

Molecular characterization of genes possibly involved in storage root development in sweetpotato

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Objectives

To unravel regulatory networks involved in the storage root development processes in sweetpotato, the genes transcriptionally regulated during the storage root induction stage were previously identified. To further characterize these genes, *ibMads-box*, *ibENOD93* and *ibExpansin* were analyzed at the molecular level.

Materials and Methods

1. Plant Material : Sweetpotato (*Ipomoea batatas* cv "Jinhongmi"),
2. Methods: RNA isolation, cDNA library construction, Northern blot hybridization, Sequencing

Results and Discussion

Previously, genes possibly related to initiation of storage root development in sweetpotato were identified from early stage storage roots (0.3-1.0 cm in diameter). Northern blot analyses identified 22 differentially expressed genes in early stage storage root and fibrous root. Among these 22 genes, putative Mads-box protein gene (*ibMads-box*), ENOD93 gene (*ibENOD93*) and Expansin gene (*ibExpansin*) were further characterized. Sequence analyses of full-length cDNAs of *ibMads-box* (1011 bp) and *ibENOD93* (579 bp) revealed ORFs of 217 and 103 amino acids, respectively. *ibExpansin* was a partial cDNA (1113 bp) consisting of 199 amino acids. Northern analysis showed transcription of *ibMads-box* is strongly induced in the storage root and basal expression level was detected in fibrous root. Transcription of *ibENOD93* was also elevated in storage root while *ibExpansin* was highly expressed in leaf, petiole as well as in storage root.