

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

Genotyping Report

FMDV serotype: O
Country: Vietnam
Year: 2016, 2017, 2018
Batch: WRLFMD/2018/00011
No. of sequences: 20
Report date: 10th May 2018
Report generated by: Nick Knowles
Report checked by: Kasia Bankowska



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Virus sample name:	VIT/23/2016
Sender reference:	16-13570
Location of origin:	Ham Tan, Binh Thuan
Country of origin:	Vietnam
Date of collection:	10/07/2016
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	04/05/2018
Last updated:	04/05/2018
VIBASys IDs: sample 36418, genome 36419, sequence viba_36420, sequencing info 36421	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_31464	VIT/8/2016	porcine	99.1	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	97.8	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	97.3	0	O	CATHAY		
viba_36477	VIT/27/2017	porcine	97.0	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	95.3	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	95.1	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	94.3	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	94.3	0	O	CATHAY		
viba_36440	VIT/3/2017	porcine	94.2	0	O	CATHAY		
viba_14613	HKN/25/2010	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	86.9	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	86.7	0	O	CATHAY		
viba_584	HKN/6/83	bovine	81.7	2	O	CATHAY		
viba_325	HKN/21/70	porcine	81.7	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.1	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	79.5	1	O	ME-SA	PanAsia-2	KAT-15
viba_617	IND/53/79	bovine	79.0	0	O	ME-SA		
viba_505	TUR/264/2009		78.8	0	O	ME-SA	PanAsia-2	SAN-09
viba_50	UGA/17/98		78.7	0	O	EA-4		
viba_285	UKG/35/2001	porcine	78.7	0	O	ME-SA	PanAsia	

Virus sample name:	VIT/24/2016
Sender reference:	16-16193
Location of origin:	Loc Thanh, Loc Ninh, Binh Phuoc
Country of origin:	Vietnam
Date of collection:	18/08/2016
Host species:	bovine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	11/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	04/05/2018
Last updated:	04/05/2018
VIBASys IDs: sample 36422, genome 36423, sequence viba_36424, sequencing info 36425	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_26288	TAI/22/2015	water buffalo	99.4	0	O	SEA	Mya-98	
viba_25518	MYA/1/2015	bovine	99.2	0	O	SEA	Mya-98	
viba_30518	TAI/34/2016	cattle	99.1	0	O	SEA	Mya-98	
viba_30498	TAI/26/2016	cattle	98.9	0	O	SEA	Mya-98	
viba_26312	TAI/30/2015	cattle	98.9	0	O	SEA	Mya-98	
viba_33981	TAI/51/2016	cattle	98.7	0	O	SEA	Mya-98	
viba_32425	MYA/4/2017a	cattle	98.7	0	O	SEA	Mya-98	
viba_30494	TAI/21/2016	cattle	98.7	0	O	SEA	Mya-98	
viba_31488	VIT/17/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_30506	TAI/31/2016	cattle	98.6	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	92.3	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	89.1	0	O	SEA		
viba_766	IRN/31/2009	cattle	84.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_860	IRN/6/2015	cattle	84.5	0	O	ME-SA	PanAsia-2	QOM-15
viba_505	TUR/264/2009		84.4	0	O	ME-SA	PanAsia-2	SAN-09
viba_719	IRN/88/2009		84.4	0	O	ME-SA	PanAsia-2	ANT-10
viba_694	CAM/3/98	bovine	84.3	0	O	SEA	Cam-94	
viba_354	PAK/16/2010	cattle	84.2	0	O	ME-SA	PanAsia-2	PUN-10
viba_491	TUR/257/2008		84.2	0	O	ME-SA	PanAsia-2	TER-08
viba_666	IRN/18/2010	cattle	84.1	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/27/2016
Sender reference:	16-20297
Location of origin:	Tam Phu, Tam Ky, Quang Nam
Country of origin:	Vietnam
Date of collection:	14/10/2016
Host species:	bovine
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	04/05/2018
Last updated:	04/05/2018
VIBASys IDs: sample 36426, genome 36427, sequence viba_36428, sequencing info 36429	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_31456	VIT/5/2016	cattle	99.5	0	O	SEA	Mya-98	
viba_26304	TAI/28/2015	cattle	99.5	0	O	SEA	Mya-98	
viba_31452	VIT/4/2016	porcine	99.5	0	O	SEA	Mya-98	
viba_31460	VIT/7/2016	cattle	99.5	0	O	SEA	Mya-98	
viba_31476	VIT/11/2016	porcine	99.4	0	O	SEA	Mya-98	
viba_23841	TAI/4/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_31480	VIT/12/2016	porcine	99.2	0	O	SEA	Mya-98	
viba_31468	VIT/9/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_23803	LAO/2/2016	water buffalo	99.2	0	O	SEA	Mya-98	
viba_36444	VIT/5/2017	porcine	99.1	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	92.1	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	89.0	0	O	SEA		
viba_576	IND/R2/75		86.6	0	O	ME-SA		
viba_694	CAM/3/98	bovine	86.4	0	O	SEA	Cam-94	
viba_505	TUR/264/2009		86.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_766	IRN/31/2009	cattle	85.8	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		85.8	0	O	ME-SA	PanAsia-2	ANT-10
viba_359	Manisa/TUR/69		85.7	0	O	ME-SA		
viba_491	TUR/257/2008		85.7	0	O	ME-SA	PanAsia-2	TER-08
viba_617	IND/53/79	bovine	85.7	0	O	ME-SA		

