

Serotype: O	Report date: 05/08/2008
WRL Ref No: NIG/1/2007	Reported by: N.J. Knowles
Sender Ref: VRD/07/518	Checked by: D.P. King
Date collected: 01/09/2007	
Date received by WRLFMD: 20/05/2008	Topotype: EA-3
Date received for sequencing: 09/06/2008	Genotype/strain: none designated
Species: Cattle	Sequence filename: NIG07-01.SEQ
Material used: BTy1	Date sequence last updated: 09/07/2008
Region sequenced: VP1	Total no. of comparisons: 1768
RT-PCR primers: O-1C244F/EUR-2B52R;	Min. no. of nt for comparison: 300
O-1C272F/EUR-2B52R;	Total turn-around time: 77 days
O-1C283F/EUR-2B52R	Sequencing time: 57 days
No. of Nt determined: 639	
No. of ambiguities: 0	
Gene length: 639	

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/SUD/3/2005	SUD05-03	639	621	0	97.18	2.82
2	O/SUD/1/2005	SUD05-01	639	620	0	97.03	2.97
3	O/SUD/2/2005	SUD05-02	639	620	0	97.03	2.97
4	O/SUD/14/2004	SUD04-14	639	615	0	96.24	3.76
5	O/SUD/15/2004	SUD04-15	639	615	0	96.24	3.76
6	O/SUD/4/2004	SUD04-04	639	615	0	96.24	3.76
7	O/SUD/1/2004	SUD04-01	639	614	0	96.09	3.91
8	O/SUD/16/2004	SUD04-16	639	614	0	96.09	3.91
9	O/SUD/25/2004	SUD04-25	639	614	0	96.09	3.91
10	O/SUD/26/2004	SUD04-26	639	614	0	96.09	3.91

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 (AJ294927)	TAW99-02	639	544	0	85.13	14.87
2	O/ISR/2/88 (DQ164899)	ISR88-02	639	543	0	84.98	15.02
3	O/MOR/1/91	MOR91-01	639	542	0	84.82	15.18
4	O/IND/53/79 [AF292107]	IND79A53	639	541	0	84.66	15.34
5	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	539	0	84.35	15.65
6	O/IND/R2/75* [AF204276]	IND75--A	639	535	0	83.72	16.28
7	O/TAI/189/87* [TRRL]	TAI87-AC	639	530	0	82.94	17.06
8	O/PHI/5/95 (DQ164946)	PHI95-05	639	508	0	79.5	20.5
9	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	507	0	79.34	20.66
10	O/HKN/6/83 (AJ294919)	HKN83-06	637	504	2	79.12	20.88

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV O from Nigeria in 2007

Software: MEGA 4.0
 No. of Taxa : 141
 Data File : n:\evd\meg\db\fmv\o\SOM2007a.meg
 Data Title : FMDV O
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates;
 seed=16245)
 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, K. Ebert & J. Wadsworth,
 5 August 2008

