

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

Genotyping Report

FMDV serotype: O
Country: Vietnam
Year: 2018
Batch: WRLFMD/2019/00010
No. of sequences: 47
Report date: 24th March 2019
Report generated by: Nick Knowles
Report checked by: Jemma Wadsworth



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

Genotyping Report

FMDV serotype: O/SEA/Mya-98
Country: Vietnam
Year: 2018, 2019
Batch: WRLFMD/2019/00010A
No. of sequences: 28
Report date: 24th March 2019
Report generated by: Nick Knowles
Report checked by: Jemma Wadsworth



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Virus sample name:	VIT/23/2018
Sender reference:	18F219
Location of origin:	Dong Yen, Quoc Oai, Ha Noi
Country of origin:	Vietnam
Date of collection:	13/11/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40642, genome 40643, sequence viba_40644, sequencing info 40645	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40736	VIT/1/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40700	VIT/37/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_491	TUR/257/2008		83.6	0	O	ME-SA	PanAsia-2	TER-08
viba_523	K83/79		83.5	0	O	EA-1		
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/24/2018
Sender reference:	18F223
Location of origin:	Bao Thang, Lao Cai
Country of origin:	Vietnam
Date of collection:	13/11/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40646, genome 40647, sequence viba_40648, sequencing info 40649	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/25/2018
Sender reference:	18F261
Location of origin:	To Hieu, Binh Gia, Lang Son
Country of origin:	Vietnam
Date of collection:	14/11/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40650, genome 40651, sequence viba_40652, sequencing info 40653	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/26/2018
Sender reference:	18F238
Location of origin:	Huong Canh, Binh Xuyen, Vinh Phuc
Country of origin:	Vietnam
Date of collection:	20/11/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40654, genome 40655, sequence viba_40656, sequencing info 40657	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/27/2018
Sender reference:	18-27160
Location of origin:	My Hoi, Cai Be, Tien Giang
Country of origin:	Vietnam
Date of collection:	29/11/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40658, genome 40659, sequence viba_40660, sequencing info 40661	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/29/2018
Sender reference:	18-28811
Location of origin:	Song Nhan, Cam My, Dong Nai
Country of origin:	Vietnam
Date of collection:	17/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40666, genome 40667, sequence viba_40668, sequencing info 40669	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/30/2018
Sender reference:	18F263
Location of origin:	Yen Trung, Yen Phong, Bac Ninh
Country of origin:	Vietnam
Date of collection:	19/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40670, genome 40671, sequence viba_40672, sequencing info 40673	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40712	VIT/40/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40720	VIT/43/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_666	IRN/18/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	84.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_576	IND/R2/75		83.9	0	O	ME-SA		
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_850	NEP/1/2015	cattle	83.6	1	O	ME-SA	PanAsia-2	KAT-15
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		83.4	0	O	ME-SA	PanAsia-2	ANT-10

Virus sample name:	VIT/31/2018
Sender reference:	18CD-1933.1
Location of origin:	Nam Hong, Hong Linh, Ha Tinh
Country of origin:	Vietnam
Date of collection:	20/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40674, genome 40675, sequence viba_40676, sequencing info 40677

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/32/2018
Sender reference:	18CD-1938.1
Location of origin:	Tinh Gia, Thanh Hoa
Country of origin:	Vietnam
Date of collection:	21/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40678, genome 40679, sequence viba_40680, sequencing info 40681	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/33/2018
Sender reference:	18F268
Location of origin:	Thanh Ha, Thanh Ba, Phu Tho
Country of origin:	Vietnam
Date of collection:	21/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	06/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40682, genome 40683, sequence viba_40684, sequencing info 40685	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.5	0	O	EA-1		
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	
viba_576	IND/R2/75		83.5	0	O	ME-SA		

Virus sample name:	VIT/34/2018
Sender reference:	18-962.1
Location of origin:	Thanh Tan, Kien Xuong, Thai Binh
Country of origin:	Vietnam
Date of collection:	22/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS2
Harvest date of material:	12/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40686, genome 40687, sequence viba_40688, sequencing info 40689	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/36/2018
Sender reference:	18F274
Location of origin:	Tu Yen, Song Lo, Vinh Phuc
Country of origin:	Vietnam
Date of collection:	26/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40694, genome 40695, sequence viba_40696, sequencing info 40697	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40712	VIT/40/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40720	VIT/43/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40672	VIT/30/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.5	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.5	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.5	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.5	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.5	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.7	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	84.2	0	O	ME-SA	PanAsia	
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_650	IRN/8/2005	ovine	84.1	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		83.9	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		83.9	0	O	ME-SA	PanAsia-2	TER-08
viba_576	IND/R2/75		83.9	0	O	ME-SA		

Virus sample name:	VIT/37/2018
Sender reference:	18-993.4
Location of origin:	Dai Xuan, Que Vo, Bac Ninh
Country of origin:	Vietnam
Date of collection:	27/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40698, genome 40699, sequence viba_40700, sequencing info 40701	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40644	VIT/23/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40736	VIT/1/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_491	TUR/257/2008		83.8	0	O	ME-SA	PanAsia-2	TER-08
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	
viba_523	K83/79		83.5	0	O	EA-1		

Virus sample name:	VIT/38/2018
Sender reference:	02.CD
Location of origin:	Cam Phuc, Cam Xuyen, Ha Tinh
Country of origin:	Vietnam
Date of collection:	27/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40702, genome 40703, sequence viba_40704, sequencing info 40705	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40748	VIT/6/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.3	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.5	0	O	EA-1		
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/39/2018
Sender reference:	18F277
Location of origin:	Tan Thanh, Kim Son, Ninh Binh
Country of origin:	Vietnam
Date of collection:	27/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40706, genome 40707, sequence viba_40708, sequencing info 40709	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/40/2018
Sender reference:	18F281
Location of origin:	Dong Cao, Pho Yen, Thai Nguyen
Country of origin:	Vietnam
Date of collection:	27/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40710, genome 40711, sequence viba_40712, sequencing info 40713

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40720	VIT/43/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40672	VIT/30/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.5	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.4	0	O	SEA		
viba_666	IRN/18/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.9	0	O	ME-SA	PanAsia	
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_576	IND/R2/75		83.9	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		83.6	0	O	ME-SA	PanAsia-2	ANT-10

Virus sample name:	VIT/41/2018
Sender reference:	18-999
Location of origin:	Dong Y, Bac Son, Lang Son
Country of origin:	Vietnam
Date of collection:	29/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS2
Harvest date of material:	10/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40714, genome 40715, sequence viba_40716, sequencing info 40717	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.4	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.9	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.9	0	O	EA-1		
viba_576	IND/R2/75		83.9	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.8	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/43/2018
Sender reference:	18CD-1987.1
Location of origin:	Vinh Lam, Vinh Linh, Quang Tri
Country of origin:	Vietnam
Date of collection:	30/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40718, genome 40719, sequence viba_40720, sequencing info 40721	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40712	VIT/40/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40672	VIT/30/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.5	0	O	SEA		
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	84.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_719	IRN/88/2009		83.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_850	NEP/1/2015	cattle	83.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_694	CAM/3/98	bovine	83.6	0	O	SEA	Cam-94	

Virus sample name:	VIT/44/2018
Sender reference:	18F287
Location of origin:	Phu Cuong, Ba Vi, Ha Noi
Country of origin:	Vietnam
Date of collection:	30/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40722, genome 40723, sequence viba_40724, sequencing info 40725