Virus sample name:	VIT/1/2017
Sender reference:	17F1
Location of origin:	Tinh Huc, Binh Lieu, Quang Ninh
Country of origin:	Vietnam
Date of collection:	07/01/2017
Host species:	water buffalo
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	11/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	04/05/2018
Last updated:	04/05/2018
VIBASys IDs: sample 36430, genome 36431, sequence viba_36432, sequencing info 36433	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_31488	VIT/17/2016	cattle	99.8	0	O	SEA	Mya-98	
viba_31484	VIT/15/2016	water buffalo	99.8	0	O	SEA	Mya-98	
viba_33981	TAI/51/2016	cattle	99.4	0	O	SEA	Mya-98	
viba_36448	VIT/7/2017	water buffalo	99.4	0	O	SEA	Mya-98	
viba_30506	TAI/31/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_33937	TAI/40/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_33977	TAI/50/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_33933	TAI/39/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_30522	TAI/35/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_33945	TAI/42/2016	cattle	99.2	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	91.6	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	88.5	0	O	SEA		
viba_491	TUR/257/2008		84.2	0	O	ME-SA	PanAsia-2	TER-08
viba_766	IRN/31/2009	cattle	84.1	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		84.0	0	O	ME-SA	PanAsia-2	ANT-10
viba_354	PAK/16/2010	cattle	83.9	0	O	ME-SA	PanAsia-2	PUN-10
viba_860	IRN/6/2015	cattle	83.8	0	O	ME-SA	PanAsia-2	QOM-15
viba_505	TUR/264/2009		83.8	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	83.6	0	O	ME-SA	PanAsia-2	
viba_666	IRN/18/2010	cattle	83.5	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/2/2017
Sender reference:	17-1801
Location of origin:	Loc Quang, Loc Ninh, Binh Phuoc
Country of origin:	Vietnam
Date of collection:	09/01/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36434, genome 36435, sequence viba_36436, sequencing info 36437	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36457	VIT/15/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_22178	VIT/36/2013	cattle	96.7	0	O	ME-SA	PanAsia	
viba_22946	MOG/1/2014	cattle	96.5	0	O	ME-SA	PanAsia	
viba_22954	MOG/3/2014	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22114	VIT/13/2013	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22122	VIT/15/2013	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22962	MOG/5/2014	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22950	MOG/2/2014	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22190	VIT/39/2013	cattle	96.4	0	O	ME-SA	PanAsia	
viba_22210	VIT/51/2013	cattle	96.2	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	92.7	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	91.6	0	O	ME-SA	Ind-2001	a
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_293	BHU/3/2009	cattle	90.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.7	0	O	ME-SA	Ind-2001	b
viba_766	IRN/31/2009	cattle	90.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_397	UAE/4/2008	gazelle	90.1	0	O	ME-SA	Ind-2001	c
viba_860	IRN/6/2015	cattle	89.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_666	IRN/18/2010	cattle	89.6	0	O	ME-SA	PanAsia-2	BAL-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/3/2017
Sender reference:	17F4
Location of origin:	Mai Pha, Son La city, Lang Son
Country of origin:	Vietnam
Date of collection:	11/01/2017
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36438, genome 36439, sequence viba_36440, sequencing info 36441	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_31464	VIT/8/2016	porcine	94.2	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	94.2	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	93.8	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	93.4	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	93.2	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	92.9	0	O	CATHAY		
viba_36477	VIT/27/2017	porcine	92.7	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	92.7	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	92.3	0	O	CATHAY		
viba_14613	HKN/25/2010	porcine	91.2	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	85.9	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	85.9	0	O	CATHAY		
viba_584	HKN/6/83	bovine	81.8	2	O	CATHAY		
viba_325	HKN/21/70	porcine	81.2	2	O	CATHAY		
viba_50	UGA/17/98		79.9	0	O	EA-4		
viba_359	Manisa/TUR/69		79.7	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	79.5	1	O	ME-SA	PanAsia-2	KAT-15
viba_617	IND/53/79	bovine	79.2	0	O	ME-SA		
viba_694	CAM/3/98	bovine	78.8	0	O	SEA	Cam-94	
viba_523	K83/79		78.8	0	O	EA-1		

