

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Date: 8 January 2010

FMDV type A

Country: Republic of Korea (South Korea)

Period: 2010

No. of isolates: 1 (VP1 sequence only)

BATCH: n/a



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Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: A WRL Ref No: none Sender Ref: A/Pochun/KOR/2010 Date collected: 07/01/2010 (before 4 am) Date received by WRLFMD: 08/01/2010 Species: Cattle Material used: Clinical material Region sequenced: VP1 RT-PCR primers: Not known No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636	Report date: 08/01/2010 Reported by: N.J. Knowles Checked by: J.M. Hammond Topotype: ASIA Genotype/strain: none designated Sequence filename: SKR10-AA.SEQ Date sequence last updated: 08/01/2010 Total no. of comparisons: 1202 Min. no. of nt for comparison: 300 Total turn-around time: 0 days Sequencing time: n/a																																																																																								
Comments: VP1 sequence received from the National Veterinary Research and Quarantine Service, Anyang, Gyeonggi 430-824, Republic of Korea.																																																																																									
Ten Most Closely Related Viruses																																																																																									
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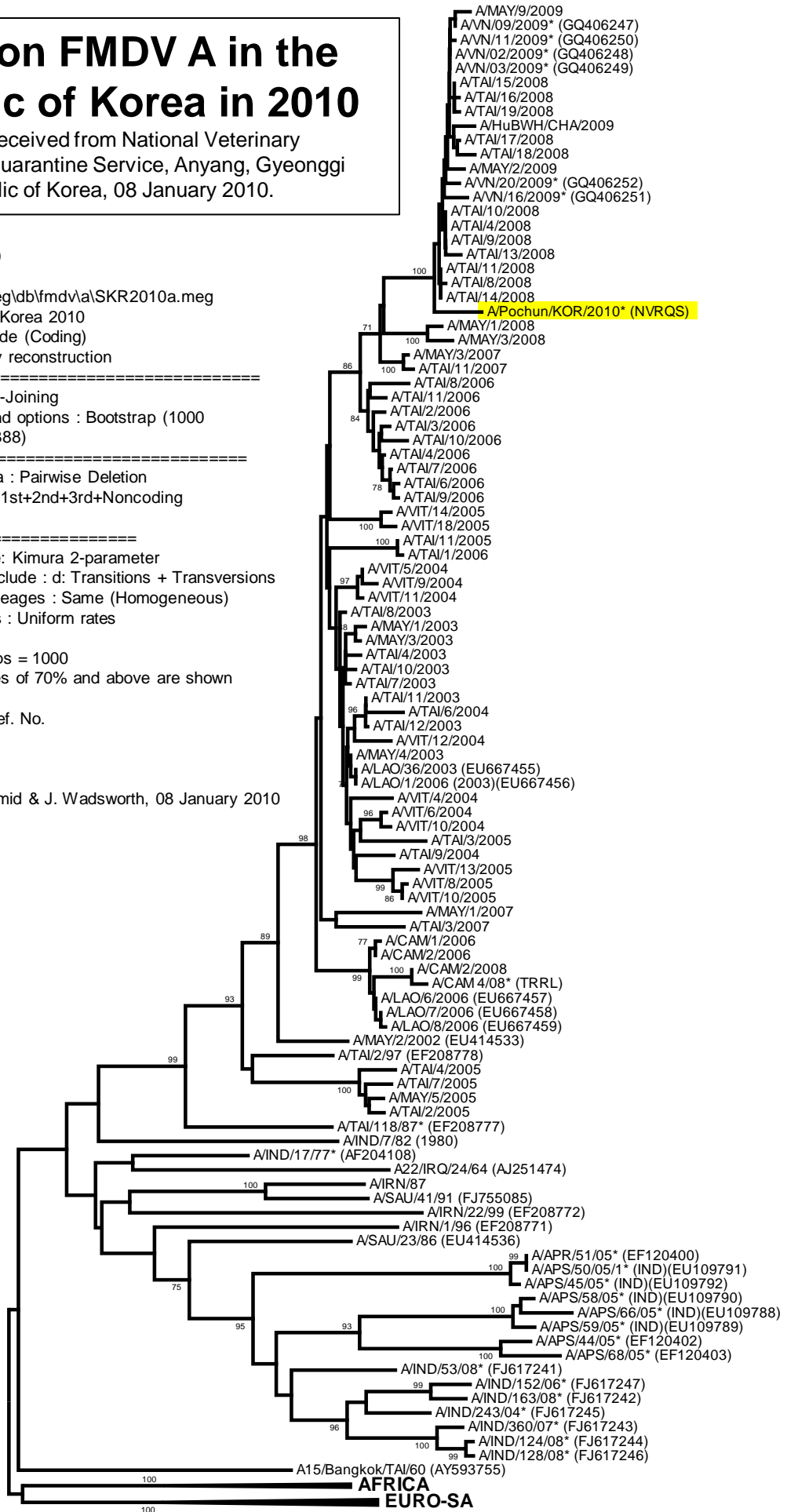
Report on FMDV A in the Republic of Korea in 2010

VP1 sequence received from National Veterinary Research and Quarantine Service, Anyang, Gyeonggi 430-824, Republic of Korea, 08 January 2010.

Software: MEGA 4.0
 No. of Taxa : 108
 Data File : n:\levd\meg\db\fmdv\A\SKR2010a.meg
 Data Title : A South Korea 2010
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=57388)
 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 : 642
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, F. Hamid & J. Wadsworth, 08 January 2010



ASIA

AFRICA
EURO-SA

0.02