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.4	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.9	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	83.8	0	O	ME-SA	PanAsia-2	
viba_719	IRN/88/2009		83.6	0	O	ME-SA	PanAsia-2	ANT-10
viba_491	TUR/257/2008		83.6	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/45/2018
Sender reference:	18F291
Location of origin:	Moc Chau, Son La
Country of origin:	Vietnam
Date of collection:	30/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40726, genome 40727, sequence viba_40728, sequencing info 40729	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_523	K83/79		84.0	0	O	EA-1		
viba_666	IRN/18/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_694	CAM/3/98	bovine	83.6	0	O	SEA	Cam-94	

Virus sample name:	VIT/46/2018
Sender reference:	18-1001.1
Location of origin:	My Hung, Luong Tai, Bac Ninh
Country of origin:	Vietnam
Date of collection:	31/12/2018
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	07/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40730, genome 40731, sequence viba_40732, sequencing info 40733

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.5	0	O	EA-1		
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	
viba_576	IND/R2/75		83.5	0	O	ME-SA		

Virus sample name:	VIT/1/2019
Sender reference:	19-01.01
Location of origin:	Nhan Thang, Gia Binh, Bac Ninh
Country of origin:	Vietnam
Date of collection:	01/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40734, genome 40735, sequence viba_40736, sequencing info 40737

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40644	VIT/23/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40700	VIT/37/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.2	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.6	0	O	ME-SA	PanAsia	
viba_491	TUR/257/2008		83.6	0	O	ME-SA	PanAsia-2	TER-08
viba_523	K83/79		83.5	0	O	EA-1		
viba_650	IRN/8/2005	ovine	83.5	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/3/2019
Sender reference:	19-1438
Location of origin:	Truong Chinh, Kon Tum, Kon Tum
Country of origin:	Vietnam
Date of collection:	04/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40738, genome 40739, sequence viba_40740, sequencing info 40741	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/4/2019
Sender reference:	19-1857
Location of origin:	Dai Thang, Dai Loc, Quang Nam
Country of origin:	Vietnam
Date of collection:	05/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40742, genome 40743, sequence viba_40744, sequencing info 40745

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40644	VIT/23/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40736	VIT/1/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40700	VIT/37/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.0	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	86.9	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_666	IRN/18/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	83.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_523	K83/79		83.7	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.4	0	O	ME-SA	PanAsia	
viba_491	TUR/257/2008		83.4	0	O	ME-SA	PanAsia-2	TER-08
viba_576	IND/R2/75		83.4	0	O	ME-SA		

Virus sample name:	VIT/6/2019
Sender reference:	19-1871
Location of origin:	Thanh Thoi B, Mo Cay Nam, Ben Tre
Country of origin:	Vietnam
Date of collection:	08/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40746, genome 40747, sequence viba_40748, sequencing info 40749	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40704	VIT/38/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40680	VIT/32/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.7	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.7	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.7	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.7	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_666	IRN/18/2010	cattle	84.3	0	O	ME-SA	PanAsia-2	BAL-09
viba_766	IRN/31/2009	cattle	84.2	0	O	ME-SA	PanAsia-2	FAR-09
viba_850	NEP/1/2015	cattle	84.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_523	K83/79		83.5	0	O	EA-1		
viba_285	UKG/35/2001	porcine	83.4	0	O	ME-SA	PanAsia	
viba_491	TUR/257/2008		83.4	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/9/2019
Sender reference:	19-2248-A
Location of origin:	Bien Gioi, Chau Thanh, Tay Ninh
Country of origin:	Vietnam
Date of collection:	11/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40750, genome 40751, sequence viba_40752, sequencing info 40753

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	99.8	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	99.8	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	99.8	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	99.8	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.5	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.0	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.0	0	O	ME-SA	PanAsia-2	BAL-09
viba_285	UKG/35/2001	porcine	83.9	0	O	ME-SA	PanAsia	
viba_850	NEP/1/2015	cattle	83.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_650	IRN/8/2005	ovine	83.8	0	O	ME-SA	PanAsia-2	
viba_491	TUR/257/2008		83.6	0	O	ME-SA	PanAsia-2	TER-08
viba_523	K83/79		83.5	0	O	EA-1		

Virus sample name:	VIT/10/2019
Sender reference:	19-2259
Location of origin:	Nghia Thanh, Chau Duc, Ba Ria Vung Tau
Country of origin:	Vietnam
Date of collection:	14/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40754, genome 40755, sequence viba_40756, sequencing info 40757	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40648	VIT/24/2018	porcine	100.0	0	O	SEA	Mya-98	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/11/2019
Sender reference:	19-2266
Location of origin:	Hung Khanh Trung A, Mo Cay Bac, Ben Tre
Country of origin:	Vietnam
Date of collection:	15/01/2019
Host species:	porcine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	08/03/2019
Primers:	FMD-3161F/FMD-4303R; O-1C244F/EUR-2B52R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40758, genome 40759, sequence viba_40760, sequencing info 40761	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40680	VIT/32/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40740	VIT/3/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_37715	VN 18-27160	porcine	100.0	0	O	SEA	Mya-98	
viba_40652	VIT/25/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40656	VIT/26/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40708	VIT/39/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40756	VIT/10/2019	porcine	100.0	0	O	SEA	Mya-98	
viba_40668	VIT/29/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40688	VIT/34/2018	porcine	100.0	0	O	SEA	Mya-98	
viba_40660	VIT/27/2018	porcine	100.0	0	O	SEA	Mya-98	