Virus sample name:	VIT/5/2017
Sender reference:	17-4434
Location of origin:	Truong Chinh, Kon Tum city, Kon Tum
Country of origin:	Vietnam
Date of collection:	22/02/2017
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:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36442, genome 36443, sequence viba_36444, sequencing info 36445	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_31456	VIT/5/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_26304	TAI/28/2015	cattle	99.2	0	O	SEA	Mya-98	
viba_31452	VIT/4/2016	porcine	99.2	0	O	SEA	Mya-98	
viba_31460	VIT/7/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_31476	VIT/11/2016	porcine	99.1	0	O	SEA	Mya-98	
viba_36428	VIT/27/2016	bovine	99.1	0	O	SEA	Mya-98	
viba_23841	TAI/4/2016	cattle	98.9	0	O	SEA	Mya-98	
viba_31480	VIT/12/2016	porcine	98.9	0	O	SEA	Mya-98	
viba_31468	VIT/9/2016	cattle	98.9	0	O	SEA	Mya-98	
viba_23803	LAO/2/2016	water buffalo	98.9	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	91.8	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	89.0	0	O	SEA		
viba_576	IND/R2/75		86.6	0	O	ME-SA		
viba_505	TUR/264/2009		86.5	0	O	ME-SA	PanAsia-2	SAN-09
viba_694	CAM/3/98	bovine	86.4	0	O	SEA	Cam-94	
viba_766	IRN/31/2009	cattle	86.3	0	O	ME-SA	PanAsia-2	FAR-09
viba_719	IRN/88/2009		86.3	0	O	ME-SA	PanAsia-2	ANT-10
viba_705	KUW/3/97	bovine	86.1	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	86.1	0	O	ME-SA	Ind-2001	c
viba_491	TUR/257/2008		86.1	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/7/2017
Sender reference:	17F33
Location of origin:	Phieng Cam, Mai Son, Son La
Country of origin:	Vietnam
Date of collection:	07/04/2017
Host species:	water buffalo
Serotype:	O
Topotype:	SEA
Lineage:	Mya-98
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36446, genome 36447, sequence viba_36448, sequencing info 36449	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36432	VIT/1/2017	water buffalo	99.4	0	O	SEA	Mya-98	
viba_31488	VIT/17/2016	cattle	99.2	0	O	SEA	Mya-98	
viba_31484	VIT/15/2016	water buffalo	99.2	0	O	SEA	Mya-98	
viba_33981	TAI/51/2016	cattle	98.7	0	O	SEA	Mya-98	
viba_30506	TAI/31/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_33937	TAI/40/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_33977	TAI/50/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_33933	TAI/39/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_30522	TAI/35/2016	cattle	98.6	0	O	SEA	Mya-98	
viba_33945	TAI/42/2016	cattle	98.6	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	91.0	0	O	SEA	Mya-98	
viba_68	TAI/189/87	bovine	88.2	0	O	SEA		
viba_766	IRN/31/2009	cattle	83.9	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		83.8	0	O	ME-SA	PanAsia-2	TER-08
viba_860	IRN/6/2015	cattle	83.7	0	O	ME-SA	PanAsia-2	QOM-15
viba_719	IRN/88/2009		83.5	0	O	ME-SA	PanAsia-2	ANT-10
viba_354	PAK/16/2010	cattle	83.4	0	O	ME-SA	PanAsia-2	PUN-10
viba_576	IND/R2/75		83.3	0	O	ME-SA		
viba_505	TUR/264/2009		83.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_694	CAM/3/98	bovine	83.2	0	O	SEA	Cam-94	

Virus sample name:	VIT/9/2017
Sender reference:	17-8338
Location of origin:	Ya Xier, Sa Thay, Kon Tum
Country of origin:	Vietnam
Date of collection:	20/04/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	Ind-2001
Sublineage:	e
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36450, genome 36452, sequence viba_36453, sequencing info 36454	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_26113	NEP/15/2015	cattle	98.6	0	O	ME-SA	Ind-2001	e
viba_26109	NEP/14/2015	cattle	98.6	0	O	ME-SA	Ind-2001	e
viba_31595	Zabaikalskiy/3/RUS/2016	cattle	98.6	0	O	ME-SA	Ind-2001	e
viba_33785	MYA/1/2017	cattle	98.6	0	O	ME-SA	Ind-2001	e
viba_31573	170206/SKR/2017	cattle	98.4	0	O	ME-SA	Ind-2001	e
viba_29935	NEP/8/2016	cattle	98.4	0	O	ME-SA	Ind-2001	e
viba_31082	BAN/GKa-236(pig)/2015	porcine	98.4	0	O	ME-SA	Ind-2001	e
viba_30859	Zabaikalskiy/2/RUS/2016	cattle	98.4	0	O	ME-SA	Ind-2001	e
viba_32441	MYA/9/2017	cattle	98.4	0	O	ME-SA	Ind-2001	e
viba_30855	Zabaikalskiy/1/RUS/2016	cattle	98.4	0	O	ME-SA	Ind-2001	e

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	93.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.8	0	O	ME-SA	Ind-2001	b
viba_705	KUW/3/97	bovine	91.2	0	O	ME-SA	Ind-2001	a
viba_397	UAE/4/2008	gazelle	89.3	0	O	ME-SA	Ind-2001	c
viba_285	UKG/35/2001	porcine	88.3	0	O	ME-SA	PanAsia	
viba_650	IRN/8/2005	ovine	87.5	0	O	ME-SA	PanAsia-2	
viba_359	Manisa/TUR/69		87.4	0	O	ME-SA		
viba_766	IRN/31/2009	cattle	87.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	87.2	0	O	ME-SA	PanAsia-2	BAL-09
viba_719	IRN/88/2009		87.2	0	O	ME-SA	PanAsia-2	ANT-10

