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

Genotyping Report

Report Date for this Batch: 15 September 2014

FMDV type A
Country: Cameroon
Period: 2013
No. of samples: 4

BATCH: WRLFMD/2014/00019

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Serotype: A	Report date: 14/09/2014
WRLFMD Ref No: CAR/4/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00019	Checked by: K. Bachanek-Bankowska
Sender Ref: 22	
Location: Garoua Boulai, East, Cameroon	Topotype: AFRICA
Date collected: 15/07/2013	Genotype/strain: G-IV
Date received by WRLFMD: 07/05/2014	Sequence filename: CAR13-04.SEQ
Date received for sequencing: 04/09/2014	Date sequence last updated: 13/09/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 20/08/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1993
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 130 days
	Sequencing time: 10 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/CAR/10/2013	CAR13-10	639	639	0	100.00	0.00	AFRICA	G-IV
2	A/CAR/11/2013	CAR13-11	639	639	0	100.00	0.00	AFRICA	G-IV
3	A/CAR/36/2013	CAR13-36	639	639	0	100.00	0.00	AFRICA	G-IV
4	A/NIG/2/2011	NIG11-02	639	617	0	96.56	3.44	AFRICA	G-IV
5	A/NIG/9/2012	NIG12-09	639	614	0	96.09	3.91	AFRICA	G-IV
6	A/NIG/36/2009	NIG09-36	639	605	0	94.68	5.32	AFRICA	G-IV
7	A/NIG/39/2009	NIG09-39	639	605	0	94.68	5.32	AFRICA	G-IV
8	A/NIG/38/2009	NIG09-38	639	604	0	94.52	5.48	AFRICA	G-IV
9	A/NIG/10/2012	NIG12-10	639	597	0	93.43	6.57	AFRICA	G-IV
10	A/NIG/8/2012	NIG12-08	639	596	0	93.27	6.73	AFRICA	G-IV

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	A/SUD/3/77 (GU566064)	SUD77-03	639	547	0	85.60	14.40	AFRICA	G-IV
2	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	536	0	83.88	16.12	AFRICA	G-I
3	A/UGA/13/66 (KF561705)	UGA66-13	639	530	0	82.94	17.06	AFRICA	G-VII
4	A/NGR/2/73 (KF561704)	NGR73-02	639	528	0	82.63	17.37	AFRICA	G-V
5	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	528	0	82.63	17.37	AFRICA	G-III
6	A/GHA/16/73 (KF561698)	GHA73-16	636	521	0	81.92	18.08	AFRICA	G-VI
7	A/EGY/1/72 (EF208756)	EGY72-01	639	522	0	81.69	18.31	AFRICA	G-II
8	A12/UK/119/32 (M10975)	UKG32119	639	514	0	80.44	19.56	EURO-SA	A_{12}
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	511	0	80.35	19.65	EURO-SA	A_5
10	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	511	0	79.97	20.03	ASIA	A15

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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FAO World Reference Laboratory for FMD Genotyping Report

Serotype: A
WRLFMD Ref No: CAR/10/2013
Batch No: WRLFMD/2014/00019
Sender Ref: 24
Location: Meiganaga, Adamaoua, Cameroon
Date collected: 17/07/2013
Date received by WRLFMD: 07/05/2014
Date received for sequencing: 04/09/2014
Species: Cattle
Material used: BTy2 27/08/2014
Region sequenced: VP1
RT-PCR primers: A-1C562F/EUR-2B52R
A-1C612F/EUR-2B52R

Report date: 14/09/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: AFRICA
Genotype/strain: G-IV
Sequence filename: CAR13-10.SEQ
Date sequence last updated: 10/09/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 1993
Min. no. of nt for comparison: 600
Total turn-around time: 130 days
Sequencing time: 10 days

Comments:

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/CAR/11/2013	CAR13-11	639	639	0	100.00	0.00	AFRICA	G-IV
2	A/CAR/36/2013	CAR13-36	639	639	0	100.00	0.00	AFRICA	G-IV
3	A/CAR/4/2013	CAR13-04	639	639	0	100.00	0.00	AFRICA	G-IV
4	A/NIG/2/2011	NIG11-02	639	617	0	96.56	3.44	AFRICA	G-IV
5	A/NIG/9/2012	NIG12-09	639	614	0	96.09	3.91	AFRICA	G-IV
6	A/NIG/36/2009	NIG09-36	639	605	0	94.68	5.32	AFRICA	G-IV
7	A/NIG/39/2009	NIG09-39	639	605	0	94.68	5.32	AFRICA	G-IV
8	A/NIG/38/2009	NIG09-38	639	604	0	94.52	5.48	AFRICA	G-IV
9	A/NIG/10/2012	NIG12-10	639	597	0	93.43	6.57	AFRICA	G-IV
10	A/NIG/8/2012	NIG12-08	639	596	0	93.27	6.73	AFRICA	G-IV

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1	A/SUD/3/77 (GU566064)	SUD77-03	639	547	0	85.60	14.40	AFRICA	G-IV
2	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	536	0	83.88	16.12	AFRICA	G-I
3	A/UGA/13/66 (KF561705)	UGA66-13	639	530	0	82.94	17.06	AFRICA	G-VII
4	A/NGR/2/73 (KF561704)	NGR73-02	639	528	0	82.63	17.37	AFRICA	G-V
5	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	528	0	82.63	17.37	AFRICA	G-III
6	A/GHA/16/73 (KF561698)	GHA73-16	636	521	0	81.92	18.08	AFRICA	G-VI
7	A/EGY/1/72 (EF208756)	EGY72-01	639	522	0	81.69	18.31	AFRICA	G-II
8	A12/UK/119/32 (M10975)	UKG32119	639	514	0	80.44	19.56	EURO-SA	A_{12}
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	511	0	80.35	19.65	EURO-SA	A_5
10	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	511	0	79.97	20.03	ASIA	A15