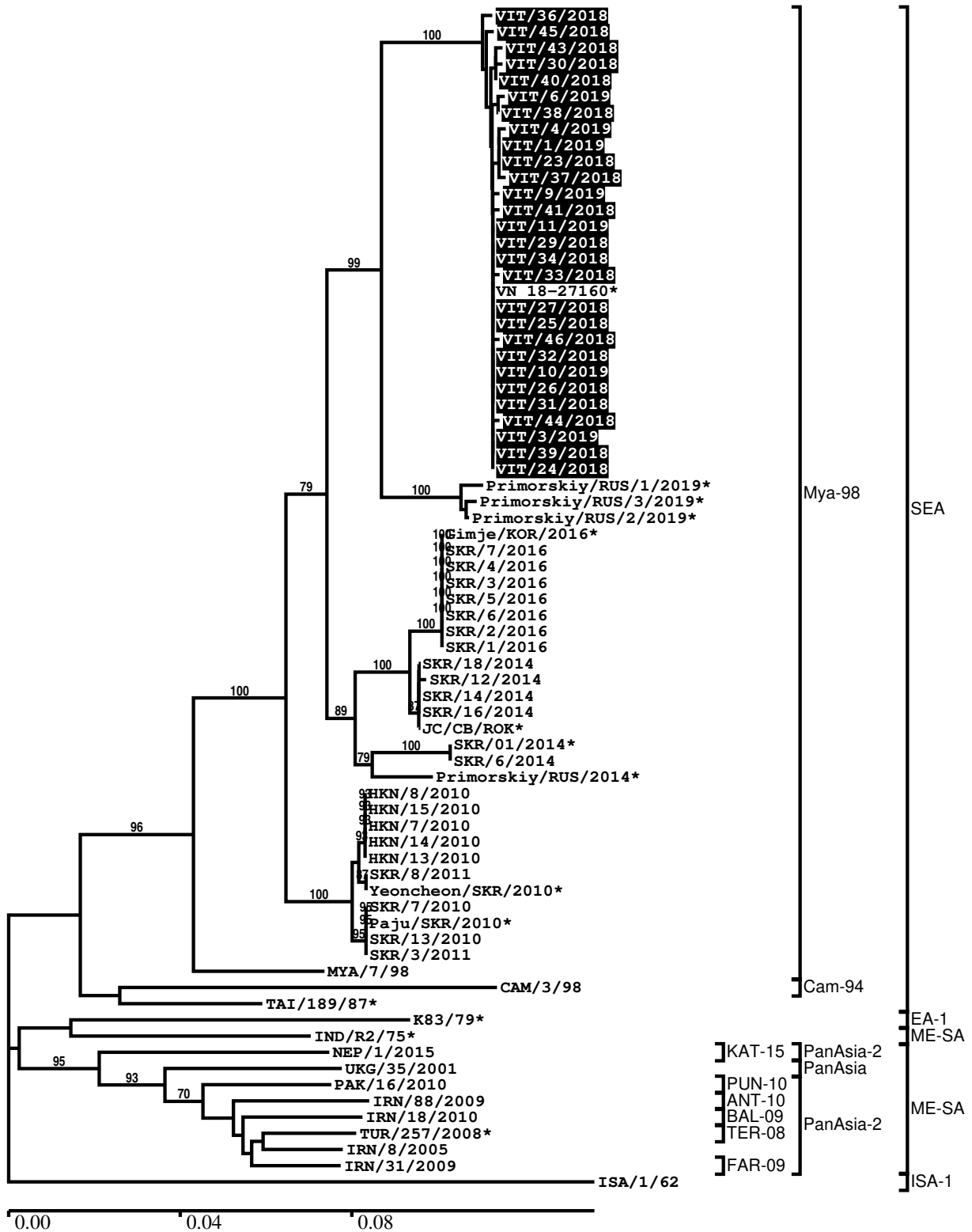
Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_199	MYA/7/98	bovine	90.4	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	87.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	84.1	1	O	ME-SA	PanAsia-2	KAT-15
viba_354	PAK/16/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	PUN-10
viba_285	UKG/35/2001	porcine	83.7	0	O	ME-SA	PanAsia	
viba_523	K83/79		83.7	0	O	EA-1		
viba_576	IND/R2/75		83.7	0	O	ME-SA		
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	

Report on FMDV O in Vietnam in 2018, 2019

Batch: WRLFMD/2019/00010A



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2019/00010A-Vietnam-O (28 sequences)
Sequence database set:	allseqs_O (4390 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	636
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	13
VIBASys version:	reflabs-1.1.2

Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	accession	host(s)	lab	country	taxonomic information
VIT/36/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/45/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/43/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/30/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/40/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/6/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/38/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/4/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/1/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/23/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/37/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/9/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/41/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/11/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/29/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/34/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/33/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VN 18-27160*	n/a	porcine	RAHO6	Vietnam	SEA/Mya-98
VIT/27/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/25/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/46/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/32/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/10/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/26/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/31/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/44/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/3/2019	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/39/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/24/2018	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
Primorskiy/RUS/1/2019*	n/a	porcine	ARRIAH	Russia	SEA/Mya-98
Primorskiy/RUS/3/2019*	n/a	porcine	ARRIAH	Russia	SEA/Mya-98
Primorskiy/RUS/2/2019*	n/a	porcine	ARRIAH	Russia	SEA/Mya-98
Gimje/KOR/2016*	n/a	porcine	QIA	Republic of Korea (South Korea)	SEA/Mya-98

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label	accession	host(s)	lab	country	taxonomic information
SKR/7/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/4/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/3/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/5/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/6/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/2/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/1/2016	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/18/2014	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/12/2014	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/14/2014	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/16/2014	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
JC/CB/ROK*	n/a	porcine	Animal and Plant Quarantine Agency	Republic of Korea (South Korea)	SEA/Mya-98
SKR/01/2014*	n/a	porcine	Animal and Plant Quarantine Agency	Republic of Korea (South Korea)	SEA/Mya-98
SKR/6/2014	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
Primorskiy/RUS/2014*	n/a	porcine	ARRIAH	Russia	SEA/Mya-98
HKN/8/2010	n/a	porcine	WRLFMD	Hong Kong SAR	SEA/Mya-98
HKN/15/2010	n/a	porcine	WRLFMD	Hong Kong SAR	SEA/Mya-98
HKN/7/2010	JQ070303	porcine	WRLFMD	Hong Kong SAR	SEA/Mya-98
HKN/14/2010	n/a	porcine	WRLFMD	Hong Kong SAR	SEA/Mya-98
HKN/13/2010	n/a	porcine	WRLFMD	Hong Kong SAR	SEA/Mya-98
SKR/8/2011	n/a	cattle	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
Yeoncheon/SKR/2010*	n/a	porcine	NVRQS	Republic of Korea (South Korea)	SEA/Mya-98
SKR/7/2010	n/a	cattle	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
Paju/SKR/2010*	n/a	cattle	NVRQS	Republic of Korea (South Korea)	SEA/Mya-98
SKR/13/2010	n/a	cattle	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
SKR/3/2011	n/a	porcine	WRLFMD	Republic of Korea (South Korea)	SEA/Mya-98
MYA/7/98	DQ164925	bovine	WRLFMD	Myanmar	SEA/Mya-98
CAM/3/98	AJ294910	bovine	WRLFMD	Cambodia	SEA/Cam-94

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label	accession	host(s)	lab	country	taxonomic information
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
K83/79*	AJ303511	n/a	WRLFMD	Kenya	EA-1
IND/R2/75*	AF204276	n/a	PD-FMD	India	ME-SA
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
PAK/16/2010	KY091285	cattle	WRLFMD	Pakistan	ME-SA/PanAsia-2/PUN-10
IRN/88/2009	KY091282	n/a	WRLFMD	Iran	ME-SA/PanAsia-2/ANT-10
IRN/18/2010	KY091283	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/BAL-09
TUR/257/2008*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
IRN/8/2005	KY091281	ovine	WRLFMD	Iran	ME-SA/PanAsia-2
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

*, not a WRLFMD Reference Number

n/a, not available

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

Genotyping Report

FMDV serotype: O/ME-SA/PanAsia
Country: Vietnam
Year: 2018
Batch: WRLFMD/2019/00010B
No. of sequences: 16
Report date: 24th March 2019
Report generated by: Nick Knowles
Report checked by: Jemma Wadsworth



