

Characterization and variability of sweetpotato virus Y, a hitherto unrecognized potyvirus infecting sweetpotato in Southern Africa

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Abstract. The biological and molecular properties of a sweetpotato virus isolate formerly known as sweetpotato virus 2 were determined. The virus had flexuous filamentous particles, induced cylindrical inclusions in infected cells and was experimentally transmitted by *Myzus persicae*. Sequence analysis of its coat protein and 3' non-translated region revealed that the virus is a distinct potyvirus, for which the name Sweetpotato virus Y (SPVY) is proposed. *Sweetpotato chlorotic stunt crinivirus* (SPCSV) synergized SPVY in *Ipomoea setosa* in mixed infections. Unlike plants that were infected only with SPVY or a Kenyan isolate (KY-38) of SPCSV and largely showed no symptoms, dually infected plants had significantly higher titres and a more uniform distribution of SPVY and showed conspicuous symptoms of SPVY infections. Comparisons of coat protein CP gene sequences of geographically diverse isolates of SPVY revealed amino acid sequence identities ranging from 86 to 100%. The results strongly suggest the existence of biologically and genetically diverse strains of SPVY from Southern Africa.