

Abstract:

Mangoe is one of the most important fruits of the continent of Asia and the tropical and subtropical regions of the world. In this study, genetic variation of 30 species of mango from some parts of the south of the country (Rudan, Manojan, Faryab, Jiroft, Anbarabad, Hishin, Dekhakh and Blok regions) was evaluated through the evaluation of the intergenic regions of trnH-psbA. DNA extraction was done by Dolaport method after young leaves were sampled. After PCR was performed using TrnH-psbA gene primers (IGS), PCR products were electrophoresed on 2% agarose gel and stained. Observation and shooting of amplified bands were done using duct gel. Duplicate products for sequencing and after sequencing, the sequences for each of the cultivars studied were recorded in the NCBI database. The quality of the sequences was investigated using Chromas software, and then, using the ClustalW method, MegAlign software was mapped and a dendrogram of phylogenic relationships and sequence similarity matrix was drawn to determine genetic relationships and genetic distances between genotypes. Sequence analysis showed that 361 positions were identified in the trnH-psbA bronchial region. There were 344 positions with removal and addition, among which 313 single-position and 31 polymorphic positions were recognized. There were also 17 positions without removal and addition. In the population studied, 17 Singletones were detected and 19 haplotypes were detected. Haplotype diversity index was 0.89. The homology of the sequence of the mango samples examined together represented a total sequence of 116 pairs of games among them. In this study, the ratio of dN / dS was 1.76. The results showed that about 33% of mango samples were of the same sequence and were not detectable by sequencing of trench-psbA. The cluster analysis also partially explained the variation among the mango samples. Based on this, it can be concluded that the sequencing of TrnH-psbA bone marrow for some of the inbred species diversity of the mango is inappropriate and may be more effective in studying inter-species variation and inter-species relationships. This is largely justified by the shortness of the trnH-psbA gene (about 450 pairs of games).

Keywords: Mango, Intra-species genetic variation, DNA barcoding, TrnH-psbA intergenic region.



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Graduate School
Faculty of Agriculture
Department of Plant Breeding and Biotechnology
Thesis for obtaining a Master's degree in Agricultural Engineering-Biotechnology in
Agriculture

Molecular analysis of trnH-psbA (IGS) genes of some southern mango genotypes

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Autumn 2018