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www: <http://www.wrlfmd.org/>

email: reporting@pirbright.ac.uk

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Virus sample name:	VIT/3/2018
Sender reference:	18-2570
Location of origin:	Binh Tan, Go Cong Tay, Tien Giang
Country of origin:	Vietnam
Date of collection:	23/01/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	28/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40574, genome 40575, sequence viba_40576, sequencing info 40577	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36497	VIT/1/2018	bovine	99.8	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	99.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.5	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	99.5	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.5	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.5	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	99.2	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_37680	TAI/16/2017	cattle	99.2	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	99.1	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.8	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	91.2	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	90.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.5	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_30238	MUR/19/2016	cattle	89.9	0	O	ME-SA	Ind-2001	e
viba_650	IRN/8/2005	ovine	89.9	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.9	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	89.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.4	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/5/2018
Sender reference:	18-3334
Location of origin:	Dao Thanh, My Tho, Tien Giang
Country of origin:	Vietnam
Date of collection:	03/02/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40578, genome 40579, sequence viba_40580, sequencing info 40581	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36461	VIT/18/2017	bovine	99.5	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	99.2	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.2	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.2	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.2	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.1	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.5	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	90.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_397	UAE/4/2008	gazelle	89.7	0	O	ME-SA	Ind-2001	c
viba_505	TUR/264/2009		89.7	0	O	ME-SA	PanAsia-2	SAN-09
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.3	0	O	ME-SA	PanAsia-2	
viba_491	TUR/257/2008		89.1	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/7/2018
Sender reference:	18-5482
Location of origin:	Tinh An, Quang Ngai, Quang Ngai
Country of origin:	Vietnam
Date of collection:	09/03/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	28/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40586, genome 40587, sequence viba_40588, sequencing info 40589	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40600	VIT/10/2018	porcine	99.7	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	99.1	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.1	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.1	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	98.9	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	98.9	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.3	0	O	ME-SA	PanAsia	
viba_293	BHU/3/2009	cattle	90.8	0	O	ME-SA	Ind-2001	d
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.0	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_30238	MUR/19/2016	cattle	89.6	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.1	0	O	ME-SA	Ind-2001	c

Virus sample name:	VIT/9/2018
Sender reference:	18-5822
Location of origin:	An Thanh Thuy, Cho Gao, Tien Giang
Country of origin:	Vietnam
Date of collection:	13/03/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40594, genome 40595, sequence viba_40596, sequencing info 40597	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36461	VIT/18/2017	bovine	99.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.4	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.4	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.4	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	99.2	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	99.2	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	99.2	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.6	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	91.3	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	90.5	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.4	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_397	UAE/4/2008	gazelle	89.7	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.6	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/10/2018
Sender reference:	18-5835
Location of origin:	Tinh Hiep, Son Tinh, Quang Ngai
Country of origin:	Vietnam
Date of collection:	14/03/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40598, genome 40599, sequence viba_40600, sequencing info 40601

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40588	VIT/7/2018	cattle	99.7	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	99.1	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.1	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.1	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	98.9	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.3	0	O	ME-SA	PanAsia	
viba_293	BHU/3/2009	cattle	90.8	0	O	ME-SA	Ind-2001	d
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.0	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_30238	MUR/19/2016	cattle	89.6	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.4	0	O	ME-SA	Ind-2001	c
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/11/2018
Sender reference:	18-8353
Location of origin:	Binh Sa, Thang Binh, Quang Nam
Country of origin:	Vietnam
Date of collection:	13/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	28/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40602, genome 40603, sequence viba_40604, sequencing info 40605	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36461	VIT/18/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	99.1	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.1	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.1	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	98.9	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	98.9	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	98.9	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.3	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.7	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	90.2	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.0	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.6	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.4	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.3	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		88.9	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/12/2018
Sender reference:	18-9129
Location of origin:	Que Trung, Nong Son, Quang Nam
Country of origin:	Vietnam
Date of collection:	28/04/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	28/02/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40606, genome 40607, sequence viba_40608, sequencing info 40609	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_37692	TAI/4/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	99.1	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	98.9	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_37680	TAI/16/2017	cattle	98.7	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	98.7	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	98.6	0	O	ME-SA	PanAsia	
viba_40576	VIT/3/2018	cattle	98.6	0	O	ME-SA	PanAsia	
viba_37696	TAI/5/2018	cattle	98.6	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	90.7	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.0	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	89.9	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	89.6	0	O	ME-SA	Ind-2001	b
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_397	UAE/4/2008	gazelle	89.0	0	O	ME-SA	Ind-2001	c
viba_650	IRN/8/2005	ovine	88.9	0	O	ME-SA	PanAsia-2	
viba_860	IRN/6/2015	cattle	88.3	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	88.3	0	O	ME-SA	PanAsia-2	BAL-09
viba_850	NEP/1/2015	cattle	88.0	1	O	ME-SA	PanAsia-2	KAT-15

Virus sample name:	VIT/13/2018
Sender reference:	18-11786
Location of origin:	Phuoc My, Phuoc Son, Quang Nam
Country of origin:	Vietnam
Date of collection:	29/05/2018
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40610, genome 40611, sequence viba_40612, sequencing info 40613	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36461	VIT/18/2017	bovine	98.9	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.6	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.6	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.6	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	98.6	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	98.6	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	98.6	0	O	ME-SA	PanAsia	
viba_37131	XJHM/CHA/2018-B	cattle	98.4	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	98.4	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.5	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	90.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.5	0	O	ME-SA	Ind-2001	b
viba_30238	MUR/19/2016	cattle	90.1	0	O	ME-SA	Ind-2001	e
viba_650	IRN/8/2005	ovine	89.9	0	O	ME-SA	PanAsia-2	
viba_505	TUR/264/2009		89.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_766	IRN/31/2009	cattle	89.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_359	Manisa/TUR/69		89.3	0	O	ME-SA		
viba_491	TUR/257/2008		89.1	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/14/2018
Sender reference:	18-13553
Location of origin:	Phuoc Tan, Xuyen Moc, Ba Ria Vung Tau
Country of origin:	Vietnam
Date of collection:	22/06/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40614, genome 40615, sequence viba_40616, sequencing info 40617	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36481	VIT/29/2017	bovine	98.9	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.9	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	98.9	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	98.9	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	98.7	0	O	ME-SA	PanAsia	
viba_40576	VIT/3/2018	cattle	98.7	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.6	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.6	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	98.6	0	O	ME-SA	PanAsia	
viba_37680	TAI/16/2017	cattle	98.6	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	91.2	0	O	ME-SA	PanAsia	
viba_293	BHU/3/2009	cattle	90.7	0	O	ME-SA	Ind-2001	d
viba_705	KUW/3/97	bovine	90.5	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	89.9	0	O	ME-SA	Ind-2001	b
viba_650	IRN/8/2005	ovine	89.9	0	O	ME-SA	PanAsia-2	
viba_30238	MUR/19/2016	cattle	89.8	0	O	ME-SA	Ind-2001	e
viba_505	TUR/264/2009		89.7	0	O	ME-SA	PanAsia-2	SAN-09
viba_766	IRN/31/2009	cattle	89.6	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.4	0	O	ME-SA	PanAsia-2	TER-08
viba_666	IRN/18/2010	cattle	89.4	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/17/2018
Sender reference:	18F207
Location of origin:	Mo Vang, Van Yen, Yen Bai
Country of origin:	Vietnam
Date of collection:	19/09/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	02/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40618, genome 40619, sequence viba_40620, sequencing info 40621

