



"Multiple alignments of HSVd sequences were obtained using ClustalW(Thompson et al., 1994). The alignment was corrected manually to maximize sequence homology. Phylogenetic analyses were performed using the following programs of the PHYLIP 3.5c package (Felsenstein, 1993). DNADIST was used to calculate genetic distances, NEIGHBOUR (UPGMA or neighbour-joining methods) to cluster the variants from the distance data, DRAWTREE to draw the resulting phylogenetic tree and SEQBOOT (100 repetitions) and CONSENSE to perform bootstrap analysis."