Virus sample name:	VIT/15/2017
Sender reference:	17-15223
Location of origin:	EaNu?l, Buon Don, Dak Lak
Country of origin:	Vietnam
Date of collection:	02/08/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36455, genome 36456, sequence viba_36457, sequencing info 36458	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36436	VIT/2/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_22178	VIT/36/2013	cattle	97.0	0	O	ME-SA	PanAsia	
viba_22114	VIT/13/2013	cattle	96.7	0	O	ME-SA	PanAsia	
viba_22122	VIT/15/2013	cattle	96.7	0	O	ME-SA	PanAsia	
viba_22190	VIT/39/2013	cattle	96.7	0	O	ME-SA	PanAsia	
viba_22946	MOG/1/2014	cattle	96.5	0	O	ME-SA	PanAsia	
viba_22210	VIT/51/2013	cattle	96.5	0	O	ME-SA	PanAsia	
viba_22202	VIT/46/2013	cattle	96.5	0	O	ME-SA	PanAsia	
viba_22206	VIT/47/2013	cattle	96.5	0	O	ME-SA	PanAsia	
viba_22958	MOG/4/2014	cattle	96.5	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	93.0	0	O	ME-SA	PanAsia	
viba_705	KUW/3/97	bovine	91.6	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	91.0	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	91.0	0	O	ME-SA	Ind-2001	b
viba_650	IRN/8/2005	ovine	90.8	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	90.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.9	0	O	ME-SA	PanAsia-2	TER-08
viba_397	UAE/4/2008	gazelle	89.7	0	O	ME-SA	Ind-2001	c
viba_354	PAK/16/2010	cattle	89.6	0	O	ME-SA	PanAsia-2	PUN-10
viba_666	IRN/18/2010	cattle	89.6	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/18/2017
Sender reference:	17F45
Location of origin:	Chieng Bang, Quynh Nhai, Son La
Country of origin:	Vietnam
Date of collection:	21/08/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36459, genome 36460, sequence viba_36461, sequencing info 36462	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36497	VIT/1/2018	bovine	99.7	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.7	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.7	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.5	0	O	ME-SA	PanAsia	
viba_36485	VIT/30/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_16348	VIT/22/2010	cattle	95.9	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.7	0	O	ME-SA	PanAsia	
viba_18652	TAI/7/2011	cattle	95.7	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.7	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	91.9	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	90.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.7	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	89.7	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.7	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	89.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_666	IRN/18/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/21/2017
Sender reference:	17-17547
Location of origin:	Tan Loi, Buon Me Thuot, Dak Lak
Country of origin:	Vietnam
Date of collection:	07/09/2017
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS2
Harvest date of material:	17/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36463, genome 36464, sequence viba_36465, sequencing info 36466	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36420	VIT/23/2016	porcine	97.3	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	97.0	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	96.1	0	O	CATHAY		
viba_36477	VIT/27/2017	porcine	94.9	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	94.8	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	93.5	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	93.4	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	93.2	0	O	CATHAY		
viba_36440	VIT/3/2017	porcine	92.7	0	O	CATHAY		
viba_14613	HKN/25/2010	porcine	91.5	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	87.2	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	86.9	0	O	CATHAY		
viba_584	HKN/6/83	bovine	81.7	2	O	CATHAY		
viba_325	HKN/21/70	porcine	81.2	2	O	CATHAY		
viba_359	Manisa/TUR/69		79.9	0	O	ME-SA		
viba_705	KUW/3/97	bovine	79.6	0	O	ME-SA	Ind-2001	a
viba_285	UKG/35/2001	porcine	79.3	0	O	ME-SA	PanAsia	
viba_850	NEP/1/2015	cattle	79.2	1	O	ME-SA	PanAsia-2	KAT-15
viba_613	ISA/9/74	bovine	79.0	0	O	ISA-1		
viba_541	OMN/7/2001	bovine	79.0	0	O	ME-SA	Ind-2001	b

Virus sample name:	VIT/22/2017
Sender reference:	17-17754
Location of origin:	Tan Trach, Can Duoc, Long An
Country of origin:	Vietnam
Date of collection:	09/09/2017
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018

VIBASys IDs: sample 36467, genome 36468, sequence viba_36469, sequencing info 36470