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40640	VIT/22/2018	water buffalo	99.4	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	98.6	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.3	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.3	0	O	ME-SA	PanAsia	
viba_37680	TAI/16/2017	cattle	98.3	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	98.3	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	98.1	0	O	ME-SA	PanAsia	
viba_40576	VIT/3/2018	cattle	98.1	0	O	ME-SA	PanAsia	
viba_37696	TAI/5/2018	cattle	98.1	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	90.4	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.0	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	89.7	0	O	ME-SA	Ind-2001	b
viba_293	BHU/3/2009	cattle	89.6	0	O	ME-SA	Ind-2001	d
viba_505	TUR/264/2009		89.6	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	89.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_860	IRN/6/2015	cattle	89.1	0	O	ME-SA	PanAsia-2	QOM-15
viba_30238	MUR/19/2016	cattle	89.0	0	O	ME-SA	Ind-2001	e
viba_491	TUR/257/2008		88.9	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/18/2018
Sender reference:	18-22002
Location of origin:	Phuoc Trung, Go Cong Dong, Tien Giang
Country of origin:	Vietnam
Date of collection:	27/09/2018
Host species:	
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40622, genome 40623, sequence viba_40624, sequencing info 40625	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40664	VIT/28/2018	porcine	99.7	0	O	ME-SA	PanAsia	
viba_40632	VIT/20/2018	cattle	99.7	0	O	ME-SA	PanAsia	
viba_40628	VIT/19/2018	porcine	99.7	0	O	ME-SA	PanAsia	
viba_40692	VIT/35/2018	cattle	99.4	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40588	VIT/7/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_40600	VIT/10/2018	porcine	98.4	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	91.0	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	91.0	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.6	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/19/2018
Sender reference:	18-23369
Location of origin:	Phu Thanh, Tan Phu Dong, Tien Giang
Country of origin:	Vietnam
Date of collection:	14/10/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40626, genome 40627, sequence viba_40628, sequencing info 40629	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40664	VIT/28/2018	porcine	100.0	0	O	ME-SA	PanAsia	
viba_40632	VIT/20/2018	cattle	100.0	0	O	ME-SA	PanAsia	
viba_40624	VIT/18/2018		99.7	0	O	ME-SA	PanAsia	
viba_40692	VIT/35/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40588	VIT/7/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_40600	VIT/10/2018	porcine	98.4	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	91.0	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	91.0	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.6	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/20/2018
Sender reference:	18-23392
Location of origin:	Phu Thanh, Tan Phu Dong, Tien Giang
Country of origin:	Vietnam
Date of collection:	17/10/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	02/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019

VIBASys IDs: sample 40630, genome 40631, sequence viba_40632, sequencing info 40633

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40664	VIT/28/2018	porcine	100.0	0	O	ME-SA	PanAsia	
viba_40628	VIT/19/2018	porcine	100.0	0	O	ME-SA	PanAsia	
viba_40624	VIT/18/2018		99.7	0	O	ME-SA	PanAsia	
viba_40692	VIT/35/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40588	VIT/7/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_40600	VIT/10/2018	porcine	98.4	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	91.0	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	91.0	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.6	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/22/2018
Sender reference:	18F258
Location of origin:	Bang Van, Ngan Son, Bac Can
Country of origin:	Vietnam
Date of collection:	11/11/2018
Host species:	water buffalo
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	02/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40638, genome 40639, sequence viba_40640, sequencing info 40641	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40620	VIT/17/2018	porcine	99.4	0	O	ME-SA	PanAsia	
viba_37707	LAO/1/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_37668	TAI/12/2017	cattle	98.3	0	O	ME-SA	PanAsia	
viba_40576	VIT/3/2018	cattle	98.1	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	97.9	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	97.9	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	97.9	0	O	ME-SA	PanAsia	
viba_37680	TAI/16/2017	cattle	97.9	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	97.9	0	O	ME-SA	PanAsia	
viba_37688	TAI/3/2018	cattle	97.8	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_285	UKG/35/2001	porcine	90.2	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	89.9	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	89.6	0	O	ME-SA	Ind-2001	b
viba_293	BHU/3/2009	cattle	89.3	0	O	ME-SA	Ind-2001	d
viba_650	IRN/8/2005	ovine	89.3	0	O	ME-SA	PanAsia-2	
viba_860	IRN/6/2015	cattle	88.9	0	O	ME-SA	PanAsia-2	QOM-15
viba_850	NEP/1/2015	cattle	88.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_666	IRN/18/2010	cattle	88.8	0	O	ME-SA	PanAsia-2	BAL-09
viba_30238	MUR/19/2016	cattle	88.7	0	O	ME-SA	Ind-2001	e
viba_397	UAE/4/2008	gazelle	88.3	0	O	ME-SA	Ind-2001	c

Virus sample name:	VIT/28/2018
Sender reference:	18-27409
Location of origin:	My Thanh Nam, Cai Lay, Tien Giang
Country of origin:	Vietnam
Date of collection:	01/12/2018
Host species:	porcine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40662, genome 40663, sequence viba_40664, sequencing info 40665	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40632	VIT/20/2018	cattle	100.0	0	O	ME-SA	PanAsia	
viba_40628	VIT/19/2018	porcine	100.0	0	O	ME-SA	PanAsia	
viba_40624	VIT/18/2018		99.7	0	O	ME-SA	PanAsia	
viba_40692	VIT/35/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	98.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.4	0	O	ME-SA	PanAsia	
viba_40588	VIT/7/2018	cattle	98.4	0	O	ME-SA	PanAsia	
viba_40600	VIT/10/2018	porcine	98.4	0	O	ME-SA	PanAsia	

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	91.0	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	91.0	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.8	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.6	0	O	ME-SA	Ind-2001	c
viba_30238	MUR/19/2016	cattle	89.5	0	O	ME-SA	Ind-2001	e
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.4	0	O	ME-SA	PanAsia-2	

Virus sample name:	VIT/35/2018
Sender reference:	19-728
Location of origin:	Cu Bao, Buon Ho, Dak Lak
Country of origin:	Vietnam
Date of collection:	24/12/2018
Host species:	cattle
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	05/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40690, genome 40691, sequence viba_40692, sequencing info 40693	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40624	VIT/18/2018		99.4	0	O	ME-SA	PanAsia	
viba_40664	VIT/28/2018	porcine	99.1	0	O	ME-SA	PanAsia	
viba_40632	VIT/20/2018	cattle	99.1	0	O	ME-SA	PanAsia	
viba_40628	VIT/19/2018	porcine	99.1	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	98.1	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	97.8	0	O	ME-SA	PanAsia	
viba_40596	VIT/9/2018	porcine	97.8	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	97.8	0	O	ME-SA	PanAsia	
viba_40588	VIT/7/2018	cattle	97.8	0	O	ME-SA	PanAsia	
viba_40600	VIT/10/2018	porcine	97.8	0	O	ME-SA	PanAsia	

