

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

## Genotyping Report

Report Date for this Batch: 21 January 2015

FMDV type SAT 3

Country: Uganda

Period: 2013

No. of sequences: 1

Originator: GenBank



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# FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: SAT3 WRLFMD Ref No: UGA/1/13* Batch No: WRLMEG/2015/00001 Sender Ref: UGA/1/13 Location: Kasese district, Uganda Date collected: 13/06/2013 Date received by WRLFMD: 21/01/2015 Date received for sequencing: n/a Species: Cattle Material used: not known Region sequenced: VP1 RT-PCR primers: Not known	Report date: 21/01/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska  Topotype: V Genotype/strain: unnamed Sequence filename: UGA13-AA.SEQ Date sequence last updated: 21/01/2015 No. of Nt determined: 654 No. of ambiguities: 0 Gene length: 654 Total no. of comparisons: 117 Min. no. of nt for comparison: 600 Total turn-around time: 0 days
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Comments: taken from the complete genome sequence (KJ820999) deposited in the GenBank database:  
 Dhikusooka MT, Tjørnehøj K, Ayebazibwe C, Namatovu A, Ruhweza S, Siegismund HR, Wekesa SN, Normann P, Belsham GJ. Foot-and-mouth disease virus serotype SAT 3 in long-horned Ankole calf, Uganda. *Emerg. Infect. Dis.* 21: 111-114.

### Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT3/UGA BUFF/27/70 (KF219685)	UGA70-27	654	528	0	80.73	19.27	V	unnamed
2	SAT3/UGA/2/97* (DQ009742)(buffalo)	UGA97B02	648	521	0	80.40	19.60	V	unnamed
3	SAT3/UGA/10/97 (=UGA/2/97)(buffalo)	UGA97-10	654	525	0	80.28	19.72	V	unnamed
4	SAT3/ZIM/P30/90 CHER-31 buffalo	ZIM90B50	654	438	0	66.97	33.03	II	unnamed
5	SAT3/BOT/P3/98 NXA-9 buffalo	BOT98NAG	654	436	0	66.67	33.33	II	unnamed
6	SAT3/ZIM/2/84	ZIM84-02	654	435	0	66.51	33.49	II	unnamed
7	SAT3/ZIM/P7/94 MT-3 buffalo	ZIM94B02	654	435	0	66.51	33.49	I	unnamed
8	SAT3/BOT/P3/98 VUM-21 buffalo	BOT98VAA	654	434	0	66.36	33.64	II	unnamed
9	SAT3/ZIM/1/83	ZIM83-01	654	434	0	66.36	33.64	I	unnamed
10	SAT3/ZIM/2/83	ZIM83-02	654	434	0	66.36	33.64	I	unnamed

### Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm))

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1	SAT3/UGA BUFF/27/70 (KF219685)	UGA70-27	654	528	0	80.73	19.27	V	unnamed
2	SAT3/UGA/2/97* (DQ009742)(buffalo)	UGA97B02	648	521	0	80.40	19.60	V	unnamed
3	SAT3/SA/57/59 (AY593850)	RSA59A57	654	424	0	64.83	35.17	I	unnamed
4	SAT3/ZAM/P2/96 (MUL-4) (DQ009741)buffalo	ZAM96-AB	648	420	0	64.81	35.19	IV	unnamed
5	SAT3/KNP/10/90* (buffalo)	KNP90-10	654	421	0	64.37	35.63	I	unnamed
6	SAT3/ZIM/P25/91 UR-7 buffalo	ZIM91B26	654	421	0	64.37	35.63	III	unnamed
7	SAT3/BEC/20/61 (AY593851)	BOT61A20	654	416	0	63.61	36.39	II	unnamed
8	SAT3/BEC/1/65 (AY593853)	BOT65A01	654	407	0	62.23	37.77	II	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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# Report on FMDV SAT 3 in Uganda in 2013

