

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

## Genotyping Report

Date: 4 July 2010

FMDV type O

Country: Kazakhstan

Period: 2010

No. of isolates: 1

VP1 sequence received from the All-Russian Research Institute  
for Animal Health (ARRIAH), Vladimir, Russian Federation.



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# FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: O	Report date: 04/07/2010
WRLFMD Ref No: none	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: Kazakhstan-2010 sample-1	
Location: Not known, Kazakhstan	Topotype: ME-SA
Date collected: 2010	Genotype/strain: PanAsia-2
Date received by WRLFMD: 02/07/2010	Sequence filename: KAZ10-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 04/07/2010
Species: Not known	No. of Nt determined: 639
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: Not known	Total no. of comparisons: 2477
	Min. no. of nt for comparison: 300
	Total turn-around time: 2 days
	Sequencing time: n/a
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/56/2006	IRN06-56	639	624	0	97.65	2.35	ME-SA	PanAsia-2
2	O/KAZ/2007 (ARRIAH)	KAZ07-AA	639	624	0	97.65	2.35	ME-SA	PanAsia-2
3	O/PAK/10/2006	PAK06-10	639	624	0	97.65	2.35	ME-SA	PanAsia-2
4	O/PAK/10/2006 (EF494503)	PAK06-AE	639	624	0	97.65	2.35	ME-SA	PanAsia-2
5	O/PAK/16/2006	PAK06-16	639	624	0	97.65	2.35	ME-SA	PanAsia-2
6	O/PAK/4/2006	PAK06-04	639	624	0	97.65	2.35	ME-SA	PanAsia-2
7	O/PAK/4/2006 (EF494500)	PAK06-AB	639	624	0	97.65	2.35	ME-SA	PanAsia-2
8	O/PAK/6/2006	PAK06-06	639	624	0	97.65	2.35	ME-SA	PanAsia-2
9	O/PAK/6/2006 (EF494501)	PAK06-AC	639	624	0	97.65	2.35	ME-SA	PanAsia-2
10	O/PAK/8/2006	PAK06-08	639	624	0	97.65	2.35	ME-SA	PanAsia-2
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/8/2005	IRN05-08	639	614	0	96.09	3.91	ME-SA	PanAsia-2
2	O/UKG/35/2001 (AJ539141)	UKG01-35	639	595	0	93.11	6.89	ME-SA	PanAsia
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	582	0	91.08	8.92	ME-SA	Ind-2001a
4	O/OMN/7/2001 (DQ164941)	OMN01-07	639	576	0	90.14	9.86	ME-SA	Ind-2001b
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	575	0	89.98	10.02	ME-SA	Pak-98
6	O/IRN/61/2001 (DQ164896)	IRN01-61	638	573	1	89.81	10.19	ME-SA	Irn-2001
7	O/BHU/3/2009	BHU09-03	639	573	0	89.67	10.33	ME-SA	Ind-2001d
8	O/UAE/4/2008	UAE08-04	636	568	0	89.31	10.69	ME-SA	Ind-2001c
9	O/IND/53/79 (AF292107)	IND79A53	639	569	0	89.05	10.95	ME-SA	unnamed
10	O/IND/R2/75* (AF204276)	IND75--A	639	563	0	88.11	11.89	ME-SA	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v3.1

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# Report on FMDV O in Kazakhstan in 2010

VP1 sequence received from ARRIAH, Russian Federation, 02/07/2010.

Software: MEGA 4.0

No. of Taxa : 297

Data File : n:\evd\meg\db\fmvd\o\KAZ2010a.meg

Data Title : O Kazakhstan 2010

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=29599)

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

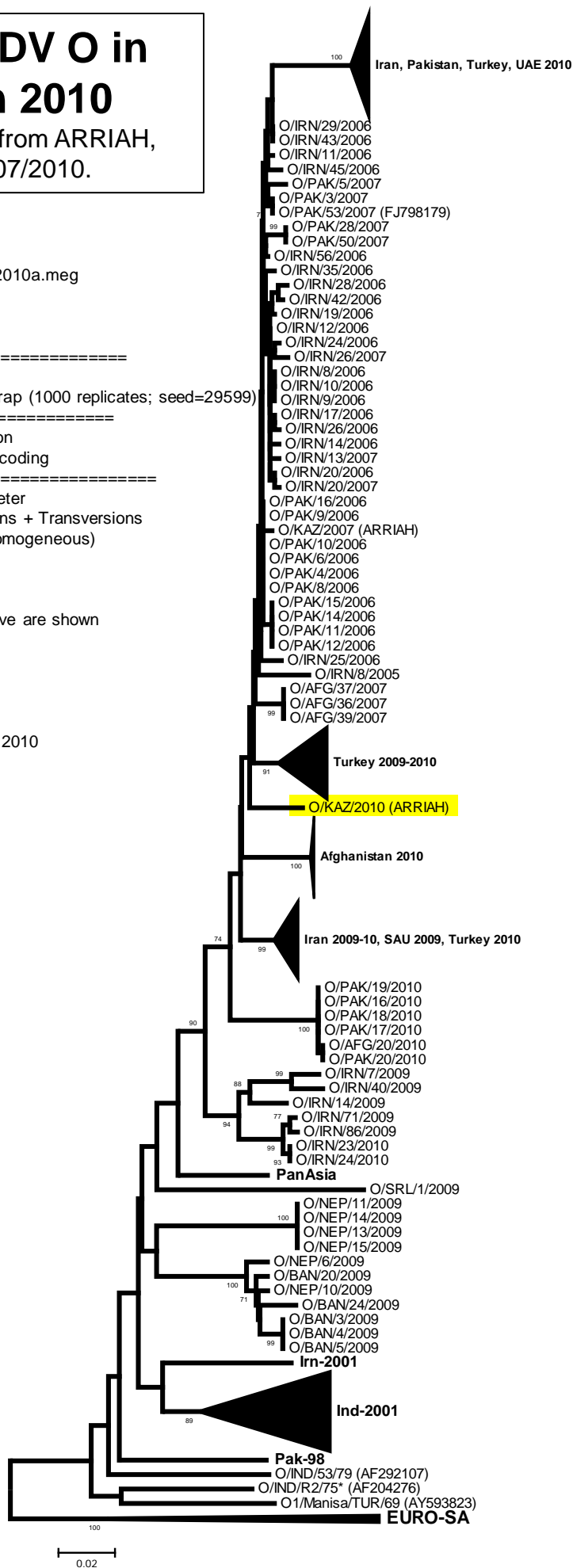
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 04 July 2010

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PanAsia-2

ME-SA

0.02