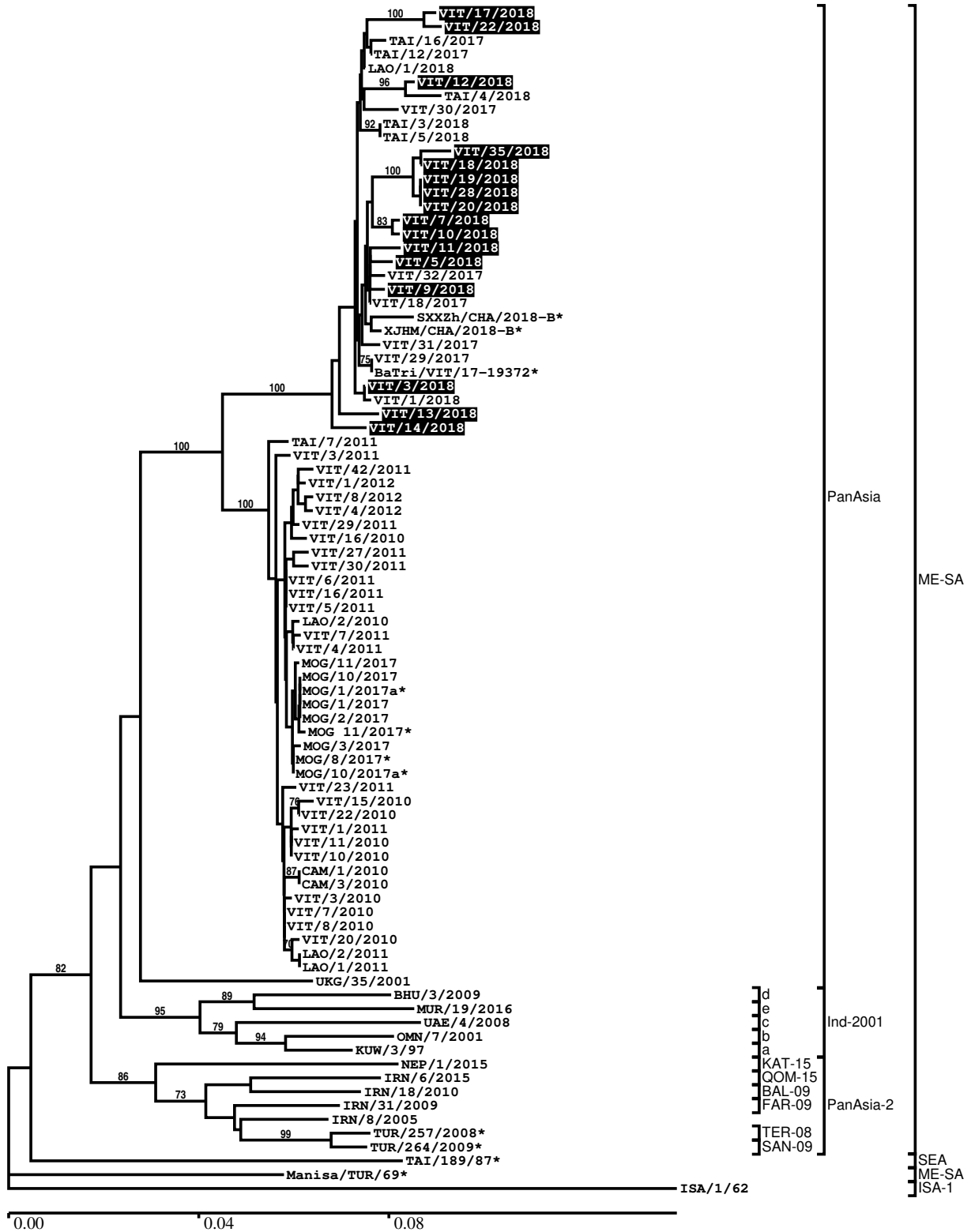
Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_293	BHU/3/2009	cattle	90.4	0	O	ME-SA	Ind-2001	d
viba_285	UKG/35/2001	porcine	90.4	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	90.2	0	O	ME-SA	Ind-2001	a
viba_541	OMN/7/2001	bovine	89.9	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_30238	MUR/19/2016	cattle	89.4	0	O	ME-SA	Ind-2001	e
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08
viba_650	IRN/8/2005	ovine	89.1	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		89.1	0	O	ME-SA		
viba_397	UAE/4/2008	gazelle	89.0	0	O	ME-SA	Ind-2001	c

Report on FMDV O in Vietnam in 2018

Batch: WRLFMD/2019/00010B



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2019/00010B-Vietnam-O (16 sequences)
Sequence database set:	allseqs_O (4390 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	636
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	14
VIBASys version:	reflabs-1.1.2

Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	accession	host(s)	lab	country	taxonomic information
VIT/17/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/22/2018	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
TAI/16/2017	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
TAI/12/2017	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
LAO/1/2018	n/a	cattle	WRLFMD	Laos	ME-SA/PanAsia
VIT/12/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
TAI/4/2018	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
VIT/30/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
TAI/3/2018	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
TAI/5/2018	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
VIT/35/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/18/2018	n/a	n/a	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/19/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/28/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/20/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/7/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/10/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/11/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/5/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/32/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/9/2018	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/18/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
SXXZh/CHA/2018-B*	n/a	cattle	LVRI	China	ME-SA/PanAsia
XJHM/CHA/2018-B*	n/a	cattle	LVRI	China	ME-SA/PanAsia
VIT/31/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/29/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
BaTri/VIT/17-19372*	n/a	cattle	RAHO6	Vietnam	ME-SA/PanAsia
VIT/3/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/1/2018	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/13/2018	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/14/2018	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
TAI/7/2011	n/a	cattle	WRLFMD	Thailand	ME-SA/PanAsia
VIT/3/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/42/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/1/2012	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/8/2012	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia

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label	accession	host(s)	lab	country	taxonomic information
VIT/4/2012	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/29/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/16/2010	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/27/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/30/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/6/2011	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/16/2011	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/5/2011	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
LAO/2/2010	n/a	cattle	WRLFMD	Laos	ME-SA/PanAsia
VIT/7/2011	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/4/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
MOG/11/2017	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG/10/2017	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG/1/2017a*	n/a	cattle	ARRIAH	Mongolia	ME-SA/PanAsia
MOG/1/2017	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG/2/2017	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG 11/2017*	n/a	cattle	ARRIAH	Mongolia	ME-SA/PanAsia
MOG/3/2017	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG/8/2017*	n/a	cattle	ARRIAH	Mongolia	ME-SA/PanAsia
MOG/10/2017a*	n/a	cattle	ARRIAH	Mongolia	ME-SA/PanAsia
VIT/23/2011	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/15/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/22/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/1/2011	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/11/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/10/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
CAM/1/2010	n/a	cattle	WRLFMD	Cambodia	ME-SA/PanAsia
CAM/3/2010	n/a	n/a	WRLFMD	Cambodia	ME-SA/PanAsia
VIT/3/2010	n/a	porcine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/7/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/8/2010	n/a	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/20/2010	n/a	water buffalo	WRLFMD	Vietnam	ME-SA/PanAsia
LAO/2/2011	n/a	water buffalo	WRLFMD	Laos	ME-SA/PanAsia
LAO/1/2011	n/a	water buffalo	WRLFMD	Laos	ME-SA/PanAsia
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
BHU/3/2009	KM921814	cattle	WRLFMD	Bhutan	ME-SA/Ind-2001/d
MUR/19/2016	MG972510	cattle	WRLFMD	Mauritius	ME-SA/Ind-2001/e
UAE/4/2008	KM921876	gazelle	WRLFMD	United Arab Emirates	ME-SA/Ind-2001/c
OMN/7/2001	DQ164941	bovine	WRLFMD	Oman	ME-SA/Ind-2001/b
KUW/3/97	DQ164904	bovine	WRLFMD	Kuwait	ME-SA/Ind-2001/a
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
IRN/6/2015	n/a	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/QOM-15
IRN/18/2010	KY091283	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/BAL-09
IRN/31/2009	KY091284	cattle	WRLFMD	Iran	ME-SA/PanAsia-2/FAR-09
IRN/8/2005	KY091281	ovine	WRLFMD	Iran	ME-SA/PanAsia-2
TUR/257/2008*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
TUR/264/2009*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
Manisa/TUR/69*	AY593823	n/a	PIADC	Turkey	ME-SA
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

*, not a WRLFMD Reference Number

n/a, not available

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

Genotyping Report

FMDV serotype: O/CATHAY
Country: Vietnam
Year: 2018
Batch: WRLFMD/2019/00010C
No. of sequences: 3
Report date: 24th March 2019
Report generated by: Nick Knowles
Report checked by: Jemma Wadsworth



