

Genetic relationship of SVDV Portugal 5/2007 to other SVDV 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 : 218
 Data File : n:\evd\meg\db\sdrv\1d\POR2007a.meg
 Data Title : SVDV POR/5/2007 VP1
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 Method : Neighbor-Joining
 Phylogeny Test and options : Bootstrap (1000 replicates; seed=5671)
 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% or greater are shown

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