

ABSTRACT

Harumanis is a premium mango cultivar widely known for its sweet taste, aroma and vibrant flesh colour. To date, the genetic identification of this mango based on multiple conserved DNA region using samples from different orchards has never been reported. The aim of this research is to identify the genetic signature of Harumanis mango at molecular level by analyzing chloroplast DNA sequences of the trnL-F and trnR-N regions. DNA samples were extracted from a total of 15 Harumanis samples collected from five selected orchards using Cetyl Trimethyl Ammonium Bromide (CTAB) extraction procedure. The extracted DNA and the PCR-amplified products were analyzed through gel electrophoresis and were then subjected to DNA Sequencing and in silico analysis. The obtained sequences were compared with the sequences available in the GeneBank. BLAST search for both the trnR-N and trnL-F regions confirmed that all the 15 samples belong to *Mangifera indica* with a 99% sequence identity. In addition, the trnL-F sequences were 99% identical to a number of specific mango cultivars such as, Tommy and Arunika. However, the trnR-N sequences were less informative as it gave hits to only two mango accessions (e.g. *Mangifera indica* voucher PDBK 2014- 0249). It is postulated that the plastid trnR-N may be a potential candidate region for the development of the Harumanis genetic signature. The results may be used to complement other molecular data for the development of a genetic barcode for Harumanis.