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www: <http://www.wrlfmd.org/>

email: reporting@pirbright.ac.uk

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Virus sample name:	VIT/6/2018
Sender reference:	18-3766
Location of origin:	My Thanh Nam, Cai Lay, Tien Giang
Country of origin:	Vietnam
Date of collection:	07/02/2018
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40582, genome 40583, sequence viba_40584, sequencing info 40585	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_40592	VIT/8/2018	porcine	97.9	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	97.5	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	96.8	0	O	CATHAY		
viba_40636	VIT/21/2018	porcine	95.7	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	93.8	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	93.7	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	93.4	0	O	CATHAY		
viba_37127	GXCX/CHA/2018-S	porcine	93.2	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	93.0	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	92.9	0	O	CATHAY		

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_418	PHI/7/96	porcine	87.8	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	87.7	0	O	CATHAY		
viba_584	HKN/6/83	bovine	82.5	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.2	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.4	0	O	ME-SA		
viba_30238	MUR/19/2016	cattle	80.3	0	O	ME-SA	Ind-2001	e
viba_850	NEP/1/2015	cattle	79.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_293	BHU/3/2009	cattle	79.7	0	O	ME-SA	Ind-2001	d
viba_617	IND/53/79	bovine	79.7	0	O	ME-SA		
viba_705	KUW/3/97	bovine	79.6	0	O	ME-SA	Ind-2001	a

Virus sample name:	VIT/8/2018
Sender reference:	18-5490
Location of origin:	Thanh Phu, Binh Long, Binh Phuoc
Country of origin:	Vietnam
Date of collection:	11/03/2018
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	01/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40590, genome 40591, sequence viba_40592, sequencing info 40593	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36469	VIT/22/2017	porcine	98.3	0	O	CATHAY		
viba_40584	VIT/6/2018	porcine	97.9	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	97.6	0	O	CATHAY		
viba_40636	VIT/21/2018	porcine	96.2	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	95.1	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	94.9	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	94.6	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	94.5	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	94.3	0	O	CATHAY		
viba_37127	GXCX/CHA/2018-S	porcine	94.0	0	O	CATHAY		

Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_418	PHI/7/96	porcine	88.9	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	88.5	0	O	CATHAY		
viba_584	HKN/6/83	bovine	84.0	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.3	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.7	0	O	ME-SA		
viba_617	IND/53/79	bovine	80.0	0	O	ME-SA		
viba_30238	MUR/19/2016	cattle	80.0	0	O	ME-SA	Ind-2001	e
viba_563	Brescia/ITL/47		79.9	4	O	EURO-SA	O2	
viba_850	NEP/1/2015	cattle	79.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_694	CAM/3/98	bovine	79.7	0	O	SEA	Cam-94	

Virus sample name:	VIT/21/2018
Sender reference:	18CD-1610.2
Location of origin:	Ky Son, Tan Ky, Nghe An
Country of origin:	Vietnam
Date of collection:	22/10/2018
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	03/03/2019
Primers:	FMD-3161F/FMD-4303R
Received for sequencing:	18/03/2019
Created:	22/03/2019
Last updated:	22/03/2019
VIBASys IDs: sample 40634, genome 40635, sequence viba_40636, sequencing info 40637	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36473	VIT/26/2017	porcine	96.8	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	96.4	0	O	CATHAY		
viba_40592	VIT/8/2018	porcine	96.2	0	O	CATHAY		
viba_40584	VIT/6/2018	porcine	95.7	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	93.2	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	92.9	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	92.9	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	92.9	0	O	CATHAY		
viba_37127	GXCX/CHA/2018-S	porcine	92.7	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	92.4	0	O	CATHAY		

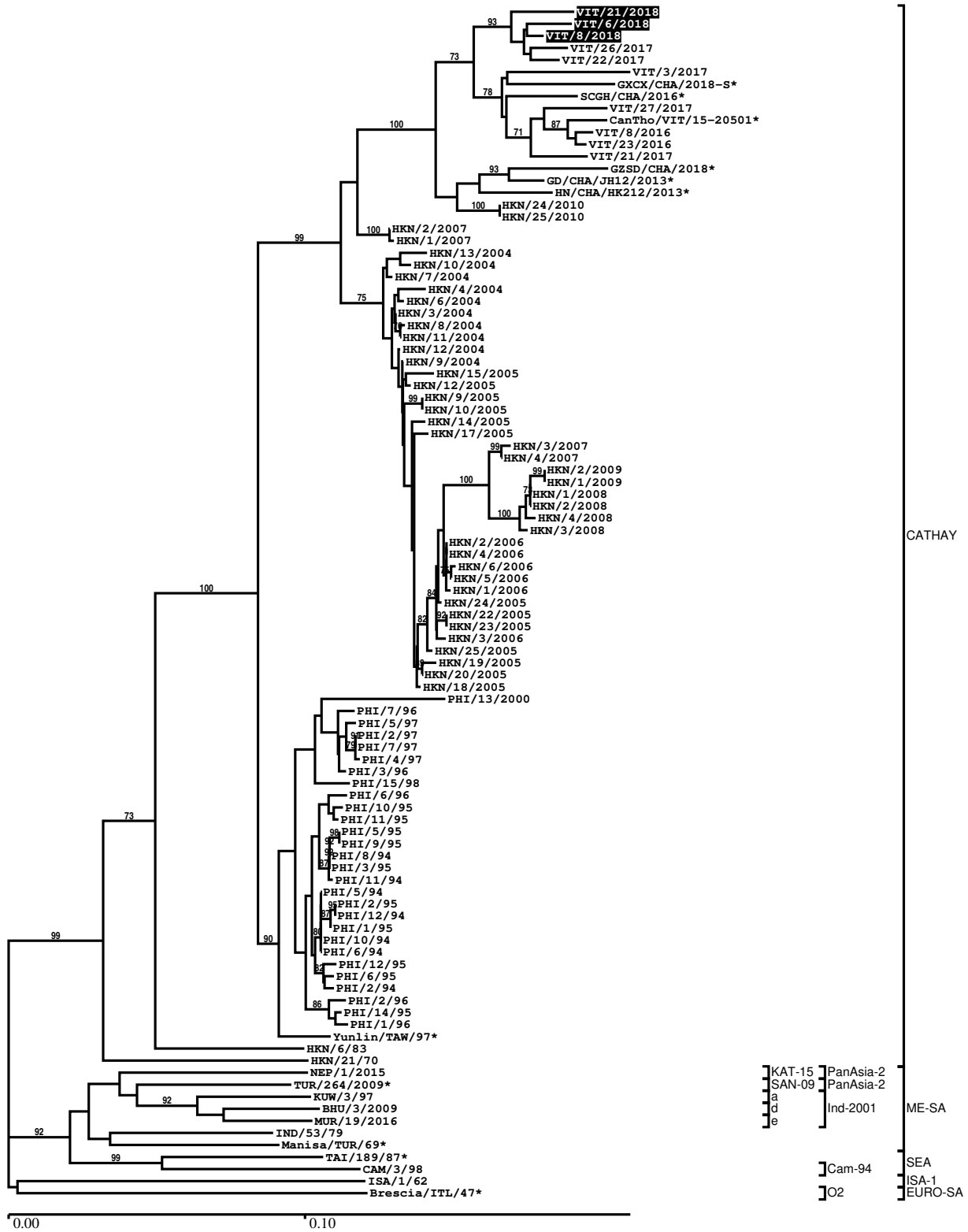
Most Closely Related Prototype Sequences

see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_480	Yunlin/TAW/97	porcine	87.8	0	O	CATHAY		
viba_418	PHI/7/96	porcine	87.4	0	O	CATHAY		
viba_584	HKN/6/83	bovine	83.3	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.8	2	O	CATHAY		
viba_617	IND/53/79	bovine	80.3	0	O	ME-SA		
viba_359	Manisa/TUR/69		79.8	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	79.8	1	O	ME-SA	PanAsia-2	KAT-15
viba_505	TUR/264/2009		79.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_705	KUW/3/97	bovine	79.3	0	O	ME-SA	Ind-2001	a
viba_694	CAM/3/98	bovine	79.3	0	O	SEA	Cam-94	

