STATUS OF FMD IN SOUTH EAST ASIA

GFRA SCIENTIFIC MEETING

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DEPARTMENT OF LIVESTOCK DEVELOPMENT

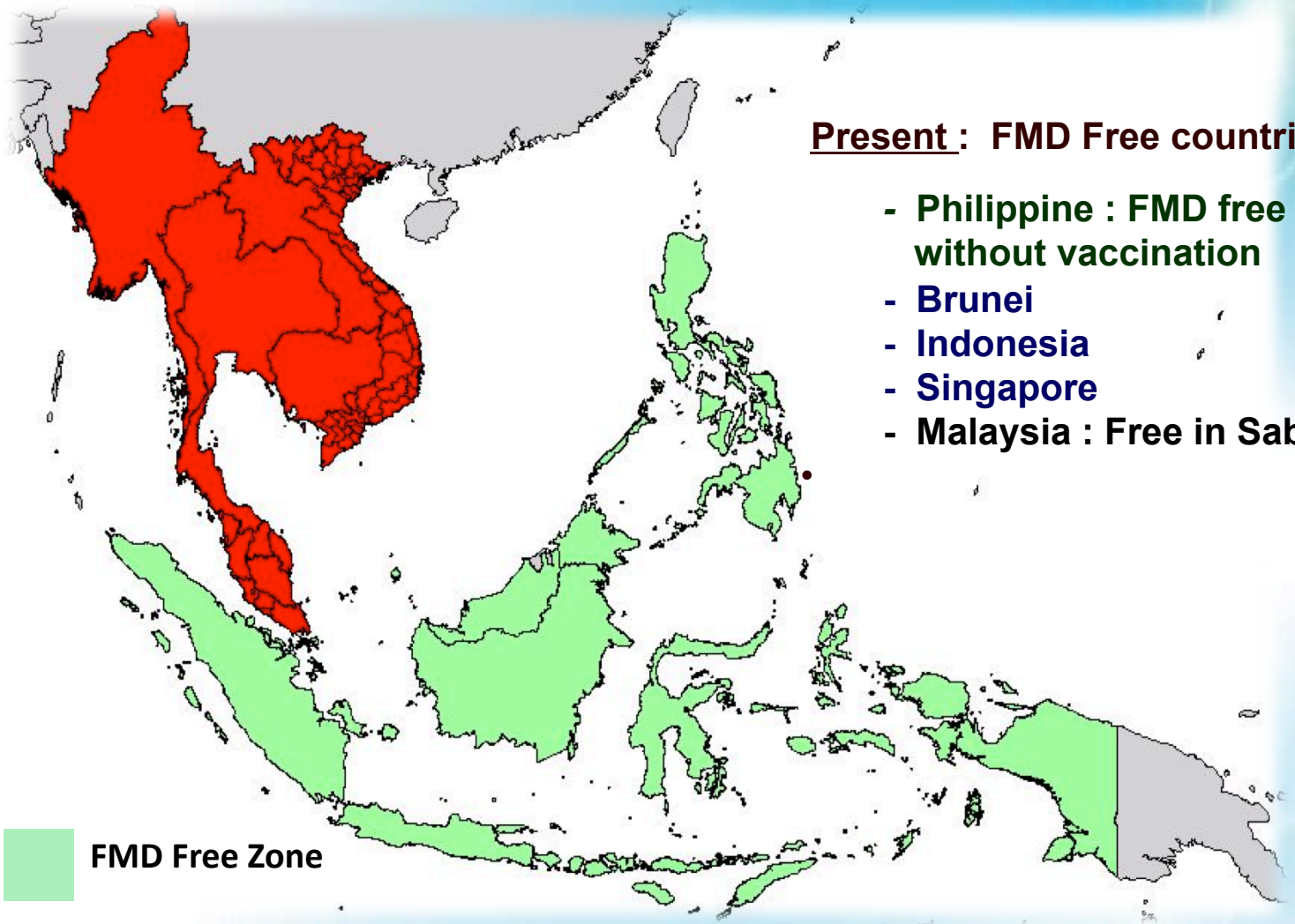
PAKCHONG, NAKHONRATCHASIMA, THAILAND

STATUS OF FMD IN SOUTH EAST ASIA

1. **Regional: pool -1**
2. **Period of coverage: 2013-2015**
3. **Countries covered:**

- Cambodia
- Myanmar
- Vietnam
- Brunei
- Philippines
- Laos PDR
- Malaysia
- Indonesia
- Singapore
- Thailand

STATUS OF FMD IN SOUTH EAST ASIA



Present : FMD Free countries / Zones

- Philippine : FMD free whole country without vaccination
- Brunei
- Indonesia
- Singapore
- Malaysia : Free in Sabah and Salawak

