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Genome organization and molecular variability in Sweetpotato chlorotic fleck virus

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Abstract. The complete nucleotide sequence of the genomic RNA of a Ugandan isolate of Sweetpotato chlorotic fleck virus (SPCFV) was shown to be 9104 nt. The SPCFV RNA not only is very similar in genomic organisation to that of carlaviruses but also encodes proteins that showed strong homologies with those of carlaviruses. Open reading frame (ORF) 1 codes for a 238 kDa protein with characteristic motifs of replication-associated proteins. ORFs 2, 3 and 4 code for proteins of 27.5, 11.5, and 7.3 kDa, respectively, that form the multifunctional triple gene block proteins. ORF 5 encodes the capsid protein (CP) of 33 kDa and ORF 6 a 15-kDa protein with a nucleic acid binding zinc finger motif (NBP). Comparison with other carlaviruses showed 12-40% similarities. Based on CP sequences, the closest relatives of SPCFV among carlaviruses are Shallot latent virus (36.2%) and Kalanchoe latent virus (37.1%). However, the SPCFV genome (9.1 kb) differs from typical carlaviruses (7.4 - 8.5 kb) by being considerably larger as a result of a larger ORF 1 (238 vs. 200-223 kDa) and a long untranslated region between ORF 4 and 5 (213 vs. ca. 34 nt for Potato virus M). To obtain a better understanding of the molecular variability of the SPCFV genome, about 2000 nts of the 3' terminal genome part of a range of geographically diverse isolates were sequenced. Comparison of the deduced amino acid sequences revealed a considerable level of geographically associated diversity among SPCFV isolates. The CP and NBP amino acid sequence similarities ranged from 88 to 100 % and from 75 to 99%, respectively. In phylogenetic analysis of CP amino acid sequences, a major East African cluster with 92-99% intragroup identity and a non-East African cluster with 88-91% intragroup identity became evident.