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Cloning and characterization of sweetpotato MADS-box gene (*IbAGL17*) isolated from tuberous root

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Objectives

We have tried to analysis of *AGL17*-related MADS-box gene, *IbAGL17*, during sweetpotato root development.

Materials and Methods

1. Material - *Ipomoea batatas* (L.) Lam. cv. Kokei 14
2. Methods - 1) Quantitative RT-PCR and Southern hybridization. 2) Tissue Printing. 3) Single rooted leaf method

Results and discussion

New MADS-box gene, *IbAGL17*, was isolated from tuberous root from sweetpotato (*Ipomoea batatas* (L.) Lam cv. Kokei 14). That gene was expressed in vegetative tissues, especially root tissues; thicken pigmented root and tuberous root. On sequence alignment, that gene fell into the *AGL17* subfamily composed of *AGL16*, *AGL17*, *ANR1*, *NMHC5* and *DEFH125*, which share high sequence similarity. A transcript of *IbAGL17* in root and petiole was found in the vascular tissues in tissue printing. These results suggest that expression pattern of *IbAGL17* may lead to a higher proliferate potential of vegetative tissues and phase transition of sweetpotato root development.