

**Table S1: Serology and OPF screening from farms in each province in 2015**

Province	Serum Tested	Serum positive	Seropositive percentage of samples	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
Hà Tĩnh	500	86	17.2 (13,21)	112	0	0
Lạng Sơn	484	20	4 (2,5)	33	0	0
Phú Thọ	500	50	10 (7,12)	62	0	0
Bắc Kạn	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Ninh Thuận	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Đồng Tháp	485	149	31 (26,34)	139	36	25.8
Bình Phước	514	84	16 (13,19)	80	2	2.5
Đắk Lắk	504	142	28 (24,32)	142	3	2.1
TOTAL	2,987	531		568	41	7.2

**Table S2: Serology and OPF screening from farms in each province in 2016**

Province	Serum Tested	Serum positive	Seropositive percentage of samples	OPF Screened (rRT-PCR)	OPF positive	Percentage OPF positive
Hà Tĩnh	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Lạng Sơn	236	31	13 (8,17)	33	2	6
Phú Thọ	253	34	13 (9,17)	32	2	6.2
Bắc Kạn	496	167	34 (29,37)	165	32	19.4
Ninh Thuận	250	177	71 (65,76)	177	20	11.2
Đồng Tháp	254	100	39 (33,45)	102	33	32.3
Bình Phước	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Đắk Lắk	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
TOTAL	1,489	509		509	89	17.4

**Table S3: Serology and OPF screening from farms in each province in 2017**

Province	Serum Tested	Serum positive	Seropositive percentage of samples	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
Hà Tĩnh	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Lạng Sơn	316	92	29 (24,34)	92	0	0
Phú Thọ	177	82	46 (39,53)	77	0	0
Bắc Kạn	982	447	46 (42,48)	443	33	7.4
Ninh Thuận	585	467	80 (76,83)	461	49	10.6
Đồng Tháp	369	210	57 (51,61)	212	85	40
Bình Phước	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Đắk Lắk	252	182	72 (66,77)	181	56	31
TOTAL	2,681	1,480		1,466	223	

**Table S4: Serology and OPF screening from farms in each province in 2018**

Province	Serum Tested	Serum positive	Seropositive percentage of samples	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
Hà Tĩnh	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Lạng Sơn	351	65	19 (14,22)	65	1	1.53
Phú Thọ	149	48	32 (24,39)	48	0	0
Bắc Kạn	752	363	48 (44,51)	347	3	0.8
Ninh Thuận	319	257	81 (76,84)	256	3	1.1
Đồng Tháp	540	284	53 (48,56)	284	31	11
Bình Phước	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Đắk Lắk	942	605	64 (61,67)	605	27	4.4
TOTAL	3,053	1,622		1,605	65	

**Table S5: Serology and OPF screening from farms in each province in 2019**

Province	Serum Tested	Serum positive	Seropositive percentage of samples	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
Hà Tĩnh	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Lạng Sơn	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Phú Thọ	117	55	47 (38,56)	55	0	0
Bắc Kạn	560	287	51 (47,55)	286	5	1.74
Ninh Thuận	136	109	80 (73,86)	109	0	0
Đồng Tháp	317	145	46 (40,51)	145	12	8.27
Bình Phước	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>	<i>na</i>
Đắk Lắk	475	304	64 (59,68)	302	11	3.64
TOTAL	1,605	900		897	28	

**Table S6: Slaughterhouse Serology and OPF sample collection summary Long An**

Sampling Round	Serum Tested	Number of positive 3ABC	Percentage 3ABC ELISA positive	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
1	30	21	70.0 (56,86)	30	7	23.3
2	30	10	33.3 (16.5, 50)	30	2	6.6
3	28	4	14.3 (1.3,27)	28	0	0
4	30	11	36.7 (19,53)	30	1	3.3
5	32	15	46.9 (29,64)	32	4	12.5
6	30	10	33.3 (16.5,50)	30	4	13.3
7	30	7	23.3 (8.2, 38)	30	4	13.3
8	30	11	36.7 (19.5,53)	30	3	10
9	30	10	33.3 (16.5, 50)	30	4	13.3
10	24	13	54.2 (34.3, 74)	24	5	20.8
11	36	17	47.2 (31,63)	36	6	16.6
12	23	9	39.1 (19.2,56)	23	0	0
13	37	11	29.7 (15,44)	37	3	8.1
14	30	9	30.0 (13.6,46)	30	1	3.3
15	20	11	55.0 (33,76 )	20	4	20
16	40	10	25.0 (11,38)	40	3	7.5
Grand Total	480	179	37.3	480	51	