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36473	VIT/26/2017	porcine	97.8	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	94.3	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	94.3	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	94.0	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	93.7	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	93.5	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	93.2	0	O	CATHAY		
viba_14613	HKN/25/2010	porcine	93.0	0	O	CATHAY		
viba_14609	HKN/24/2010	porcine	93.0	0	O	CATHAY		
viba_36477	VIT/27/2017	porcine	92.6	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	83.9	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.5	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.7	0	O	ME-SA		
viba_617	IND/53/79	bovine	80.1	0	O	ME-SA		
viba_694	CAM/3/98	bovine	79.9	0	O	SEA	Cam-94	
viba_293	BHU/3/2009	cattle	79.9	0	O	ME-SA	Ind-2001	d
viba_850	NEP/1/2015	cattle	79.9	1	O	ME-SA	PanAsia-2	KAT-15
viba_505	TUR/264/2009		79.8	0	O	ME-SA	PanAsia-2	SAN-09

Virus sample name:	VIT/26/2017
Sender reference:	17-19073
Location of origin:	Xuyen A slaughter house, Cu Chi, Ho Chi Minh
Country of origin:	Vietnam
Date of collection:	02/10/2017
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36471, genome 36472, sequence viba_36473, sequencing info 36474	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36469	VIT/22/2017	porcine	97.8	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	94.6	0	O	CATHAY		
viba_36420	VIT/23/2016	porcine	94.3	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	94.3	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	94.2	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	94.0	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	93.5	0	O	CATHAY		
viba_36477	VIT/27/2017	porcine	92.9	0	O	CATHAY		
viba_36440	VIT/3/2017	porcine	92.9	0	O	CATHAY		
viba_14613	HKN/25/2010	porcine	92.7	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	87.7	0	O	CATHAY		
viba_418	PHI/7/96	porcine	87.5	0	O	CATHAY		
viba_584	HKN/6/83	bovine	83.3	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.9	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.9	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	80.6	1	O	ME-SA	PanAsia-2	KAT-15
viba_505	TUR/264/2009		80.2	0	O	ME-SA	PanAsia-2	SAN-09
viba_617	IND/53/79	bovine	80.1	0	O	ME-SA		
viba_705	KUW/3/97	bovine	79.8	0	O	ME-SA	Ind-2001	a
viba_293	BHU/3/2009	cattle	79.7	0	O	ME-SA	Ind-2001	d

Virus sample name:	VIT/27/2017
Sender reference:	17-19537
Location of origin:	An Dien, Ben Cat, Binh Duong
Country of origin:	Vietnam
Date of collection:	06/10/2017
Host species:	porcine
Serotype:	O
Topotype:	CATHAY
Lineage:	
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	RS1
Harvest date of material:	12/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36475, genome 36476, sequence viba_36477, sequencing info 36478	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36420	VIT/23/2016	porcine	97.0	0	O	CATHAY		
viba_31464	VIT/8/2016	porcine	96.7	0	O	CATHAY		
viba_26337	CanTho/VIT/15-20501	porcine	95.4	0	O	CATHAY		
viba_36465	VIT/21/2017	porcine	94.9	0	O	CATHAY		
viba_31216	SCGH/CHA/2016	porcine	94.3	0	O	CATHAY		
viba_31208	GD/CHA/JH12/2013	porcine	93.5	0	O	CATHAY		
viba_36473	VIT/26/2017	porcine	92.9	0	O	CATHAY		
viba_36440	VIT/3/2017	porcine	92.7	0	O	CATHAY		
viba_36469	VIT/22/2017	porcine	92.6	0	O	CATHAY		
viba_14613	HKN/25/2010	porcine	91.5	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	86.6	0	O	CATHAY		
viba_480	Yunlin/TAW/97	porcine	86.6	0	O	CATHAY		
viba_584	HKN/6/83	bovine	82.9	2	O	CATHAY		
viba_325	HKN/21/70	porcine	82.6	2	O	CATHAY		
viba_359	Manisa/TUR/69		80.3	0	O	ME-SA		
viba_850	NEP/1/2015	cattle	80.0	1	O	ME-SA	PanAsia-2	KAT-15
viba_285	UKG/35/2001	porcine	79.4	0	O	ME-SA	PanAsia	
viba_617	IND/53/79	bovine	79.4	0	O	ME-SA		
viba_505	TUR/264/2009		79.3	0	O	ME-SA	PanAsia-2	SAN-09
viba_860	IRN/6/2015	cattle	79.2	0	O	ME-SA	PanAsia-2	QOM-15

Virus sample name:	VIT/29/2017
Sender reference:	17-20463
Location of origin:	An Phu, Cu Chi, Ho Chi Minh
Country of origin:	Vietnam
Date of collection:	20/10/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36479, genome 36480, sequence viba_36481, sequencing info 36482	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_35454	BaTri/VIT/17-19372	cattle	100.0	0	O	ME-SA	PanAsia	
viba_36461	VIT/18/2017	bovine	99.7	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36485	VIT/30/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_16348	VIT/22/2010	cattle	95.9	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.7	0	O	ME-SA	PanAsia	
viba_18652	TAI/7/2011	cattle	95.7	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.7	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	91.0	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	90.4	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.9	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	89.7	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.4	0	O	ME-SA	Ind-2001	c
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_666	IRN/18/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	BAL-09
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/30/2017
Sender reference:	17F75
Location of origin:	Phi Nhu, Dien Bien Dong, Dien Bien
Country of origin:	Vietnam
Date of collection:	26/10/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36483, genome 36484, sequence viba_36485, sequencing info 36486	

