

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

Genome Sequencing Report

Report Date for this Batch: 24 October 2016

FMDV type O

Country: Mauritius

Period: 2016

No. of sequences: 6



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Genome Sequencing Report

Date: 24/10/2016

Sequencing platform: Illumina MiSeq

Sequencing methodology:

Software for genome assembly: DNASTAR NGEN & Lasergene SeqManPro v.12

Reported by: K. Bachanek-Bankowska & N.J. Knowles

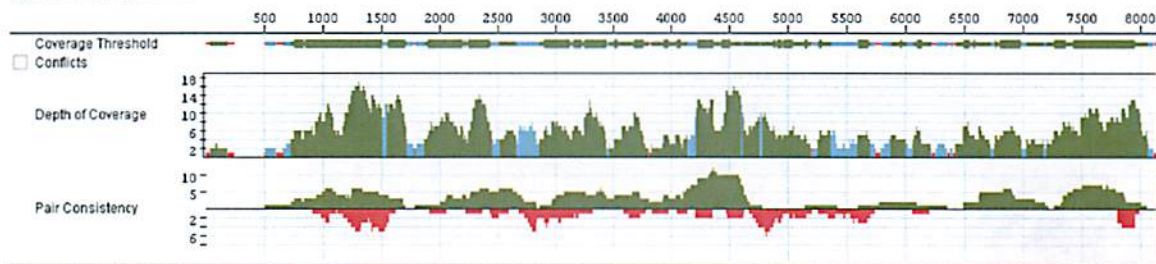
WRLFMD Ref. No.	Sender Ref.	Material sequenced	No. Nt. Determined [excl. poly(C) tract & poly(A) tail]
O/MUR/1/2016	O/1A/MAU/2016	Epithelium suspension	8062
O/MUR/5/2016	O/2B/MAU/2016	Epithelium suspension	8069
O/MUR/9/2016	O/3A/MAU/2016	Epithelium suspension	8077
O/MUR/19/2016	O/F1/ROD/2016	Epithelium suspension	8094
O/MUR/21/2016	O/F2/ROD/2016	Epithelium suspension	8093
O/MUR/23/2016	O/F3/ROD/2016	Epithelium suspension	8093

Comments

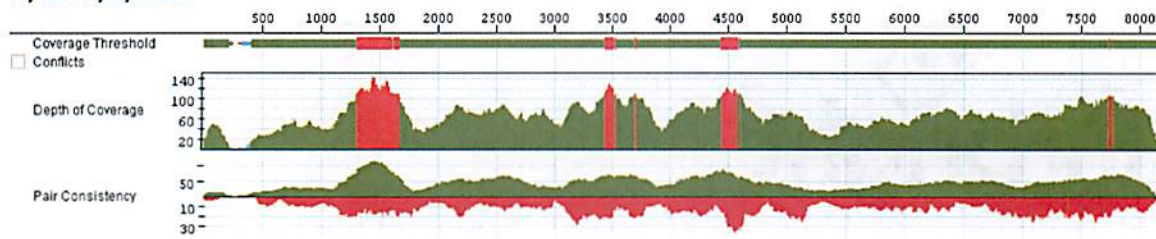
All six genome sequences had a 73 nt deletion in the middle of the s-fragment when compared to most O/ME-SA/Ind-2001d viruses so far sequenced. However, deletions in the same position (and of a similar size) have been observed in Ind-2001d viruses from Bangladesh, Bhutan, Algeria, Tunisia and Morocco. O/MUR/1/2016 was not included in Fig. 2 since the genome sequence was incomplete.

Coverage maps (Fig. 1):

