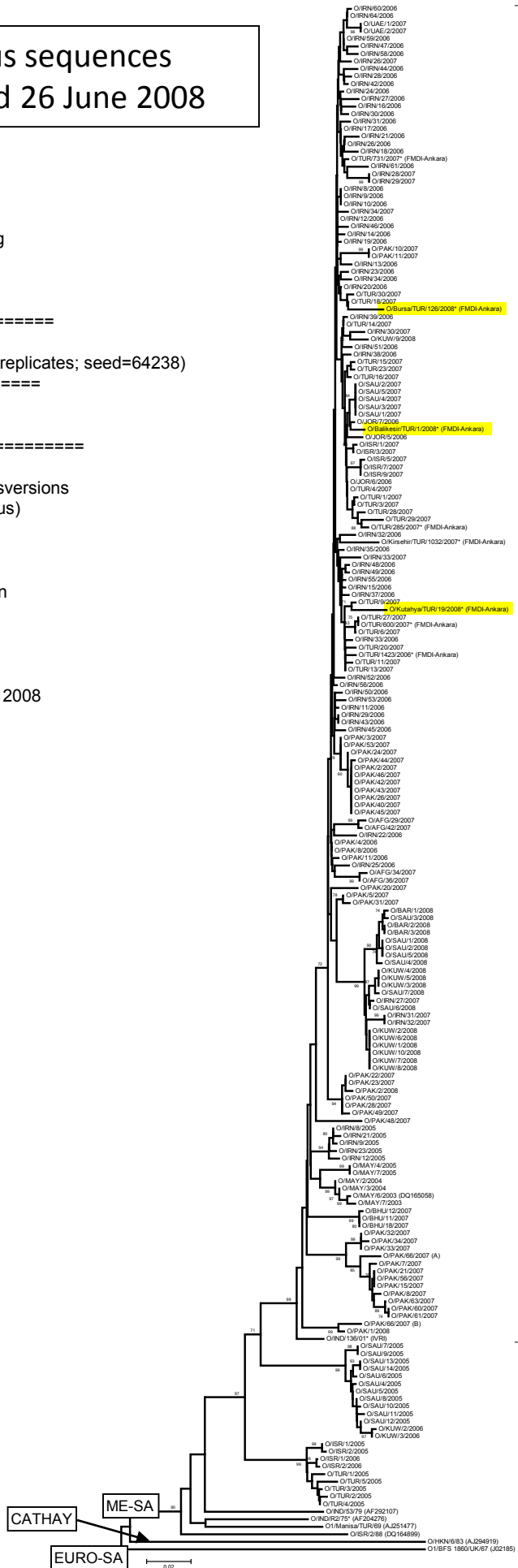


Report on FMD type O virus sequences from FMDI-Ankara received 26 June 2008

No. of Taxa : 206
 Data File : n:\evd\meg\db\fmdv\o\tUR2008a.meg
 Data Title : Turkey 2008 (FMDI-Ankara)
 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 : 639
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and less are shown

* , not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Ebert, 26 June 2008



PanAsia-2

PanAsia

Report on FMD type O virus sequences from FMDI-Ankara received 26 June 2008 (only the PanAsia-2 lineage is shown)

No. of Taxa : 206
 Data File : n:\levd\meg\db\fmdv\o\tur2008a.meg
 Data Title : Turkey 2008 (FMDI-Ankara)
 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 : 639
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and less are shown

* , not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Ebert, 26 June 2008