FMD Free Zone

FMD Infected Areas

Source : OIE SRR-SEA

STATUS OF FMD IN SOUTH EAST ASIA

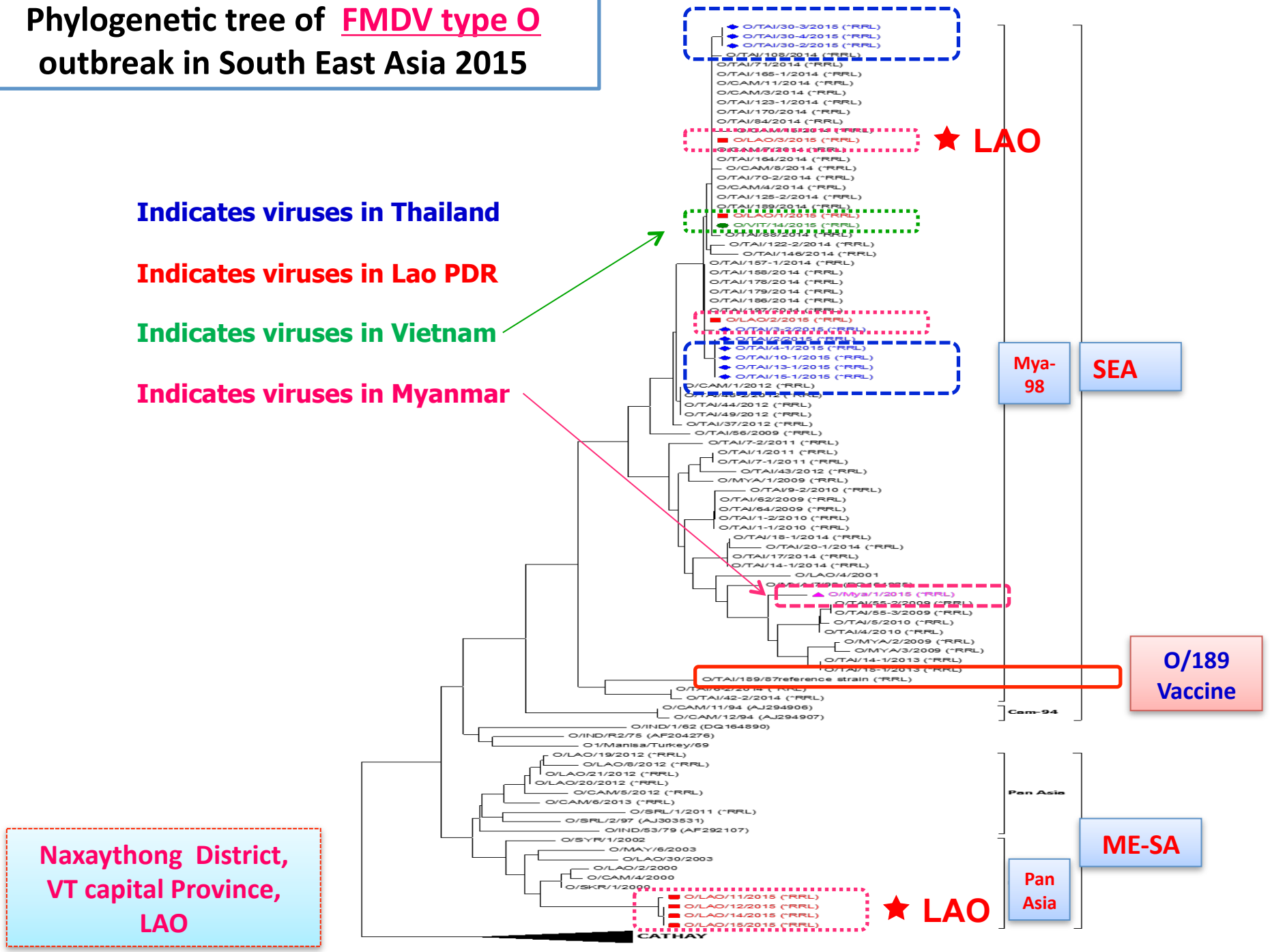
Serotype	Topotype	Remarks
O	South East Asia	Myanmar 98 and Cambodia94; endemic in SE Asia: report in China, Korea and Japan in 2010
	Pan Asia	Detected SE Asia in late 1990s
	Cathay	1st detected in Hong Kong in early 1990s
A	South East Asia	Indigenous in SE Asia; reported in China in 2009 and Korea in 2010
Asia1	Asian	Reported in Vietnam in 2007; China in 2009 and Cambodia 2015

