6.15 Detection and Phylogenetic Analysis of Potyviruses Associated with Some Important Crops in Sudan.

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A survey was conducted to identify and evaluate the genetic variability among Potyvirus species infecting some vegetables crops grown in Sudan. A total of 200 symptomatic leaf samples were tested for infection using serological as well as Reverse Transcription-Polymerase Chain Reaction (RT-PCR) assays. For RT-PCR technique, both degenerate genus- and species-specific primers were utilized. New primers were also designed based on known conservative regions in the potyviral genome and proved to be highly specific for Potyvirus species detection. Five viral species were identified: Leek yellow stripe virus (LYSV), Onion yellow dwarf virus (OYDV), Potato virus Y (PVYNTN, PVYN-Wi), Zucchini yellow mosaic virus (ZYMV) and Papaya ringspot virus-P (PRSV-P). However, the latter was reported for the first time in Sudan. Partial nucleotide sequences of different viral genomic regions have been deposited in international GenBank (NCBI), translated into amino acid sequences and matched with the GenBank database using the ExPASy online translation tool. Phylogenetic analysis of Potato and Garlic viruses revealed that some Sudan’s isolates (PVY, LYSV and OYDV) were significantly divergent from those retrieved from the GenBank in their partial coat protein genomic regions. However, phylogenetic analysis of PRSV-P and ZYMV did not reveal such a significant divergence. The approaches and protocols developed in this study provide a baseline for developing a strong protection strategy against Potyvirus diseases in Sudan.