

Serotype: O	Report date: 11/02/2008						
WRL Ref No: BAR/1/2008							
Sender Ref: none							
Date collected: 08/01/2008							
Date received by WRLFMD: 29/01/2008	Topotype: ME-SA						
Date received for sequencing: 04/02/2008	Genotype/strain: PanAsia 2						
Species: Cattle	Sequence filename: BAR08-01.SEQ						
Material used: BTy1	Date sequence last updated: 08/02/2008						
Region sequenced: VP1	Total no. of comparisons: 1704						
RT-PCR primers: O-1C244F/EUR2B-52R; O-1C272F/EUR2B-52R	Min. no. of nt for comparison: 300						
No. of Nt determined: 639	Total turn-around time: 13 days						
No. of ambiguities: 0	Sequencing time: 7 days						
Gene length: 639							
Comments:							
<b>Ten Most Closely Related Viruses</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/BAR/2/2008	BAR08-02	639	637	0	99.69	0.31
2	O/BAR/3/2008	BAR08-03	639	637	0	99.69	0.31
3	O/IRN/27/2007	IRN07-27	639	631	0	98.75	1.25
4	O/IRN/31/2007	IRN07-31	639	628	0	98.28	1.72
5	O/IRN/32/2007	IRN07-32	639	628	0	98.28	1.72
6	O/PAK/5/2007	PAK07-05	638	622	1	97.49	2.51
7	O/PAK/31/2007	PAK07-31	637	620	2	97.33	2.67
8	O/PAK/10/2006	PAK06-10	639	621	0	97.18	2.82
9	O/PAK/16/2006	PAK06-16	639	621	0	97.18	2.82
10	O/PAK/4/2006	PAK06-04	639	621	0	97.18	2.82
<b>Relationships to Reference Virus Strains</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAW/2/99	TAW99-02	639	594	0	92.96	7.04
2	O/IND/53/79 [AF292107]	IND79A53	639	566	0	88.58	11.42
3	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	562	0	87.95	12.05
4	O/IND/R2/75* [AF204276]	IND75--A	639	558	0	87.32	12.68
5	O/ISR/2/88 (DQ164899)	ISR88-02	639	547	0	85.6	14.4
6	O/TAI/189/87* [TRRL]	TAI87-AC	639	547	0	85.6	14.4
7	O/MOR/1/91	MOR91-01	639	543	0	84.98	15.02
8	O/PHI/5/95 (DQ164946)	PHI95-05	639	525	0	82.16	17.84
9	O/HKN/6/83	HKN83-06	637	515	2	80.85	19.15
10	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	508	0	79.5	20.5
nt, nucleotides							
*, not a WRLFMD reference number							

Serotype: O  
WRL Ref No: BAR/2/2008  
Sender Ref: none  
Date collected: 08/01/2008  
Date received by WRLFMD: 29/01/2008  
Date received for sequencing: 04/02/2008  
Species: Cattle  
Material used: BTy1  
Region sequenced: VP1  
RT-PCR primers: O-1C244F/EUR2B-52R;  
O-1C272F/EUR2B-52R  
No. of Nt determined: 639  
No. of ambiguities: 0  
Gene length: 639

Report date: 11/02/2008  
Topotype: ME-SA  
Genotype/strain: PanAsia 2  
Sequence filename: BAR08-02.SEQ  
Date sequence last updated: 08/02/2008  
Total no. of comparisons: 1704  
Min. no. of nt for comparison: 300  
Total turn-around time: 13 days  
Sequencing time: 7 days

Comments:

### Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/BAR/3/2008	BAR08-03	639	639	0	100	0
2	O/BAR/1/2008	BAR08-01	639	637	0	99.69	0.31
3	O/IRN/27/2007	IRN07-27	639	631	0	98.75	1.25
4	O/IRN/31/2007	IRN07-31	639	628	0	98.28	1.72
5	O/IRN/32/2007	IRN07-32	639	628	0	98.28	1.72
6	O/PAK/5/2007	PAK07-05	638	622	1	97.49	2.51
7	O/PAK/10/2006	PAK06-10	639	622	0	97.34	2.66
8	O/PAK/16/2006	PAK06-16	639	622	0	97.34	2.66
9	O/PAK/4/2006	PAK06-04	639	622	0	97.34	2.66
10	O/PAK/6/2006	PAK06-06	639	622	0	97.34	2.66

### Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAW/2/99	TAW99-02	639	595	0	93.11	6.89
2	O/IND/53/79 [AF292107]	IND79A53	639	566	0	88.58	11.42
3	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	564	0	88.26	11.74
4	O/IND/R2/75* [AF204276]	IND75--A	639	560	0	87.64	12.36
5	O/ISR/2/88 (DQ164899)	ISR88-02	639	549	0	85.92	14.08
6	O/TAI/189/87* [TRRL]	TAI87-AC	639	548	0	85.76	14.24
7	O/MOR/1/91	MOR91-01	639	545	0	85.29	14.71
8	O/PHI/5/95 (DQ164946)	PHI95-05	639	524	0	82	18
9	O/HKN/6/83	HKN83-06	637	514	2	80.69	19.31
10	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	510	0	79.81	20.19

nt, nucleotides

\*, not a WRLFMD reference number

Serotype: O  
WRL Ref No: BAR/3/2008  
Sender Ref: none  
Date collected: 08/01/2008  
Date received by WRLFMD: 29/01/2008  
Date received for sequencing: 04/02/2008  
Species: Cattle  
Material used: BTy1  
Region sequenced: VP1  
RT-PCR primers: O-1C244F/EUR2B-52R;  
O-1C272F/EUR2B-52R  
No. of Nt determined: 639  
No. of ambiguities: 0  
Gene length: 639

Report date: 11/02/2008  
Topotype: ME-SA  
Genotype/strain: PanAsia 2  
Sequence filename: BAR08-03.SEQ  
Date sequence last updated: 08/02/2008  
Total no. of comparisons: 1704  
Min. no. of nt for comparison: 300  
Total turn-around time: 13 days  
Sequencing time: 7 days

Comments:

### Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/BAR/2/2008	BAR08-02	639	639	0	100	0
2	O/BAR/1/2008	BAR08-01	639	637	0	99.69	0.31
3	O/IRN/27/2007	IRN07-27	639	631	0	98.75	1.25
4	O/IRN/31/2007	IRN07-31	639	628	0	98.28	1.72
5	O/IRN/32/2007	IRN07-32	639	628	0	98.28	1.72
6	O/PAK/5/2007	PAK07-05	638	622	1	97.49	2.51
7	O/PAK/10/2006	PAK06-10	639	622	0	97.34	2.66
8	O/PAK/16/2006	PAK06-16	639	622	0	97.34	2.66
9	O/PAK/4/2006	PAK06-04	639	622	0	97.34	2.66
10	O/PAK/6/2006	PAK06-06	639	622	0	97.34	2.66

### Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAW/2/99	TAW99-02	639	595	0	93.11	6.89
2	O/IND/53/79 [AF292107]	IND79A53	639	566	0	88.58	11.42
3	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	564	0	88.26	11.74
4	O/IND/R2/75* [AF204276]	IND75--A	639	560	0	87.64	12.36
5	O/ISR/2/88 (DQ164899)	ISR88-02	639	549	0	85.92	14.08
6	O/TAI/189/87* [TRRL]	TAI87-AC	639	548	0	85.76	14.24
7	O/MOR/1/91	MOR91-01	639	545	0	85.29	14.71
8	O/PHI/5/95 (DQ164946)	PHI95-05	639	524	0	82	18
9	O/HKN/6/83	HKN83-06	637	514	2	80.69	19.31
10	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	510	0	79.81	20.19

nt, nucleotides

\*, not a WRLFMD reference number

# Report on FMD type O viruses from Bahrain in 2008

No. of Taxa : 184

Data File : n:\evd\meg\db\fmdv\o\BAR2008a.meg

Data Title : Bahrain 2008

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

Method : Neighbor-Joining

Phylogeny Test and options : Bootstrap (1000 replicates; seed=64843)

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, 11 February 2008