Batch: WRLMEG/2015/00001

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

Analysis ----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 657

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

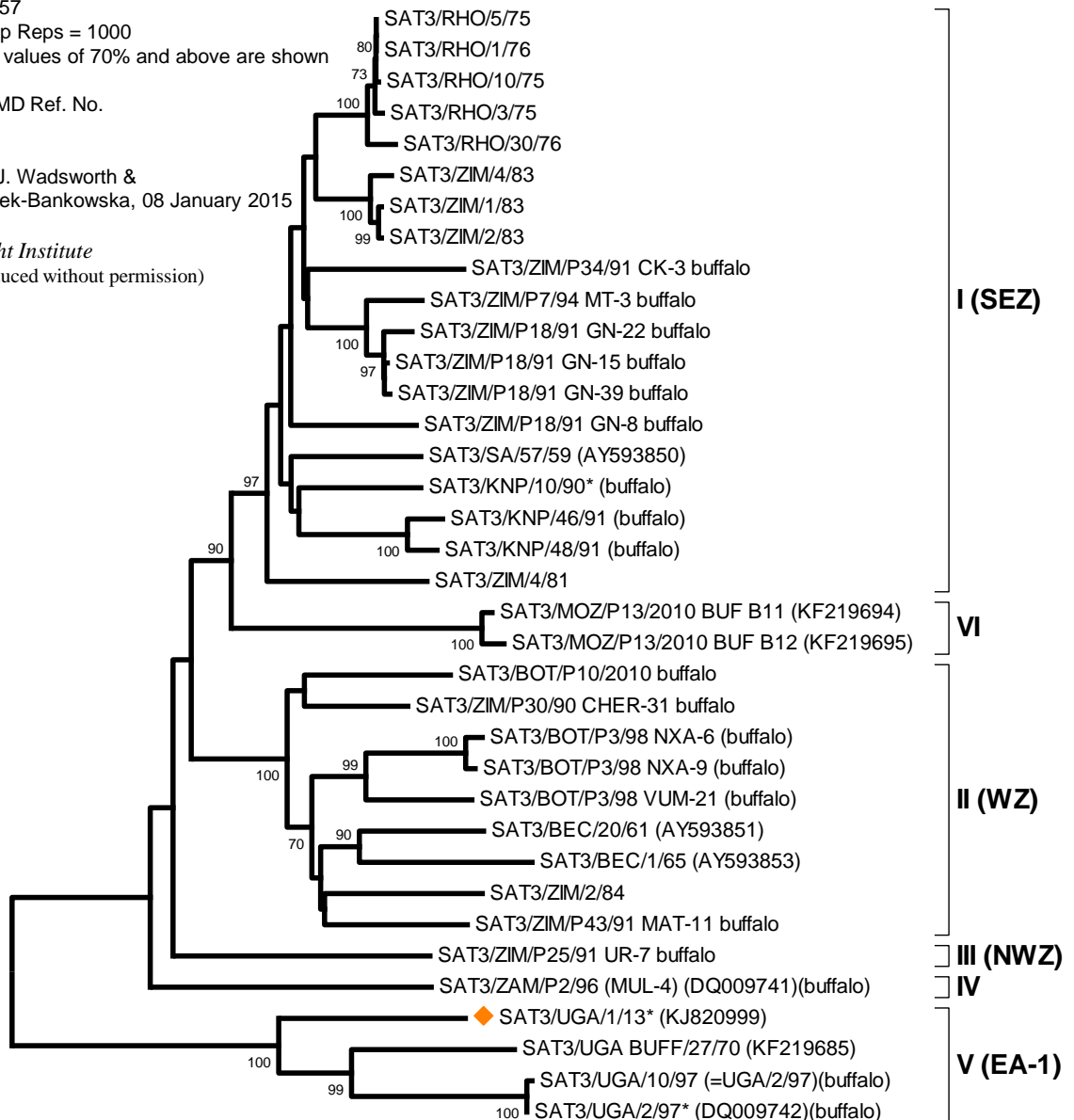
\*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth &

K. Bachanek-Bankowska, 08 January 2015

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