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FAO World Reference Laboratory for FMD Genotyping Report

Serotype: A	Report date: 14/09/2014
WRLFMD Ref No: CAR/11/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00019	Checked by: K. Bachanek-Bankowska
Sender Ref: 25	
Location: Djohong, Adamaoua, Cameroon	Topotype: AFRICA
Date collected: 17/07/2013	Genotype/strain: G-IV
Date received by WRLFMD: 07/05/2014	Sequence filename: CAR13-11.SEQ
Date received for sequencing: 04/09/2014	Date sequence last updated: 13/09/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 20/08/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1993
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 130 days
	Sequencing time: 10 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/CAR/10/2013	CAR13-10	639	639	0	100.00	0.00	AFRICA	G-IV
2	A/CAR/36/2013	CAR13-36	639	639	0	100.00	0.00	AFRICA	G-IV
3	A/CAR/4/2013	CAR13-04	639	639	0	100.00	0.00	AFRICA	G-IV
4	A/NIG/2/2011	NIG11-02	639	617	0	96.56	3.44	AFRICA	G-IV
5	A/NIG/9/2012	NIG12-09	639	614	0	96.09	3.91	AFRICA	G-IV
6	A/NIG/36/2009	NIG09-36	639	605	0	94.68	5.32	AFRICA	G-IV
7	A/NIG/39/2009	NIG09-39	639	605	0	94.68	5.32	AFRICA	G-IV
8	A/NIG/38/2009	NIG09-38	639	604	0	94.52	5.48	AFRICA	G-IV
9	A/NIG/10/2012	NIG12-10	639	597	0	93.43	6.57	AFRICA	G-IV
10	A/NIG/8/2012	NIG12-08	639	596	0	93.27	6.73	AFRICA	G-IV

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1	A/SUD/3/77 (GU566064)	SUD77-03	639	547	0	85.60	14.40	AFRICA	G-IV
2	A/KEN/42/66 (K18/66)(KF561699)	KEN66-42	639	536	0	83.88	16.12	AFRICA	G-I
3	A/UGA/13/66 (KF561705)	UGA66-13	639	530	0	82.94	17.06	AFRICA	G-VII
4	A/NGR/2/73 (KF561704)	NGR73-02	639	528	0	82.63	17.37	AFRICA	G-V
5	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	528	0	82.63	17.37	AFRICA	G-III
6	A/GHA/16/73 (KF561698)	GHA73-16	636	521	0	81.92	18.08	AFRICA	G-VI
7	A/EGY/1/72 (EF208756)	EGY72-01	639	522	0	81.69	18.31	AFRICA	G-II
8	A12/UK/119/32 (M10975)	UKG32119	639	514	0	80.44	19.56	EURO-SA	A_{12}
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	511	0	80.35	19.65	EURO-SA	A_5
10	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	511	0	79.97	20.03	ASIA	A15

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FAO World Reference Laboratory for FMD Genotyping Report

Serotype: A	Report date: 14/09/2014
WRLFMD Ref No: CAR/36/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00019	Checked by: K. Bachanek-Bankowska
Sender Ref: 33	
Location: Madardam, Far North, Cameroon	Topotype: AFRICA
Date collected: 27/07/2013	Genotype/strain: G-IV
Date received by WRLFMD: 07/05/2014	Sequence filename: CAR13-36.SEQ
Date received for sequencing: 04/09/2014	Date sequence last updated: 13/09/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 21/08/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1993
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
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Most Closely Related Viruses

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1	A/CAR/10/2013	CAR13-10	639	639	0	100.00	0.00	AFRICA	G-IV
2	A/CAR/11/2013	CAR13-11	639	639	0	100.00	0.00	AFRICA	G-IV
3	A/CAR/4/2013	CAR13-04	639	639	0	100.00	0.00	AFRICA	G-IV
4	A/NIG/2/2011	NIG11-02	639	617	0	96.56	3.44	AFRICA	G-IV
5	A/NIG/9/2012	NIG12-09	639	614	0	96.09	3.91	AFRICA	G-IV
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3	A/UGA/13/66 (KF561705)	UGA66-13	639	530	0	82.94	17.06	AFRICA	G-VII
4	A/NGR/2/73 (KF561704)	NGR73-02	639	528	0	82.63	17.37	AFRICA	G-V
5	A21/Lumbwa/KEN/64 (AY593761)	KEN64-AA	639	528	0	82.63	17.37	AFRICA	G-III
6	A/GHA/16/73 (KF561698)	GHA73-16	636	521	0	81.92	18.08	AFRICA	G-VI
7	A/EGY/1/72 (EF208756)	EGY72-01	639	522	0	81.69	18.31	AFRICA	G-II
8	A12/UK/119/32 (M10975)	UKG32119	639	514	0	80.44	19.56	EURO-SA	A_{12}
9	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	511	0	80.35	19.65	EURO-SA	A_5
10	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	511	0	79.97	20.03	ASIA	A15

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Report on FMDV A in Cameroon in 2013

Batch: WRLFMD/2014/00019

◆ 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 : 639
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,
14 September 2014

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