**Table S7: Slaughterhouse Serology and OPF sample collection summary Tay Ninh**

Sampling Round	Serum Tested	Number of positive 3ABC	Percentage 3ABC ELISA positive	OPF Screened (rRT-PCR)	OPF positive for FMDV RNA	Percentage OPF positive
1	30	28	93.3 (84, 100)	30	9	30
2	30	14	46.7 (29,64)	30	6	20
3	30	21	70.0 (53,86)	30	7	23.3
4	30	10	33.3 (16.5,50)	30	5	16.6
5	30	14	46.7 (29,64)	30	7	23.3
6	30	7	23.3 (8,38)	30	1	3.3
7	30	18	60.0 (42,77)	30	5	16.6
8	30	21	70.0 (53,86)	30	4	13.3
9	30	8	26.7 (11,42)	30	5	16.6
10	30	9	30.0 (13,46)	30	1	3.3
11	30	17	56.7 (39,74)	30	7	23.3
12	30	15	50.0 (32,74)	30	2	6.6
13	30	11	36.7 (19.5, 53.8)	30	2	6.6
14	30	20	66.7 (49.8,83)	30	4	13.3
15	30	13	43.3 (25.6, 70)	30	2	6.6
16	30	23	76.7 (61,91)	30	4	13.3
Grand Total	480	277	57.7	480	71	

**Table S8: Large cluster information of serotype O**

Name	Type	Area	Dates detected	Species	MRCA	Number of sequences	Closest lineage	Within cluster GD
Cluster 1	Farm and Outbreak	North	2010-12-22 to 2014-07-14	Pig, Cattle, Buffalo	2008.6 (1998.7,2020)	54	O/ME-SA/Pan Asia	0.028
	Farm and Outbreak	Central	2010-12-26 to 2012-05-23	Pig, Buffalo				
	Farm and Outbreak	South	2010-12-21 to 2017-01-09*	Pig, Cattle, Buffalo				
Cluster 2 <sup>†</sup>	Farm and Outbreak	North	2017-10-01 to 2018-11-11	Pig, Cattle, Buffalo, Goat	2015.9 (2013.4,2019.6)	90	O/ME-SA/Pan Asia	0.011
	Outbreak	Central	2018-04-13	Cattle				
	Farm and Slaughterhouse	South	2017-01-10 to 2018-07-01	Cattle, Buffalo				
Cluster 6 <sup>†</sup>	Outbreak	North	2018-11-13 to 2019-01-15	Pig	2017.9 (2017.5, 2019.1)	21	Mya-98	0.021
	Outbreak	Central	2018-12-27 to 2019-01-05					
	Outbreak	South	2018-11-13 to					
Cluster 8	Outbreak	North	2015-10-30 to 2017-09-23*	Pig, Cattle	2011.7	12	O/ME-SA/Ind2001d	0.021
		South	2015-09-04 to 2015-10-22	Pig, Cattle, Buffalo	(2006.6,2020.9)			
Cluster 9 <sup>†</sup>	Outbreak	North	2016-01-16 to 2016-11-18	Cattle	2013.1 (2007.2,2019.2)	13	Mya-98 B	0.066
	Outbreak	Central	2013-10-07 to 2016-10-14	Pig (2016-11-18)				
	Farm and Slaughterhouse	South	2016-08-18 to 2017-12-15					

Cluster 10 <sup>†</sup>	Outbreak	North	2016-11-16	Cattle Pig (2015-09-10)	20 09.7 (2002.9,2018.8)	22	O/ME-SA/Pan Asia	0.027
	Farm, Outbreak and Slaughterhouse	South	2013-05-17 to 2017-08-01					

<sup>†</sup> Clusters that were circulating in southern Vietnam during period of slaughterhouse sampling

\* 2017 sequence does not cluster with other sequences in cluster 1 and 8, thus this clusters were not considered to be circulating after 2012 and 2015.

