

VACCINE MATCHING STUDIES OF RECENT FMDV SEROTYPE A AND O ISOLATES FROM SOUTHEAST ASIA (2015–2017)

Singanallur, Nagendrakumar¹; Seeeyo, Kingkarn²; Vo Van Hung³; Horsington, Jacquelyn¹; Udon, Romphruke²; Nguyen, Phuong³; Huy, Hoang³; Ngo, Long^{3*}; Rodtian, Pranee² & Vosloo, Wilna¹

¹CSIRO Australian Animal Health Laboratory, Australia

²OIE-Regional Reference Laboratory for FMD in SEA, Thailand

³Centre for Veterinary Diagnostics, Ho Chi Minh City, Vietnam

**In memory of our friend and colleague*

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Spatial distribution of FMD outbreaks 2015–2016



	No. of outbreaks		
	2015	2016	2017*
Cambodia	43	71	49
Lao PDR	10	45	17
Malaysia	10	71	17
Myanmar	39	27	53
Thailand	183	262	31
Viet Nam	60	37	3
Total	345	513	170

**Up to July*

Source: Yu Qiu, OIE SRR-SEA, Bangkok

Summary of events 2015–2017



Eastward movement
from Pool 2
2015 - O/Ind/2001d
2016 – O/Ind/2001d
2017 – Asia1/G-VIII

Antigen matching studies by LP-ELISA – Serotype O

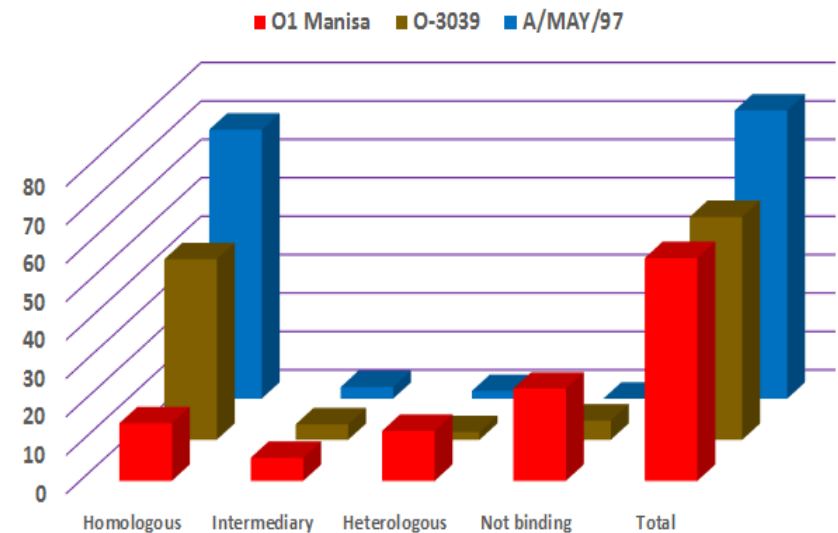
- Bovine vaccinate serum
 - O₁ Manisa
 - O-3039
- Homologous reagents
- Field isolates from Thailand, Lao PDR, Vietnam, Cambodia & Myanmar
- 58 isolates studied
 - 41 from OIE RRL, Pakchong, Thailand
 - 17 from RAHO6, Ho Chi Minh City, Vietnam

Antigen matching studies by LP-ELISA – Serotype A

- Bovine vaccinate serum
 - A/MAY/97
- Homologous reagents
- Field isolates from Thailand, Vietnam & Cambodia
- 75 isolates studied
 - 49 from OIE RRL, Pakchong, Thailand
 - 26 from RAHO6, Ho Chi Minh City, Vietnam

