



Maximum likelihood phylogenetic tree of partial nucleotide sequences amplified from yam potexviruses using primers YamX-3F and YamX-5R. Previously reported sequences of the same region (208 nt) in the genomes of YVX, yam potexvirus 1 and yam potexvirus 2 were included as references. Evolutionary distances were computed using the HKY model [43]. Bootstrap values of 1,000 replicates are shown at nodes when above 70%. Black triangles represent the sequences generated in this study and the corresponding domain of the YVX complete genome is indicated by a black circle. Accession numbers are provided and the scale bar shows the number of substitutions per base.

- 43 Hasegawa, M.; Kishino, H.; Yano, T. Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *J. Mol. Evol.* 1985, 22, 160–174.