



Cassava Proteome Technologies: approaches and strategies to increase starch yield and nutritional quality varieties

Songbi Chen¹, Kaimian Li¹, Luiz JCB Carvalho²

¹Tropical Crops Genetic Resources, Chinese Academy of Tropical Agricultural Sciences, Danzhou, China;

²Genetic Resources and Biotechnology, Embrapa, Brazil.

Proteomics is a leading technology for the high-throughput analysis of proteins on a genome-wide scale. It has become a major field of functional genomics. In plant it is used to find new genes, validate gene functions, evaluate the roles of transgenic plants and improve the efficiency of molecular breeding by design. Its applications are currently being extended to analyze various functional aspects of proteins such as posttranslational modifications, protein-protein interactions, activities and structures. Cassava is widely grown as a staple food and animal feed in countries of tropics and subtropics. In Asia, cassava products are for multiple uses for multiple markets. Cassava proteome technologies will provide the insight on the improvement of crop integrated breeding for starch yield and nutritional quality varieties.

In this study proteomics provides a broad view of cassava varieties at the level of proteins. It is intended to give an understanding of the technologies behind proteomics and its application to address biological questions regarding source-flux-sink interactions, high starch accumulation, nutritional-quality characteristics and etc. It was used to characterize the proteomes of source, flux and sink organs of cassava varieties. More than 2,000 protein spots in protein-expression images of cassava were analyzed and the identified proteins were classified into 14 functional groups. The results indicated the differential-protein expression and the unique metabolic pathways in starch accumulation and nutritional quality in storage roots. The cross-talking between photosynthetic pathway in leaves, signal transduction in petioles and starch-accumulation pathways in the storage roots were also discussed in the present study. These data involved proteomic evaluation of crosstalk of metabolic pathways would direct provide a guide to the improvement of cassava breeding for high starch yield and nutritional quality varieties. In addition, proteomic approach would be used to identify the cassava mutant and decrease the breeding cycles. This work may pave the way towards to evaluate cassava varieties in global protein levels, and also reveal the biological regulatory networks for cassava proteomics-assisted breeding.

Key words: Cassava, proteome technology, starch accumulation, nutritional quality.