

Abstract

Cassava green mite (CGM) of the *Mononychellus* genus is an invasive species in Africa introduced from South America. Its genetic diversity over geographical localities has never been assessed in Kenya. We extracted DNA on internal transcribed spacer 2 (ITS2) and cytochrome oxidase subunit I (COI) and compared phylogenetic variations of CGM from the three sites in Kenya. We searched for species identify from the NCBI Genebank and found identical species nucleotide from Congo and Benin. Sequences from the three sites in Kenya were found to be 100% similar to CGM nucleotide from the Cong-Benin accessions (X79902.1) on ITS2 gene region. On COI, a 98-99% site sequences similarity was observed on *M. progresivus* accession X79901.1. The CGM race sequence from coastal Kenya was found to have the highest phylogenetic divergence from the Congo-Benin sequences. A small biogeographic genetic divergence was evident from the analyses among the sites. While the results confirm *M. progresivus* species identity in Kenya it also indicates intra-species phylogenetic variations on the COI gene region.