**Table S9: Large cluster information for serotype A**

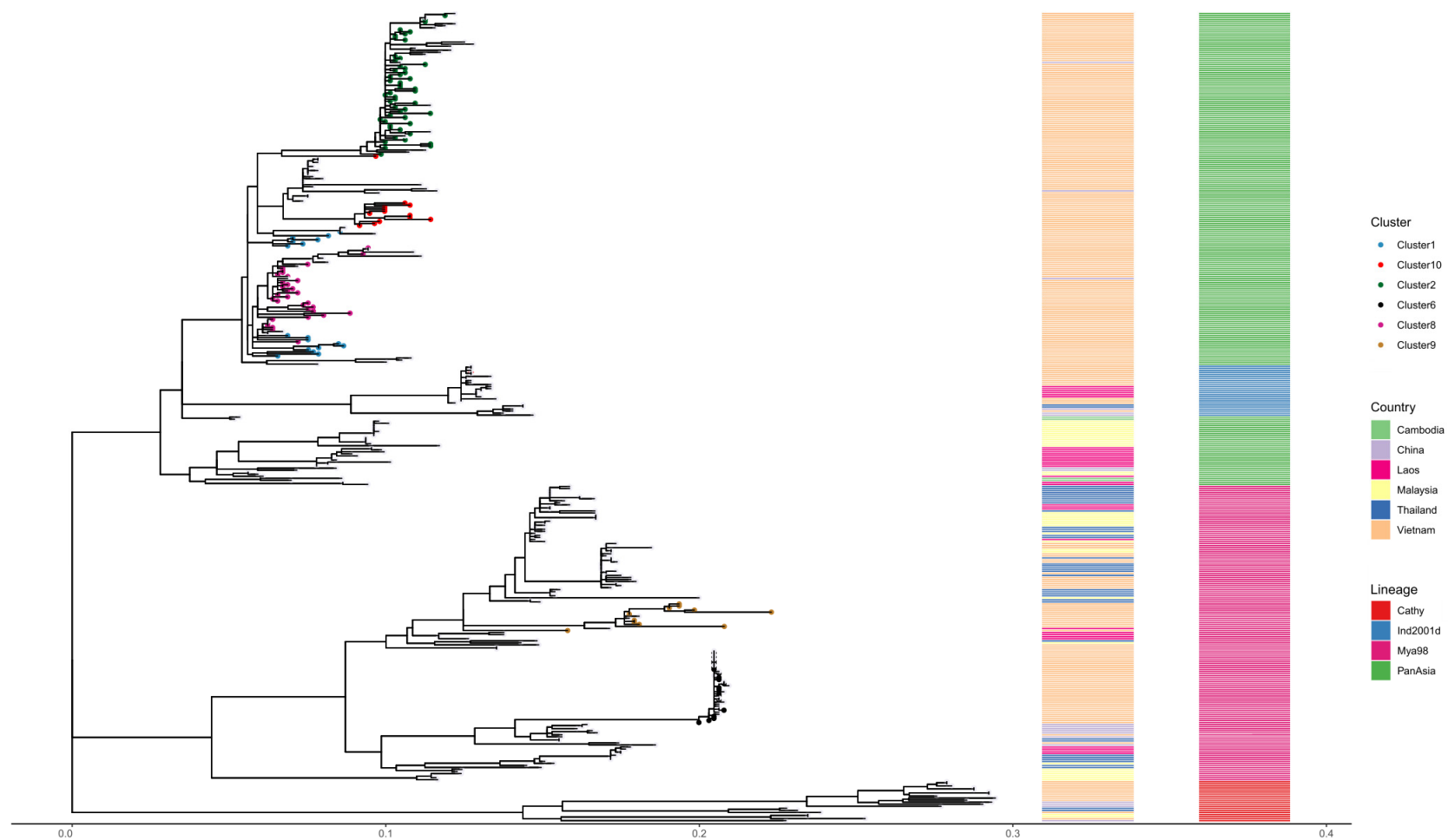
Name	Type	Area	Dates detected	Species	MRCA	Number of sequences	Closest lineage	Within cluster GD
cluster9	Farm	North	2017-08-25 to 2018-01-08	Cattle	2015.3 (2012.2, 2019.5)	56	Sea/97	0.01
	Farm and outbreak	Central	2017-01-08 to 2019-01-05					
cluster5 <sup>†</sup>	Outbreak	North	2017-08-29 to 2017-09-11	Cattle	2015.8 (2013.1,2019.5)	20	Sea/97	0.01
	Farm and outbreak	Central	2017-01-08 to 2017-08-05					
	Slaughterhouse	South	2017-10-17 to 2018-03-29					
cluster4 <sup>†</sup>	Outbreak	North	2013-12-01 to 2014-04-24	Cattle Pig (2014-04-24)	2012.4 (2006.4,2019.4)	21	Sea/97	0.02
	Outbreak	Central	2013-10-09 to 2016-10-13	Cattle Pig (2015-09-10)				
	Outbreak and Slaughterhouse	South	2017-10-31 to 2019-06-01	Buffalo				
cluster10 <sup>†</sup>	Farm	South	2017-01-06 to 2019-06-01	Cattle	2016.8 (2015.5,2020.1)	12	Sea/97	0.04
	Slaughterhouse		2018-01-24 to 2019-02-27					

