Characterization of *IbAGL17* Related to Tuberous Root Development in Sweet Potato (*Ipomoea batatas* (L.) Lam.)

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Concerns about food shortages due to growing population is rising, so food crops are quite critical research subjects. *Ipomoea batatas* (L.) Lam. is the 7th most important food crop in the world, which roots are especially rich in starch, vitamins C and minerals. Moreover, sweet potato contains many pigments, such as anthocyanin and carotene, and grow well even in barren land. Genetically being hexaploid (2n = 6x = 96), it has large genome size (1.6 Gb). However, the information for genome analysis has not been fully studied. We identified that *IbAGL17*, a MADS-box gene isolated from the sweet potato, was strikingly expressed in thickened pigmented roots and tuberous roots. Furthermore, *IbAGL17* expressed highly on the plant from 40 days when there was rapid starch accumulation for tuberization. MADS-box transcription factors have been found to participate in not only reproductive development but also vegetative development. The coding sequence of *IbAGL17* were 657 bp and contained seven exons and six introns, composing of 219 amino acids. Evolutionally the sequence showed the highest similarity with *AtAGL21* of *Arabidopsis thaliana*, regulating auxin accumulation in lateral roots so that stimulates lateral root initiation and growth. *IbMADS1* of *Ipomoea batatas* had the next highest similarity, appeared to be related with cell proliferation and starch accumulation. Likewise, we suggest that *IbAGL17* would affect on growth of the roots like other AGL17 subfamily genes, found the regulatory roles in the root development. Particularly, sweet potato has tuberous roots working as vegetative organs and reproductive organs. It indicated that *IbAGL17* may act on the development of sweet potato tuber as MADS-box gene. This study finally would provide basic information and enlightenment about tuberization, which help increase crop yield of the sweet potato. In conclusion, it would contribute to solve the chronic global food problem.