

Trichan Piyaarphakorn 2014: Expression of *AVP1*, *EXO* and *MRB1* Members from Cassava in Potato. Master of Science (Genetics), Major Field: Genetics, Department of Genetics. Thesis Advisor: Assistant Professor Chatchawan Jantasuriyarat, Ph.D. 184 pages.

Cassava (*Manihot esculenta* Crantz.) is an important economic crop of Thailand. It produces storage roots rich in carbohydrate in the form of starch which is widely exploited in many industrial purposes in addition to its use in human and animal consumption. Recently, cassava starch has also been the source for bioethanol production in the growing renewable energy industry. This study aimed to investigate genes in the network controlling organ growth as part of the attempt to gain an understanding of the genetics underlying storage root development in cassava. Such knowledge would be directly beneficial to the varietal improvement scheme to obtain high-yielding cassava cultivars to accommodate for the continuous rise in demands. The study focused on 3 groups of genes; *AVP1*, *EXO* and *MRB1*, whose role in organ development control has been well-documented. Genome database search and evolutionary analysis using phylogenetic trees constructed from amino acid alignment have allowed for the identification of 5 cassava members of the *AVP1* and *EXO* family and 2 members of the *MRB1* family. Further investigation by study of gene expression profiles has indicated 2 genes; *MeAVP1_1* & *MeAVP1_2* in the *AVP1* family, 2 genes; *MeEXO1* & *MeEXO3*, in the *EXO* family and 1 gene; *MeMRB1* in the *MRB1* family, which are likely to play role in cassava storage root growth. Consequently, overexpression constructs were made for these candidate genes and used in genetic transformation of potato to help assess their possible function in storage organ development. Potato transgenic lines were identified by PCR analysis and transgene copy number and expression then determined by Southern blot and semi-quantitative RT-PCR respectively. Evaluation of phenotypic consequences of transgene expression will be determined in these transgenic lines. The information obtained from this study would help strengthen the knowledge platform and lead to comprehensive understanding of the regulation of cassava storage root development in the future.

Student's signature

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