<sup>†</sup> Clusters that were circulating in southern Vietnam during period of slaughterhouse sampling

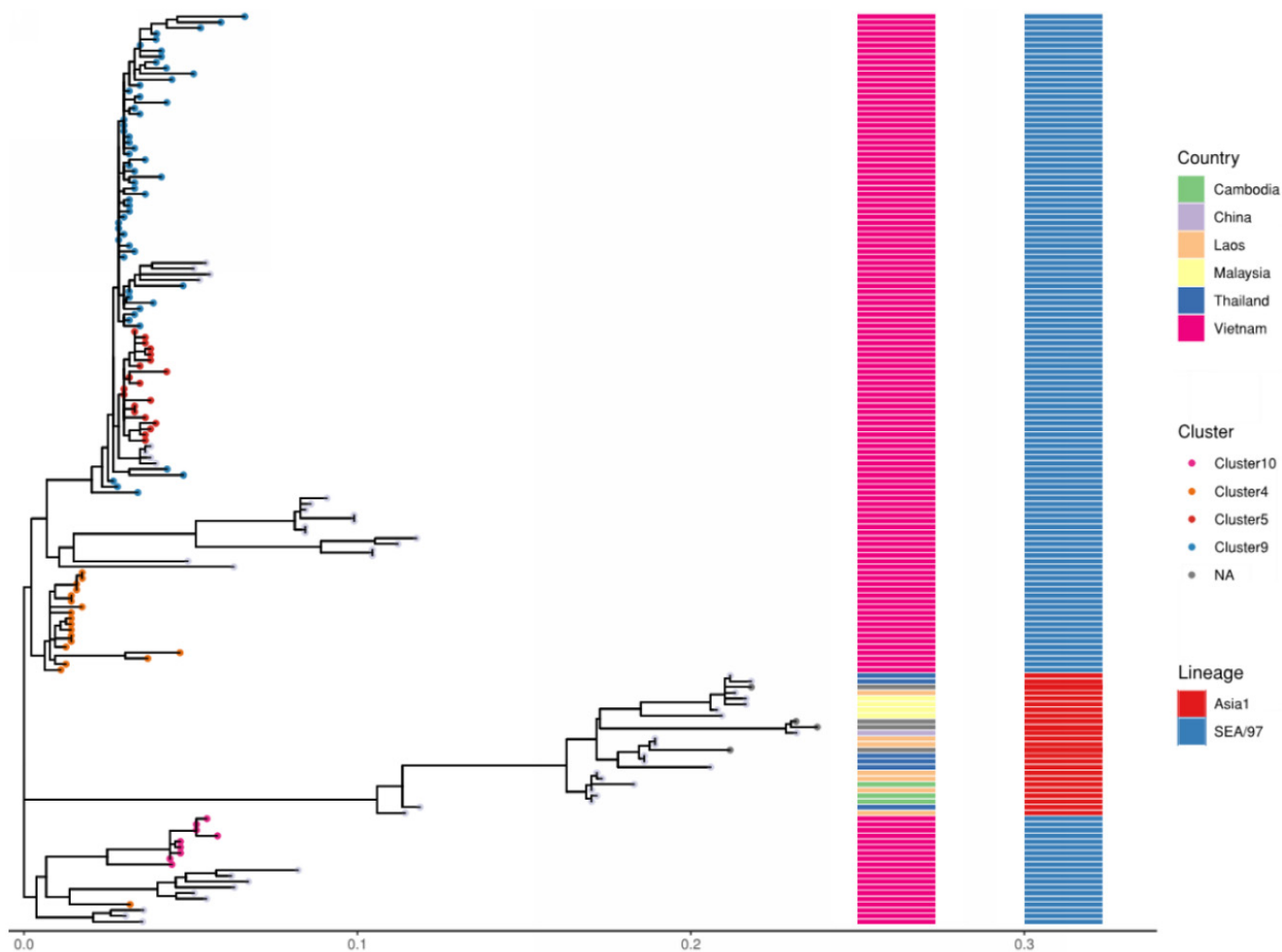
**Table S10: Model selection results from the Bayesian Evolutionary Sampling Tree (BEAST) where the best model, relaxed clock coalescent sky grid model was selected.**

