Integrating genetic diversity, metabolites profiles, transcript profiles, and protein profile allowed identification of gene sets useful to improve storage root quality in cassava storage root.

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A research program at EMBRAPA Genetic Resources and Biotechnology exploits natural genetic variation to overcome genetic bottlenecks during domestication and to improve yield and quality of cassava storage root. Here, we integrate results genetic diversity, metabolite profiles (carotenoid synthesis), microarray-based transcript and proteomic profile to unveil complex biological and metabolic networks using diversity from landraces and F1 progeny. Based on correlation analysis, we mined candidate regulatory genes to identify putative biological pathway network that differentiate storage root phenotypes and genes coding for enzymes in carotenoid synthesis to identify putative mutations in the pathway. Proteomic profile was used to mine candidate proteins associated to carotenoid accumulation. Results from this analysis provided evidences to indicate that carotenoid metabolite revealed by HPLC profiles correlate differentially with specific expressed genes coding for enzymes such PSY, PDS and LyCb as well as with specific putative regulatory genes network with gene nodes as FLC, ABI1, JAR1, MPK4, BRI1 and ATG50240. Proteomic profile revealed that small Heat Shock Proteins (sHSP) were the most abundant protein in the carotenoid-protein complex and that HSP21 protein play major roles in the accumulation of β-carotene in cassava storage root. It was also observed that the gene coding for HSP18.1 and HSP21 are highly expressed in intense yellow root than in white.