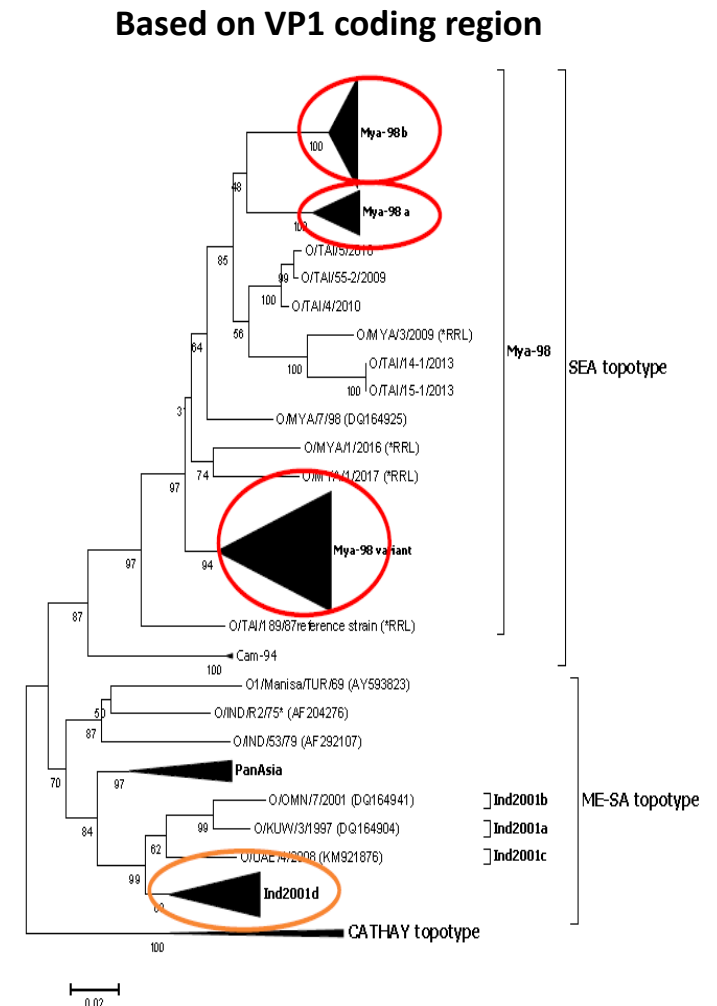
Relative homology with the reference vaccine strains (based on r1 values by LPELISA)

	O1 Manisa	O-3039	A Malaysia 97
Homologous (%)	25.9	81.0	93.3
Intermediary (%)	10.3	6.9	4.0
Heterologous (%)	22.4	3.5	2.7
Not binding (%)	41.4	8.6	0.0
Total samples	58	58	75



Serotype O - circulating lineages (2015–2017)

- Genotypes/lineages 2015–2017
 - O/SEA genotype variants
 - O Cathay toptotype variants
 - O/SEA/Mya-98 lineage
 - O/ME-SA/Ind 2001d variants
- Two separate incursions of O/ME-SA/Ind2001d sub-lineage
 - Lao PDR and Vietnam (2015)
 - Myanmar and Thailand (2016-2017)
- Three sub-lineages of O/SEA/Mya-98 were recorded (2009-2013; 2015-2016 and 2016-2017)
- RRL: Mya-98 – 12; Ind2001d – 13; Others could not be characterised due to lack of sequences
- RAHO6: Mya-98 – 7; Ind2001d – 5, Cathay – 6 & PanAsia – 1; Others could not be characterised due to lack of sequences



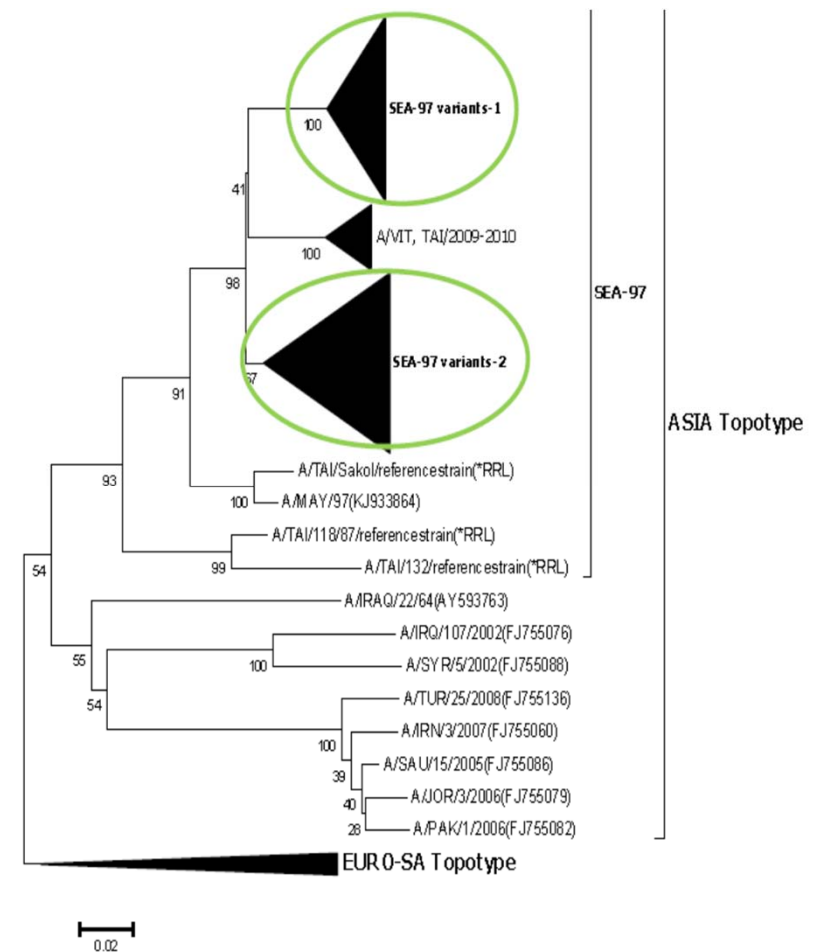
Sequences generated by OIE RRL, Pakchong



