

Genetic relationships of Italian SVD viruses isolated during 2005-2007 to other SVD viruses

Mid-point-rooted Neighbor-joining tree using MEGA 3.1. Based on a comparison of complete (or nearly complete) VP1 sequences. This is part of the tree shown on page 1.

Software: MEGA 3.1
 No. of Taxa : 217
 Data File : N:\evd\MEG\db\SVDV\1D\ITL2007a.meg
 Data Title : SVDV VP1
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 Method : Neighbor-Joining
 Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
 Include Sites : =====
 Gaps/Missing Data : Pairwise Deletion
 Codon Positions : 1st+2nd+3rd+Noncoding
 Substitution Model : =====
 Model : Nucleotide: Kimura 2-parameter
 Substitutions to Include : d: Transitions + Transversions
 Pattern among Lineages : Same (Homogeneous)
 Rates among sites : Uniform rates
 No. of Sites : 849
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

N.J. Knowles & Ginette Wilden, 18 June 2007