Most Closely Related Sequences

sequence	virus name	Host	% Id.	# Ambig.	serotype	topotype	lineage	sublineage
viba_36461	VIT/18/2017	bovine	99.1	0	O	ME-SA	PanAsia	
viba_36497	VIT/1/2018	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	98.7	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	98.6	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.4	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.4	0	O	ME-SA	PanAsia	
viba_16275	VIT/3/2010	porcine	95.4	0	O	ME-SA	PanAsia	
viba_18716	VIT/1/2011	water buffalo	95.3	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	90.4	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	89.7	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.6	0	O	ME-SA	PanAsia-2	SAN-09
viba_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_650	IRN/8/2005	ovine	89.3	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.1	0	O	ME-SA	Ind-2001	c
viba_666	IRN/18/2010	cattle	88.9	0	O	ME-SA	PanAsia-2	BAL-09
viba_491	TUR/257/2008		88.9	0	O	ME-SA	PanAsia-2	TER-08

Virus sample name:	VIT/31/2017
Sender reference:	17-21869
Location of origin:	Tan Xuan, Ba Tri, Ben Tre
Country of origin:	Vietnam
Date of collection:	10/11/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	14/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36487, genome 36488, sequence viba_36489, sequencing info 36490	

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_36497	VIT/1/2018	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36493	VIT/32/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.2	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36485	VIT/30/2017	bovine	98.6	0	O	ME-SA	PanAsia	
viba_16348	VIT/22/2010	cattle	95.7	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.6	0	O	ME-SA	PanAsia	
viba_18652	TAI/7/2011	cattle	95.6	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.6	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	91.8	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	90.4	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.2	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		90.0	0	O	ME-SA	PanAsia-2	SAN-09
viba_650	IRN/8/2005	ovine	89.6	0	O	ME-SA	PanAsia-2	
viba_397	UAE/4/2008	gazelle	89.6	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
viba_860	IRN/6/2015	cattle	89.3	0	O	ME-SA	PanAsia-2	QOM-15

Virus sample name:	VIT/32/2017
Sender reference:	18-440
Location of origin:	Tan My Chanh, My Tho, Tien Giang
Country of origin:	Vietnam
Date of collection:	25/12/2017
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy1
Harvest date of material:	13/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36491, genome 36492, sequence viba_36493, sequencing info 36494	

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_36497	VIT/1/2018	bovine	99.4	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.4	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36485	VIT/30/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_16348	VIT/22/2010	cattle	95.6	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.4	0	O	ME-SA	PanAsia	
viba_18652	TAI/7/2011	cattle	95.4	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.4	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	91.6	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	90.8	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.7	0	O	ME-SA	Ind-2001	b
viba_505	TUR/264/2009		89.9	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_766	IRN/31/2009	cattle	89.4	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.3	0	O	ME-SA	PanAsia-2	TER-08
viba_666	IRN/18/2010	cattle	88.9	0	O	ME-SA	PanAsia-2	BAL-09

Virus sample name:	VIT/1/2018
Sender reference:	18-2731
Location of origin:	Binh Phu, Go Cong Tay, Tien Giang
Country of origin:	Vietnam
Date of collection:	25/01/2018
Host species:	bovine
Serotype:	O
Topotype:	ME-SA
Lineage:	PanAsia
Sublineage:	
Sequence length:	633
Ambiguities:	0
Material submitted for sequencing:	BTy2
Harvest date of material:	17/04/2018
Primers:	O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R
Received for sequencing:	30/04/2018
Created:	10/05/2018
Last updated:	10/05/2018
VIBASys IDs: sample 36495, genome 36496, sequence viba_36497, sequencing info 36498	

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_36493	VIT/32/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_35454	BaTri/VIT/17-19372	cattle	99.4	0	O	ME-SA	PanAsia	
viba_36481	VIT/29/2017	bovine	99.4	0	O	ME-SA	PanAsia	
viba_36489	VIT/31/2017	bovine	99.2	0	O	ME-SA	PanAsia	
viba_36485	VIT/30/2017	bovine	98.7	0	O	ME-SA	PanAsia	
viba_16348	VIT/22/2010	cattle	95.9	0	O	ME-SA	PanAsia	
viba_16307	VIT/11/2010	cattle	95.7	0	O	ME-SA	PanAsia	
viba_18652	TAI/7/2011	cattle	95.7	0	O	ME-SA	PanAsia	
viba_16303	VIT/10/2010	cattle	95.7	0	O	ME-SA	PanAsia	

