

**Report from the Molecular Epidemiology Section of the Experimental Epidemiology Group to the
Head of the World Reference Laboratory for FMD (Non-QAU Form)**

Serotype: O	Date: 08/06/2003						
Virus isolate: KEN/3/2002	Reported by: N.J. Knowles						
Material used: RS1	Signed (file copy only):						
Region sequenced: VP1	Seq. filename: KEN02-03						
RT-PCR primer set: O-1C272F/NK61							
Topotype: East Africa 2 (EA-2)	No. of ambiguities: 2						
Genotype/strain:	Date seq. last updated: 05/04/2003						
No. of nt determined / no. in gene: 637 / 639	Total no. of comparisons made: 1304						
<p>Comments: This virus is a representative of a newly recognised topotype – East Africa 2 (EA-2). It appears that members of this topotype have, in the past, recombined with viruses of the Middle East-South Asia (ME-SA) topotype with a cross-over point somewhere in the 3' half of the VP1 gene. This makes it difficult, if not impossible, to distinguish the two topotypes when only sequences at the 3' end of VP1 are compared, e.g. the viruses shown below in italics (IND, SAU & TUR) are probably members of the ME-SA topotype.</p>							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	UG 5/02/O* (Onderstepoort)	UGA02-AA	489	464	1	94.89	5.11
2	UG 11/02/O* (Onderstepoort)	UGA02-AB	495	468	0	94.55	5.45
3	<i>O/IND/146/99*</i>	<i>IND99-AC</i>	<i>156</i>	<i>147</i>	<i>9</i>	<i>94.23</i>	<i>5.77</i>
4	<i>O/SAU/76/94</i>	<i>SAU94-76</i>	<i>152</i>	<i>143</i>	<i>1</i>	<i>94.08</i>	<i>5.92</i>
5	<i>O/TUR/5/90</i>	<i>TUR90-05</i>	<i>156</i>	<i>146</i>	<i>9</i>	<i>93.59</i>	<i>6.41</i>
6	<i>O/TUR/5/97</i>	<i>TUR97-05</i>	<i>156</i>	<i>146</i>	<i>1</i>	<i>93.59</i>	<i>6.41</i>
7	O/KEN/18/98	KEN98-18	384	359	17	93.49	6.51
8	<i>O/TUR/19/91</i>	<i>TUR91-19</i>	<i>166</i>	<i>155</i>	<i>2</i>	<i>93.37</i>	<i>6.63</i>
9	<i>O/TUR/18/90</i>	<i>TUR90-18</i>	<i>165</i>	<i>154</i>	<i>3</i>	<i>93.33</i>	<i>6.67</i>
10	O/UGA/3/2002	UGA02-03	636	593	3	93.24	6.76
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/MOR/1/91	MOR91-01	207	175	3	84.54	15.46
2	O/IND/53/79	IND79A53	637	534	2	83.83	16.17
3	O/IND/R2/75*	IND75--A	637	533	2	83.67	16.33
4	O/ISR/1/88	ISR88-01	193	161	5	83.42	16.58
5	O/TAW/2/99	TAW99-02	637	530	2	83.20	16.80
6	O1/Manisa/TUR/69	TUR69--E	637	527	2	82.73	17.27
7	O/TAI/189/87*	TAI87--B	527	431	3	81.78	18.22
8	O/PHI/5/95	PHI95-05	516	408	6	79.07	20.93
9	O/HKN/6/83	HKN83-06	635	502	4	79.06	20.94
10	O1/BFS 1860/UK/67	UKG67--A	637	502	2	78.81	21.19
nt, nucleotides							
*, not a WRLFMD reference number							

cc. Head of Experimental Epidemiology Group
cc. Head of Vesicular Diseases Group

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Head of the World Reference Laboratory for FMD (Non-QAU Form)**

Serotype: O	Date: 08/06/2003
Virus isolate: KEN/5/2002	Reported by: N.J. Knowles
Material used: BTy1	Signed (file copy only):
Region sequenced: VP1	Seq. filename: KEN02-05
RT-PCR primer set: O-1C272F/NK61	
Topotype: East Africa 2 (EA-2)	No. of ambiguities: 0
Genotype/strain:	Date seq. last updated: 05/04/2003
No. of nt determined / no. in gene: 639 / 639	Total no. of comparisons made: 1304

Comments: This virus is a representative of a newly recognised topotype – East Africa 2 (EA-2). It appears that members of this topotype have, in the past, recombined with viruses of the Middle East-South Asia (ME-SA) topotype with a cross-over point somewhere in the 3' half of the VP1 gene. This makes it difficult, if not impossible, to distinguish the two topotypes when only sequences at the 3' end of VP1 are compared, e.g. the viruses shown below in italics (IND, SAU, TUR & UAE) are probably members of the ME-SA topotype.