Serotype A - circulating lineages (2015–2017)

- Genotypes/lineages (2015–2017)
 - A/Asia/SEA-97 – still dominant
 - In 2011–2012 a new lineage, TAI 2012, was detected and has become dominant since 2015–2017
 - Within this new lineage, new variants have been detected from Cambodia since 2015
- RRL isolates – 20 belonged to SEA-97 variants while 22 belonged to TAI 2012 sublineage
- RAHO6 isolates – 16 belonged to SEA-97 variants; others could not be characterised (sequences not available)

Based on VP1 coding region



Sequences generated by OIE RRL, Pakchong



Antigen Matching vs Phylogeny

Serotype	Genotype/Lineage	Homologous	Intermediary	Heterologous	Not Binding
O1 Manisa	O/ME-SA/PanAsia	0	1	0	0
	O/ME-SA/Ind2001d	8	2	4	4
	O/SEA/Mya-98	6	3	6	4
	O/Cathay	0	0	0	6
	Uncharacterised	1	0	3	10 *
O-3039	O/ME-SA/PanAsia	1	0	0	0
	O/ME-SA/Ind2001d	16	2	0	0
	O/SEA/Mya-98	15	2	2	0
	O/Cathay	1	0	0	5
	Uncharacterised	14	0	0	0

*At least 6 could be Cathay

Antigen Matching vs Phylogeny

Serotype	Genotype/Lineage	Homologous	Intermediary	Heterologous	Not Binding
A/MAY/97	ASIA/SEA-97	35	1	0	0
	ASIA/SEA-97 (TAI 2012)	18	2	2	0
	Uncharacterised	17	0	0	0

Conclusions

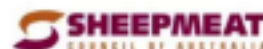
- Appearance of new lineages of viruses within Pool 1 (SEA)
 - Indicates a dynamic endemic situation
 - New variants emerging due to poor vaccines or less coverage
- ‘Trans-pool’ migration is of major concern - Pool 2 (ME-SA)
 - Indicating possible changes in animal movement patterns
 - Bigger potential risk for vaccine failures
 - More pronounced outbreaks due to naïve population

Conclusions

- Suitable commercial vaccine strains for the current situation
 - Serotype A: A Malaysia 97
 - Serotype O: O-3039
- Continued, real-time monitoring for the emergence of variant strains in SEA by both vaccine matching studies and phylogenetic analysis is required for effective control of the disease in this region
- Australia is committed to working closely with the countries in the region for management and control of the disease

**IMPROVED SURVEILLANCE, PREPAREDNESS AND RETURN TO TRADE FOR
EMERGENCY ANIMAL DISEASE INCURSIONS USING FOOD AND MOUTH DISEASE AS A MODEL**

PROJECT PARTNERS



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Thank you

Transboundary Animal Disease Mitigation Team

CSIRO HEALTH & BIOSECURITY / AUSTRALIAN ANIMAL HEALTH LABORATORY

Nagendra Singanallur
Research Scientist

t +61 3 5227 5020

e nagendra.singanallur@csiro.au

CSIRO HEALTH & BIOSECURITY / AUSTRALIAN ANIMAL HEALTH LABORATORY

www.csiro.au