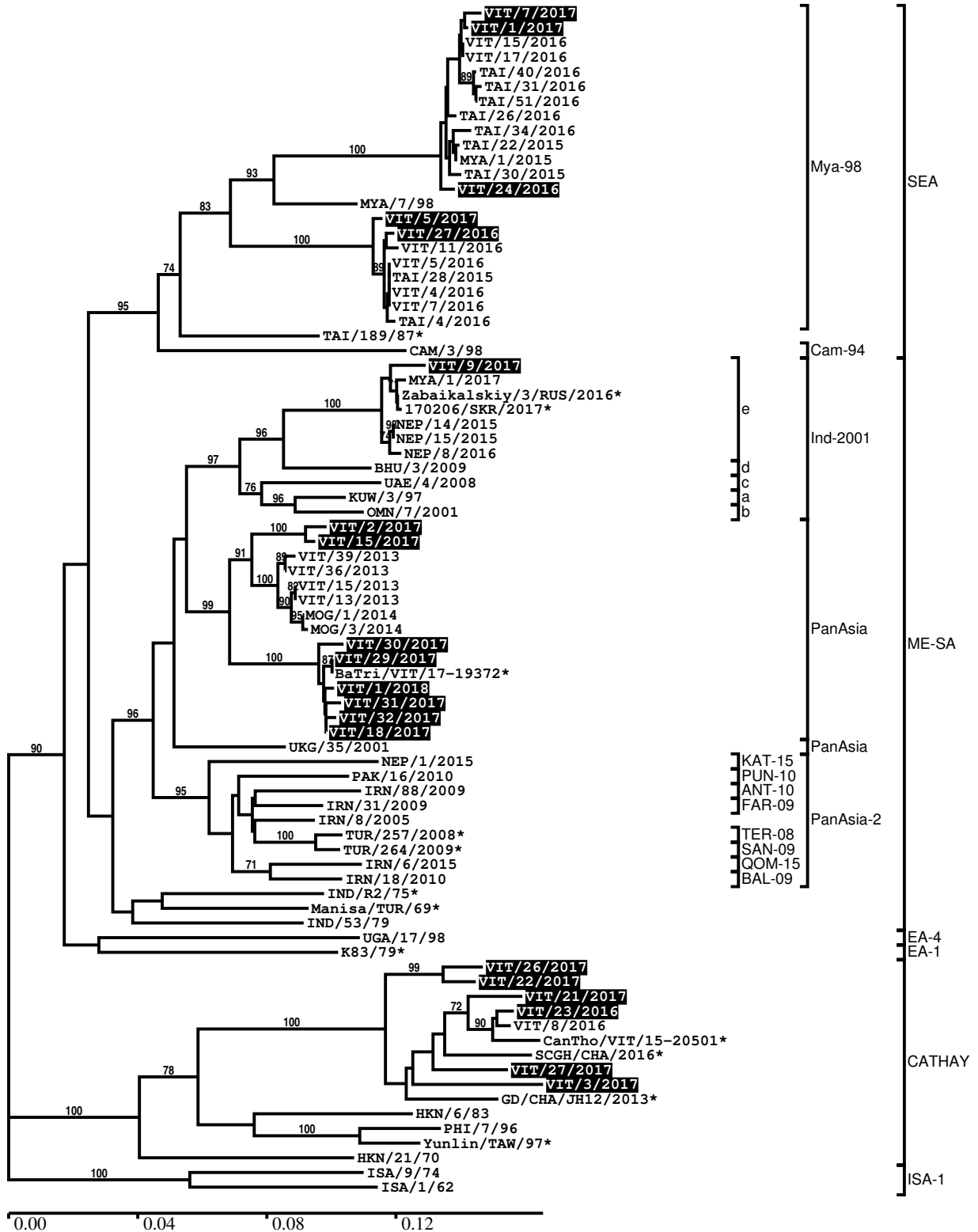
Most Closely Related Prototype Sequences

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	91.9	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	90.7	0	O	ME-SA	Ind-2001	d
viba_541	OMN/7/2001	bovine	90.7	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	90.1	0	O	ME-SA	Ind-2001	c
viba_650	IRN/8/2005	ovine	89.7	0	O	ME-SA	PanAsia-2	
viba_766	IRN/31/2009	cattle	89.7	0	O	ME-SA	PanAsia-2	FAR-09
viba_491	TUR/257/2008		89.6	0	O	ME-SA	PanAsia-2	TER-08
viba_666	IRN/18/2010	cattle	89.3	0	O	ME-SA	PanAsia-2	BAL-09

