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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00021

Sender Details:



Date Received: 6th April 2010
Country of Origin: Kenya
Date Reported: 18th June 2010

Dear Dr. Sabenzia Nabalayo Wekesa,

Re.: Serotype SAT2

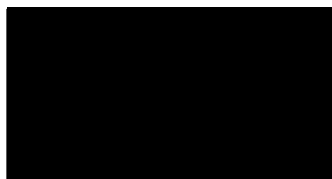
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Please note this sample was collected more than 12 months ago.

Results Approved By:



Official Stamp:



Date:

18/6/10



To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: elizabeth.wilson@bbsrc.ac.uk)

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

Genotyping Report

Date: 16 June 2010

FMDV type SAT 2

Country: Kenya

Period: 2009

No. of isolates: 1

BATCH: WRLFMD/2010/00021



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT2	Report date: 16/06/2010
WRLFMD Ref No: KEN/122/2009	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00021	Checked by: D.P. King
Sender Ref: K122/09	
Location: Rongai, Rift Valley, Kenya	Topotype: IV
Date collected: 01/01/2009	Genotype/strain: Unnamed
Date received by WRLFMD: 06/04/2010	Sequence filename: KEN09122.SEQ
Date received for sequencing: 27/05/2010	Date sequence last updated: 16/06/2010
Species: Cattle	No. of Nt determined: 648
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 529
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300
	Total turn-around time: 71 days
	Sequencing time: 20 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/KEN/11/2009	KEN09-11	648	636	0	98.15	1.85	IV	unnamed
2	SAT2/KEN/13/2009	KEN09-13	648	636	0	98.15	1.85	IV	unnamed
3	SAT2/UGA/01/2004* (GU323171)	UGA04-AA	347	308	0	88.76	11.24	IV	unnamed
4	SAT2/UGA/08/2004* (GU323176)	UGA04-AF	347	308	0	88.76	11.24	IV	unnamed
5	SAT2/NYE/29/90	NYE90-29	648	574	0	88.58	11.42	IV	unnamed
6	SAT2/UGA/11/2004* (GU323178)	UGA04-AH	347	307	0	88.47	11.53	IV	unnamed
7	SAT2/ETH/2/90 (1989)(AY343936)	ETH90-AB	647	571	1	88.25	11.75	IV	unnamed
8	SAT2/UGA/03/2004* (GU323173)	UGA04-AC	347	306	0	88.18	11.82	IV	unnamed
9	SAT2/MAL/1/2004 (OVI)	MAL04-01	384	338	0	88.02	11.98	IV	unnamed
10	SAT2/ETH/1/91 (AY343937)	ETH91-AA	648	569	0	87.81	12.19	IV	unnamed
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	568	0	87.65	12.35	IV	unnamed
2	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	562	0	86.73	13.27	IV	unnamed
3	SAT2/MAL/1/2003	MAL03-01	648	518	0	79.94	20.06	I	unnamed
4	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	518	0	79.94	20.06	III	unnamed
5	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	514	1	79.44	20.56	III	unnamed
6	SAT2/SA/106/59 (AY593848)	RSA59--A	648	511	0	78.86	21.14	I	unnamed
7	SAT2/ZIM/14/2002	ZIM02-14	648	507	0	78.24	21.76	I	unnamed
8	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	496	0	76.54	23.46	II	unnamed
9	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	483	0	74.54	25.46	V	unnamed
10	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	482	0	74.38	25.62	II	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.1

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Report on FMDV SAT 2 in Kenya in 2009

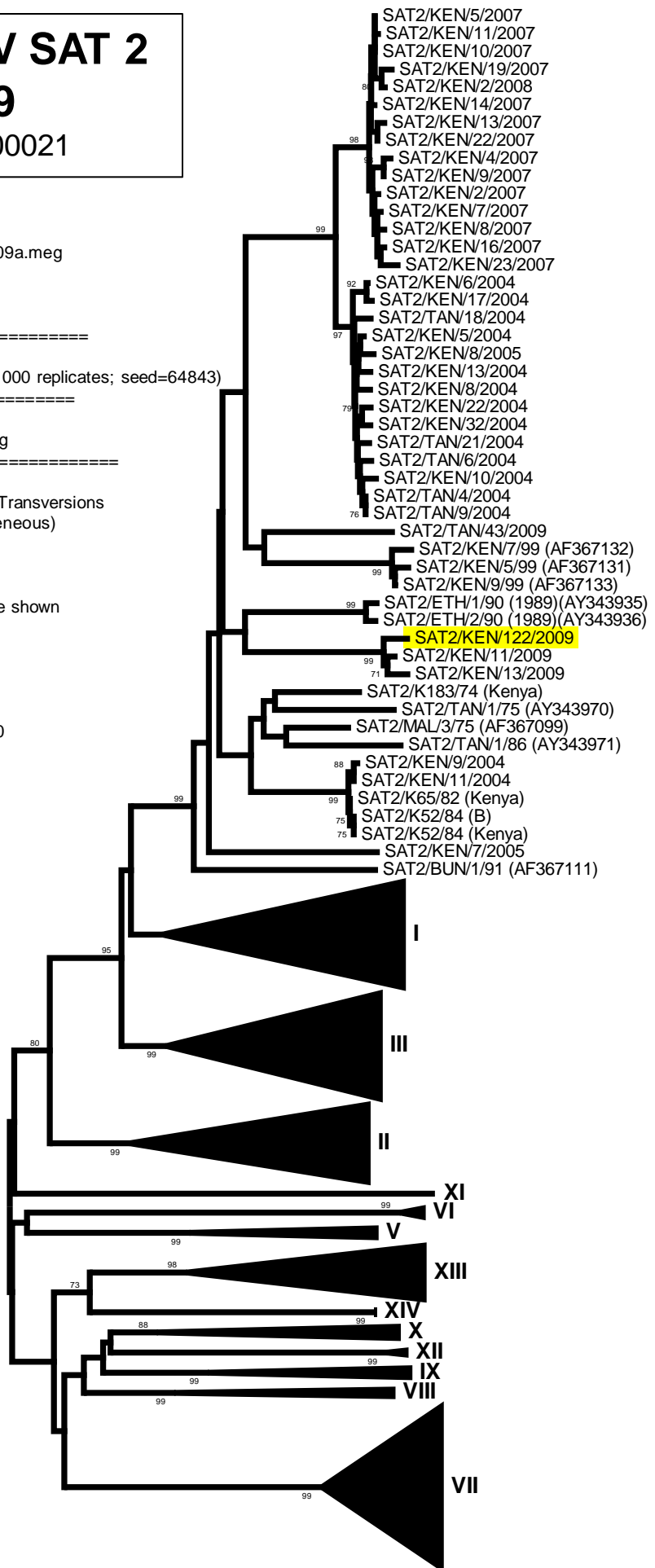
Batch: WRLFMD/2010/00021

Software: MEGA 4.0
 No. of Taxa : 302
 Data File : n:\evd\meg\db\fmv\sat2\TAN2009a.meg
 Data Title : Kenya & Tanzania 2009
 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 : 651
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 16 June 2010

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