Serotype O				
	Path sampling	Path Sampling average	Steppingstone sampling	Steppingstone sampling average
Relaxed clock exponential	-8507.962087	-8507.037632	-8510.304413	-8509.431206
	-8506.113178		-8508.558	
Relaxed clock expansion	-8508.172778	-8508.342028	-8508.451305	-8508.291626
	-8508.511278		-8508.131947	
Relaxed clock constant	-8458.92312	-8458.449227	-8459.655856	-8459.274212
	-8457.975333		-8458.892568	
Relaxed clock coalescent sky grid	-8137.909934	-8138.998022	-8138.659178	-8139.871078
	-8140.086109		-8141.082978	
Serotype A				
	Path sampling	Path Sampling average	Steppingstone sampling	Steppingstone sampling average
Relaxed clock exponential	-5696.304571	-5695.588948	-5696.86083	-5696.043596
	-5694.873326		-5695.226363	
Relaxed clock expansion	-5697.271664	-5698.113582	-5698.07718	-5698.947185
	-5698.955501		-5699.817189	
Relaxed clock constant	-5706.882944	-5693.61778	-5706.951335	-5706.906472
	-5680.352616		-5706.86161	
Relaxed clock coalescent sky grid	-5686.396487	-5683.374551	-5688.637852	-5685.418112
	-5680.352616		-5682.198372	





[Figure S1: Serotype O clusters shown in a maximum likelihood tree with other circulating FMD sequences obtained from South East Asian countries Cambodia, Laos, Malaysia, Thailand. Different node colors show the different clusters, only clusters with <10 sequences are labelled. Different bars show different lineages and the country where FMD sequence was isolated. ]



[Figure S2: Serotype A clusters shown in a maximum likelihood tree with other circulating FMD sequences obtained from South East Asian countries Cambodia, Laos, Malaysia, Thailand. Different node colors show the different clusters, only clusters with <10 sequences are labelled. Different bars show different lineages and the country where FMD sequence was isolated.]