Report on FMDV O in Vietnam in 2016, 2017, 2018

Batch: WRLFMD/2018/00011



*, not a WRLFMD Reference Number

Analysis Parameters

VP1 subsequence extractor:	vp1_O
Query sequence set:	WRLFMD/2018/00011-Vietnam-O (20 sequences)
Sequence database set:	allseqs_O (3785 sequences)
Prototype sequence set:	!prototypes_O (48 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:	27
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/7/2017	n/a	water buffalo	WRLFMD	Vietnam	SEA/Mya-98
VIT/1/2017	n/a	water buffalo	WRLFMD	Vietnam	SEA/Mya-98
VIT/15/2016	n/a	water buffalo	WRLFMD	Vietnam	SEA/Mya-98
VIT/17/2016	n/a	cattle	WRLFMD	Vietnam	SEA/Mya-98
TAI/40/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/31/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/51/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/26/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/34/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/22/2015	n/a	water buffalo	WRLFMD	Thailand	SEA/Mya-98
MYA/1/2015	n/a	bovine	WRLFMD	Myanmar	SEA/Mya-98
TAI/30/2015	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
VIT/24/2016	n/a	bovine	WRLFMD	Vietnam	SEA/Mya-98
MYA/7/98	DQ164925	bovine	WRLFMD	Myanmar	SEA/Mya-98
VIT/5/2017	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/27/2016	n/a	bovine	WRLFMD	Vietnam	SEA/Mya-98
VIT/11/2016	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/5/2016	n/a	cattle	WRLFMD	Vietnam	SEA/Mya-98
TAI/28/2015	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
VIT/4/2016	n/a	porcine	WRLFMD	Vietnam	SEA/Mya-98
VIT/7/2016	n/a	cattle	WRLFMD	Vietnam	SEA/Mya-98
TAI/4/2016	n/a	cattle	WRLFMD	Thailand	SEA/Mya-98
TAI/189/87*	KY091288	bovine	TRRL	Thailand	SEA
CAM/3/98	AJ294910	bovine	WRLFMD	Cambodia	SEA/Cam-94
VIT/9/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/Ind-2001/e
MYA/1/2017	MG972517	cattle	WRLFMD	Myanmar	ME-SA/Ind-2001/e
Zabaikalskiy/3/RUS/2016*	MG972584	cattle	ARRIAH	Russia	ME-SA/Ind-2001/e
170206/SKR/2017*	n/a	cattle	QIA	Republic of Korea (South Korea)	ME-SA/Ind-2001/e
NEP/14/2015	MG972546	cattle	WRLFMD	Nepal	ME-SA/Ind-2001/e
NEP/15/2015	MG972547	cattle	WRLFMD	Nepal	ME-SA/Ind-2001/e
NEP/8/2016	MG972556	cattle	WRLFMD	Nepal	ME-SA/Ind-2001/e
BHU/3/2009	KM921814	cattle	WRLFMD	Bhutan	ME-SA/Ind-2001/d
UAE/4/2008	KM921876	gazelle	WRLFMD	United Arab Emirates	ME-SA/Ind-2001/c

continued on next page

label	accession	host(s)	lab	country	taxonomic information
KUW/3/97	DQ164904	bovine	WRLFMD	Kuwait	ME-SA/Ind-2001/a
OMN/7/2001	DQ164941	bovine	WRLFMD	Oman	ME-SA/Ind-2001/b
VIT/2/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/15/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/39/2013	KX944728	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/36/2013	KX944726	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/15/2013	KX944717	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/13/2013	KX944715	cattle	WRLFMD	Vietnam	ME-SA/PanAsia
MOG/1/2014	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
MOG/3/2014	n/a	cattle	WRLFMD	Mongolia	ME-SA/PanAsia
VIT/30/2017	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/1/2018	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/31/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/32/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
VIT/18/2017	n/a	bovine	WRLFMD	Vietnam	ME-SA/PanAsia
UKG/35/2001	AJ539141	porcine	PIADC	United Kingdom	ME-SA/PanAsia
NEP/1/2015	n/a	cattle	WRLFMD	Nepal	ME-SA/PanAsia-2/KAT-15
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/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	FMADI-Ankara	Turkey	ME-SA/PanAsia-2/TER-08
TUR/264/2009*	n/a	n/a	FMADI-Ankara	Turkey	ME-SA/PanAsia-2/SAN-09
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
IND/R/75*	AF204276	n/a	PD-FMD	India	ME-SA
Manisa/TUR/69*	AY593823	n/a	PIADC	Turkey	ME-SA
IND/53/79	AF292107	bovine	PD-FMD	India	ME-SA
UGA/17/98	HM211075	n/a	WRLFMD	Uganda	EA-4
K83/79*	AJ303511	n/a	WRLFMD	Kenya	EA-1
VIT/26/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/22/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/21/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/23/2016	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/8/2016	n/a	porcine	WRLFMD	Vietnam	CATHAY
CanTho/VIT/15-20501*	n/a	porcine	RAHO6	Vietnam	CATHAY
SCGH/CHA/2016*	KX161429	porcine	LVRI	China	CATHAY
VIT/27/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
VIT/3/2017	n/a	porcine	WRLFMD	Vietnam	CATHAY
GD/CHA/JH12/2013*	KU204894	porcine	SMU	China	CATHAY
HKN/6/83	AJ294919	bovine	WRLFMD	Hong Kong SAR	CATHAY
PHI/7/96	AJ294926	porcine	WRLFMD	Philippines	CATHAY
Yunlin/TAW/97*	AF308157	porcine	PIADC	Taiwan	CATHAY
HKN/21/70	AJ294911	porcine	WRLFMD	Hong Kong SAR	CATHAY
ISA/9/74	AJ303502	bovine	WRLFMD	Indonesia	ISA-1
ISA/1/62	AJ303500	n/a	WRLFMD	Indonesia	ISA-1

*, not a WRLFMD Reference Number

n/a, not available