

P0924

Amylase gene expression and genetic diversity among Amazonian sweet cassava samples

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On nutrient improvement project for staple foods requires the knowledge of the extent of genetic variation among plant cultivars. Starch accumulation in cassava roots as well as biological and functional properties are determined by a balance between biosynthesis and degradation processes. In this work we demonstrate the use of RAPD to detect and measure the genetic diversity of cassava cultivars from eastern Amazon, with distinct sweet taste, by DNA fingerprinting and evaluation of the expression for amylase gene. Nine cassava accessions were sampled to prepare DNA templates from 100mg of each young cassava leaf. RAPD was performed using twenty commercial primers and the amplified DNA samples were run in agarose gel. RAPD patterns were grouped following Pearson's coefficient that was used to construct the dendrogram. RAPD with primer OPW-12 showed that most varieties of this work, except one, showed a very similar fingerprint pattern, indicating that they were likely related. Real time RT-PCR analysis showed that the MEamy2 gene (amylase) was differentially expressed in cassava cultivars, as expected.