

Proceedings of the 2012 JKUAT Scientific, Technological and Industrialization Conference, Science Technology and Innovation for sustainable development 15th – 16th November 2012. Pg. 9-17, JKUAT, Nairobi, Kenya

PARTIAL NUCLEOTIDE SEQUENCES OF SWEET POTATO LEAF CURL VIRUS OCCURRING IN KENYA AND ITS PHYLOGENETIC RELATIONSHIP WITH OTHER MEMBERS OF BEGOMOVIRUSES

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Abstract

Sweet potato leaf curl virus has been reported in different sweet potato growing regions of Kenya. Partial nucleotide sequences of Kenyan Sweet potato leaf curl virus isolates were compared with other isolates from different parts of the world. Sequences from ORFs AV1 (in the virion sense) and ORFs AC1, AC2, and AC4 (in the complementary sense) were analyzed using OMEGA 5 software. Samples from Central, and Coast Kenya were closely related to isolates from Spain and India with nucleotide sequence identities that varied from 61 to 96%. AV1 sequences of four samples from central were related with over 92% nucleotide sequence identity. AC2 fragments of Isolates from Western and Coast had 95% and 96% nucleotide sequence identity and amino acid sequence identity respectively indicating that the AC2 protein may have had common ancestry. The study reports the first partial sequences of begomovirus infecting sweet potato inform different parts of Kenya and their phylogenetic relationship with other begomoviruses from other parts of the world.