, and enlargement stages. The resulting TDFs revealed a pattern of up (19% TU-82-155 and 6% PI318846-3) and down (29% TU-82-155) regulated expressions. About 45% of TDFs in TU-82-155 and 4% PI318846-3 were transiently expressed. This study aided in identifying critical transcripts involved in root initiation and enlargement in developmental stages of both TU-82-155 and PI318846-3. TDFs are currently being characterized for function assignment of genes involved in these critical processes. These studies could be of use in further elucidating and understanding of gene expression in response

to environmental stimuli such as microgravity conditions in space farming of crops.
NASA/USDA/CSREES funded.