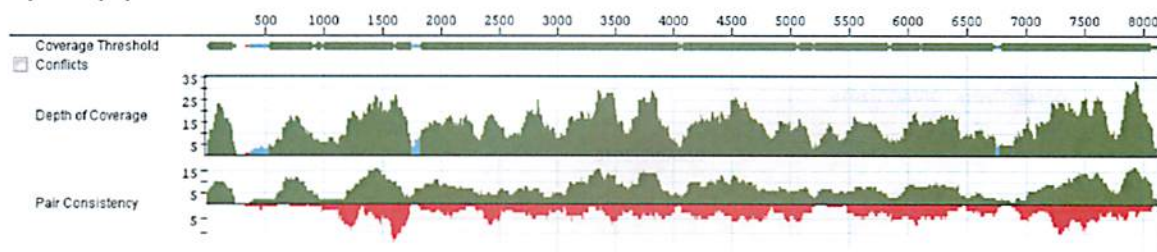
O/MUR/1/2016



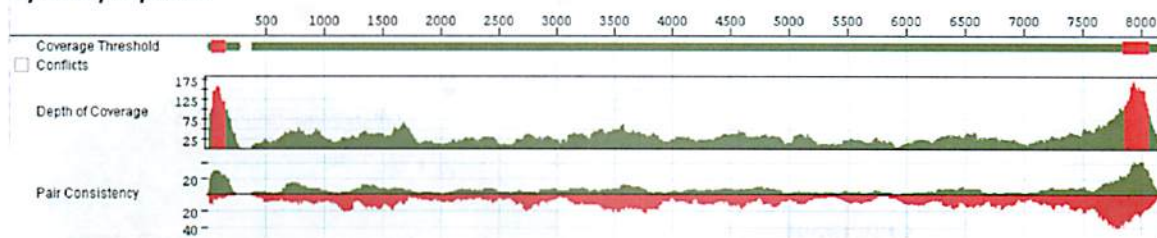
O/MUR/5/2016



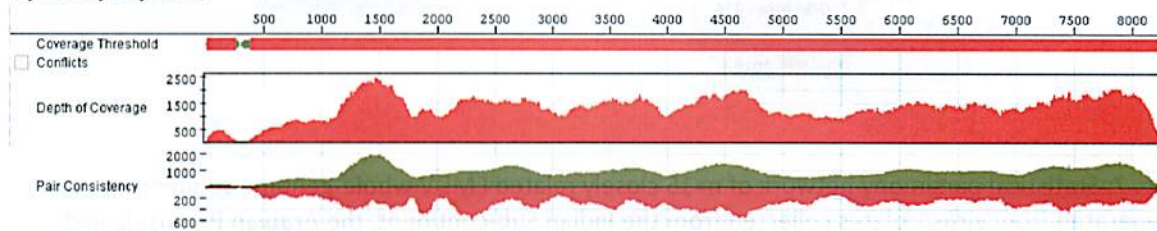
O/MUR/9/2016



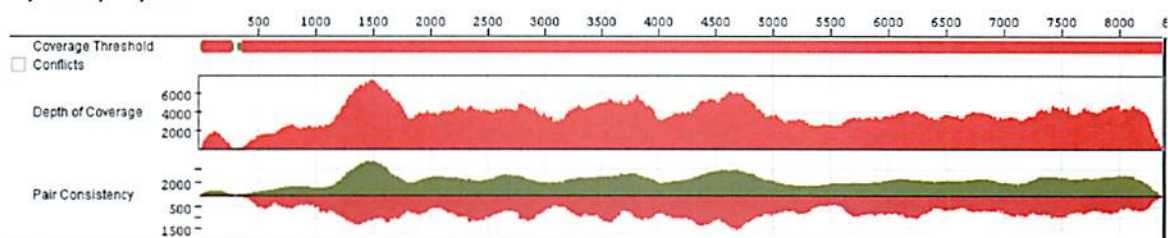
O/MUR/19/2016



O/MUR/21/2016



O/MUR/23/2016



Legend:

A thin red line represents a region sequenced only once.

A medium blue line is for a region sequenced on one strand only, even if the coverage in that region meets the Coverage Threshold value.

A medium green line indicates a region sequenced on both strands but failing the Minimum Number on Each Strand parameter.

A thick green line represents a region sequenced on both strands and that matches or exceeds the Coverage Threshold and Minimum Number on Each Strand values.

A thick red line represents a region that exceeds the Maximum Expected Coverage parameter.

The graph labelled Depth of Coverage represents the depth of sequences throughout the assembly. The numbers to the left of the graph indicate the actual number of sequences represented.

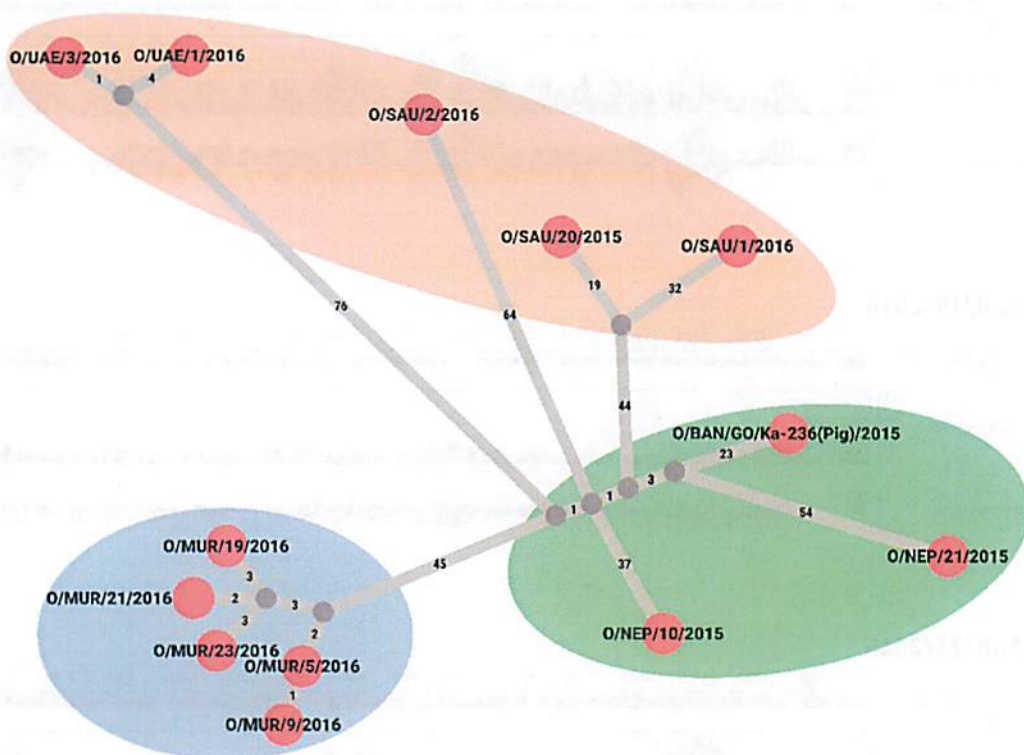


Fig. 2. Statistical parsimony network of $n=15$ closely related FMDV whole-genome sequences generated from virus isolates collected from the Indian Sub-continent, the Arabian Peninsula and Mauritius. The network was generated in the TCS 1.2.1 software and constructed in Cytoscape 3.4.0.