Report on FMDV O in Vietnam in 2018

Batch: WRLFMD/2019/00010C



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2019/00010C-Vietnam-O (3 sequences)
Sequence database set:	allseqs_O (4390 sequences)
Prototype sequence set:	!prototypes_O (49 sequences)
Number of related sequences reported:	10
Minimal VP1 subsequence match length	600
Sequence alignment method:	muscle (default parameters)
Sequence alignment length:	633
Phylogeny reconstruction method:	fdnadist, fneighbor
Number of bootstrap samples:	1000
Random seed for bootstrapping:	1
Displaying bootstrap values above:	70.0%
Number of sequences in tree capped at:	100
Number of prototype sequences in tree:	13
VIBASys version:	reflabs-1.1.2

Sequences in the Phylogenetic Tree

All sequences in the tree are in taxonomic group FMDV/O

label	accession	host(s)	lab	country	taxonomic information
VIT/21/2018	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/6/2018	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/8/2018	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/26/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/22/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/3/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
GXCX/CHA/2018-S*	n/a	porcine	LVRI	China	CATHAY
SCGH/CHA/2016*	KX161429	porcine	LVRI	China	CATHAY
VIT/27/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
CanTho/VIT/15-20501*	n/a	porcine	RAHO6	Vietnam	CATHAY
VIT/8/2016	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/23/2016	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/21/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
MGZSD/CHA/2018*	MG840803	porcine	LVRI	China	CATHAY
GD/CHA/JH12/2013*	KU204894	porcine	SMU	China	CATHAY
HN/CHA/HK212/2013*	KU204893	porcine	SMU	China	CATHAY
HKN/24/2010	KM243162	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/25/2010	KM243163	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/2/2007	KM243151	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/1/2007	KM243150	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/13/2004	KM243126	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/10/2004	DQ164887	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/7/2004	DQ164884	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/4/2004	DQ164882	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/6/2004	DQ164883	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/3/2004	DQ164881	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/8/2004	DQ164885	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/11/2004	DQ164888	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/12/2004	DQ164889	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/9/2004	DQ164886	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/15/2005	KM243134	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/12/2005	KM243132	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/9/2005	KM243129	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/10/2005	KM243130	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/14/2005	KM243133	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/17/2005	KM243135	porcine	WRLFMD	Hong Kong SAR	CATHAY

continued on next page

label	accession	host(s)	lab	country	taxonomic information
HKN/3/2007	KM243152	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/4/2007	KM243153	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/2/2009	KM243160	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/1/2009	KM243159	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/1/2008	KM243155	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/2/2008	KM243156	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/4/2008	KM243158	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/3/2008	KM243157	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/2/2006	KM243145	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/4/2006	KM243147	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/6/2006	KM243149	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/5/2006	KM243148	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/1/2006	KM243144	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/24/2005	KM243142	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/22/2005	KM243140	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/23/2005	KM243141	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/3/2006	KM243146	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/25/2005	KM243143	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/19/2005	KM243137	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/20/2005	KM243138	porcine	WRLFMD	Hong Kong SAR	CATHAY
HKN/18/2005	KM243136	porcine	WRLFMD	Hong Kong SAR	CATHAY
PHI/13/2000	DQ164948	n/a	WRLFMD	Philippines	CATHAY
PHI/7/96	AJ294926	porcine	WRLFMD	Philippines	CATHAY
PHI/5/97	KM243062	porcine	WRLFMD	Philippines	CATHAY
PHI/2/97	KM243059	porcine	WRLFMD	Philippines	CATHAY
PHI/7/97	KM243064	porcine	WRLFMD	Philippines	CATHAY
PHI/4/97	KM243061	porcine	WRLFMD	Philippines	CATHAY
PHI/3/96	KM243055	porcine	WRLFMD	Philippines	CATHAY
PHI/15/98	KM243088	porcine	WRLFMD	Philippines	CATHAY
PHI/6/96	KM243057	porcine	WRLFMD	Philippines	CATHAY
PHI/10/95	KM243046	porcine	WRLFMD	Philippines	CATHAY
PHI/11/95	KM243047	porcine	WRLFMD	Philippines	CATHAY
PHI/5/95	DQ164946	n/a	WRLFMD	Philippines	CATHAY
PHI/9/95	KM243045	porcine	WRLFMD	Philippines	CATHAY
PHI/8/94	KM243037	porcine	WRLFMD	Philippines	CATHAY
PHI/3/95	KM243043	porcine	WRLFMD	Philippines	CATHAY
PHI/11/94	KM243039	porcine	WRLFMD	Philippines	CATHAY
PHI/5/94	KM243035	porcine	WRLFMD	Philippines	CATHAY
PHI/2/95	KM243042	porcine	WRLFMD	Philippines	CATHAY
PHI/12/94	KM243040	porcine	WRLFMD	Philippines	CATHAY
PHI/1/95	KM243041	porcine	WRLFMD	Philippines	CATHAY
PHI/10/94	KM243038	porcine	WRLFMD	Philippines	CATHAY
PHI/6/94	KM243036	porcine	WRLFMD	Philippines	CATHAY
PHI/12/95	KM243048	porcine	WRLFMD	Philippines	CATHAY
PHI/6/95	KM243044	porcine	WRLFMD	Philippines	CATHAY
PHI/2/94	KM243034	porcine	WRLFMD	Philippines	CATHAY
PHI/2/96	KM243054	porcine	WRLFMD	Philippines	CATHAY
PHI/14/95	KM243050	porcine	WRLFMD	Philippines	CATHAY
PHI/1/96	KM243053	porcine	WRLFMD	Philippines	CATHAY
Yunlin/TAW/97*	AF308157	porcine	PIADC	Taiwan	CATHAY
HKN/6/83	AJ294919	bovine	WRLFMD	Hong Kong SAR	CATHAY
HKN/21/70	AJ294911	porcine	WRLFMD	Hong Kong SAR	CATHAY
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
TUR/264/2009*	n/a	n/a	FMDI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
KUW/3/97	DQ164904	bovine	WRLFMD	Kuwait	ME-SA/Ind-2001/a
BHU/3/2009	KM921814	cattle	WRLFMD	Bhutan	ME-SA/Ind-2001/d
MUR/19/2016	MG972510	cattle	WRLFMD	Mauritius	ME-SA/Ind-2001/e
IND/53/79	AF292107	bovine	PD-FMD	India	ME-SA
Manisa/TUR/69*	AY593823	n/a	PIADC	Turkey	ME-SA
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
CAM/3/98	AJ294910	bovine	WRLFMD	Cambodia	SEA/Cam-94
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1
Brescia/ITL/47*	M55287	n/a	BFAV	Italy	EURO-SA/O2

*, not a WRLFMD Reference Number
n/a, not available