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/KEN/18/98	KEN98-18	384	364	17	94.79	5.21
2	<i>O/IND/1/88</i>	<i>IND88-01</i>	<i>161</i>	<i>151</i>	<i>4</i>	<i>93.79</i>	<i>6.21</i>
3	O/KEN/7/2002	KEN02-07	639	599	0	93.74	6.26
4	<i>O/TUR/27/90</i>	<i>TUR90-27</i>	<i>174</i>	<i>163</i>	<i>0</i>	<i>93.68</i>	<i>6.32</i>
5	<i>O/SAU/11/85</i>	<i>SAU85-11</i>	<i>157</i>	<i>147</i>	<i>7</i>	<i>93.63</i>	<i>6.37</i>
6	<i>O/TUR/5/90</i>	<i>TUR90-05</i>	<i>156</i>	<i>146</i>	<i>9</i>	<i>93.59</i>	<i>6.41</i>
7	<i>O/SAU/44/91</i>	<i>SAU91-44</i>	<i>156</i>	<i>146</i>	<i>3</i>	<i>93.59</i>	<i>6.41</i>
8	<i>O/UAE/1/92</i>	<i>UAE92-01</i>	<i>154</i>	<i>144</i>	<i>1</i>	<i>93.51</i>	<i>6.49</i>
9	<i>O/SAU/69/93</i>	<i>SAU93-69</i>	<i>143</i>	<i>133</i>	<i>6</i>	<i>93.01</i>	<i>6.99</i>
10	<i>O/IND/146/99*</i>	<i>IND99-AC</i>	<i>156</i>	<i>145</i>	<i>9</i>	<i>92.95</i>	<i>7.05</i>

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/ISR/1/88	ISR88-01	193	167	5	86.53	13.47
2	O/TAW/2/99	TAW99-02	639	551	0	86.23	13.77
3	O/MOR/1/91	MOR91-01	207	178	3	85.99	14.01
4	O/IND/53/79	IND79A53	639	547	0	85.60	14.40
5	O/IND/R2/75*	IND75--A	639	547	0	85.60	14.40
6	O1/Manisa/TUR/69	TUR69--E	639	539	0	84.35	15.65
7	O1/BFS 1860/UK/67	UKG67--A	639	523	0	81.85	18.15
8	O/TAI/189/87*	TAI87--B	527	431	3	81.78	18.22
9	O/HKN/6/83	HKN83-06	637	510	2	80.06	19.94
10	O/PHI/5/95	PHI95-05	516	409	6	79.26	20.74

nt, nucleotides

*, not a WRLFMD reference number

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Head of the World Reference Laboratory for FMD (Non-QAU Form)**

Serotype: O	Date: 08/06/2003
Virus isolate: KEN/7/2002	Reported by: N.J. Knowles
Material used: RS1	Signed (file copy only):
Region sequenced: VP1	Seq. filename: KEN02-07
RT-PCR primer set: O-1C272F/NK61	
Topotype: East Africa 2 (EA-2)	No. of ambiguities: 0
Genotype/strain:	Date seq. last updated: 05/04/2003
No. of nt determined / no. in gene: 639 / 639	Total no. of comparisons made: 1304

Comments: This virus is a representative of a newly recognised topotype – East Africa 2 (EA-2). It appears that members of this topotype have, in the past, recombined with viruses of the Middle East-South Asia (ME-SA) topotype with a cross-over point somewhere in the 3' half of the VP1 gene. This makes it difficult, if not impossible, to distinguish the two topotypes when only sequences at the 3' end of VP1 are compared, e.g. the viruses shown below in italics (IND, SAU & TUR) are probably members of the ME-SA topotype.

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	<i>O/TUR/3/2002*</i>	<i>TUR02-AD</i>	158	149	7	94.30	5.70
2	O/KEN/18/98	KEN98-18	384	362	17	94.27	5.73
3	<i>O/IND/54/98*</i>	<i>IND98-AA</i>	165	155	0	93.94	6.06
4	O/KEN/5/2002	KEN02-05	639	599	0	93.74	6.26
5	<i>O/IND/178/99* (1998)</i>	<i>IND98-AQ</i>	153	143	6	93.46	6.54
6	<i>O/SAU/76/94</i>	<i>SAU94-76</i>	152	142	1	93.42	6.58
7	<i>O/IND/289/97*</i>	<i>IND97-AW</i>	165	154	0	93.33	6.67
8	<i>O/IND/209/99* (1998)</i>	<i>IND98-AU</i>	165	154	0	93.33	6.67
9	<i>O/IND/61/97* (1996)</i>	<i>IND96-AB</i>	165	154	0	93.33	6.67
10	<i>O/IND/143/99*</i>	<i>IND99-AB</i>	164	153	1	93.29	6.71

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/MOR/1/91	MOR91-01	207	179	3	86.47	13.53
2	O/ISR/1/88	ISR88-01	193	166	5	86.01	13.99
3	O/IND/R2/75*	IND75--A	639	549	0	85.92	14.08
4	O/TAW/2/99	TAW99-02	639	547	0	85.60	14.40
5	O1/Manisa/TUR/69	TUR69--E	639	544	0	85.13	14.87
6	O/IND/53/79	IND79A53	639	537	0	84.04	15.96
7	O/TAI/189/87*	TAI87--B	527	428	3	81.21	18.79
8	O/HKN/6/83	HKN83-06	637	515	2	80.85	19.15
9	O1/BFS 1860/UK/67	UKG67--A	639	516	0	80.75	19.25
10	O/PHI/5/95	PHI95-05	516	412	6	79.84	20.16

nt, nucleotides

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