STATUS OF FMD IN SOUTH EAST ASIA

Tissue sample submission to RRL: Antigen Detection During 2014 - 2015

Year	Country	No. of sample (Tissue)	ELISA typing results				RT-PCR results	
			O	A	Asia1	NVD	Positive	Negative
2014	Cambodia	17	5	-	-	12	7	10
	Lao PDR	5	-	3	-	2	4	1
	Thailand	355	88	116	-	151	269	86
2015	Thailand	118	60	18	-	40	96	22
	Lao PDR	15	7	7	-	1	14	1
	Vietnam	20	1	19	-	-	20	-
	Myanmar	1	-	-	-	1	1	-
	Cambodia	17	4	3	2	8	11	6

Phylogenetic tree of FMDV type O outbreak in South East Asia 2015

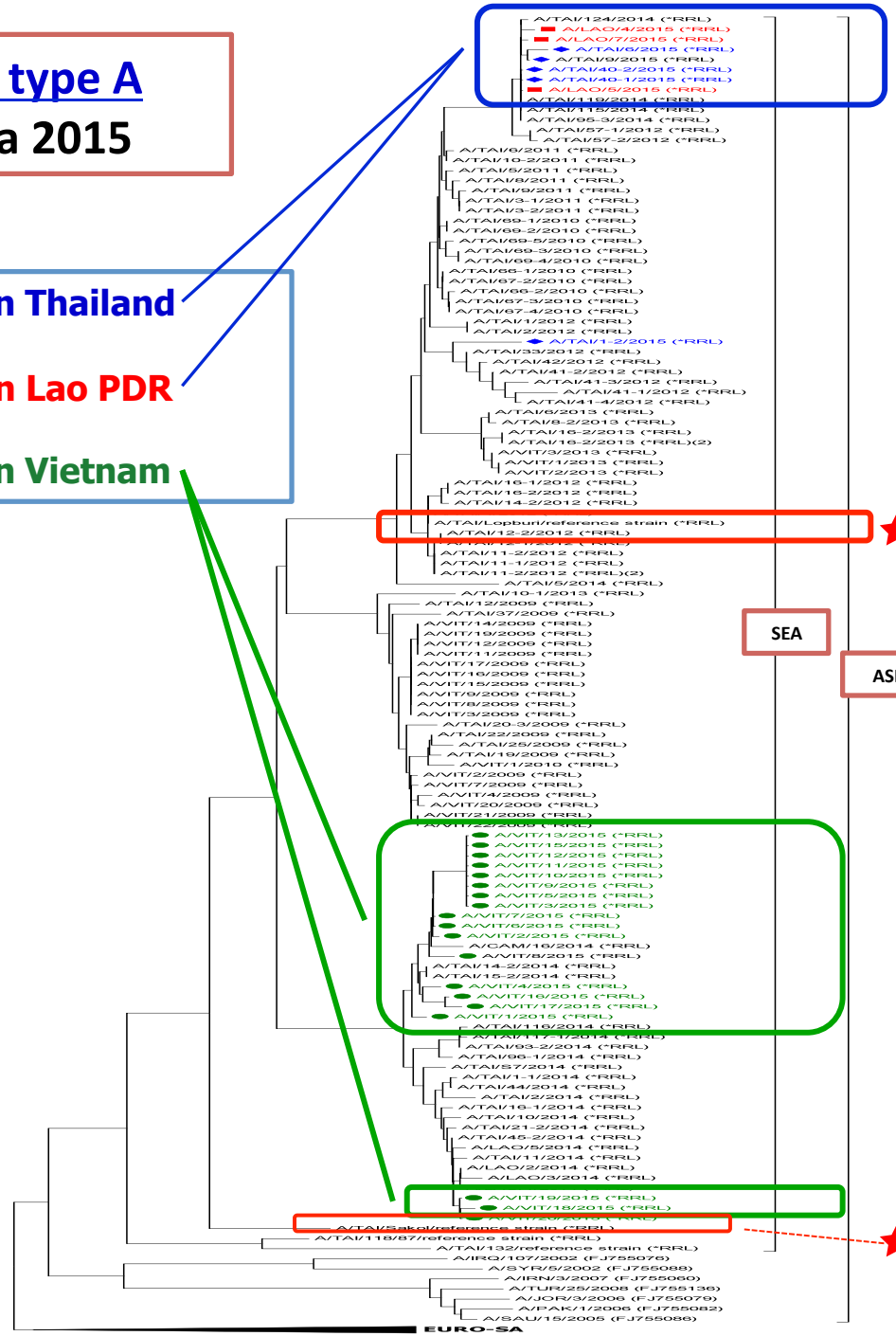


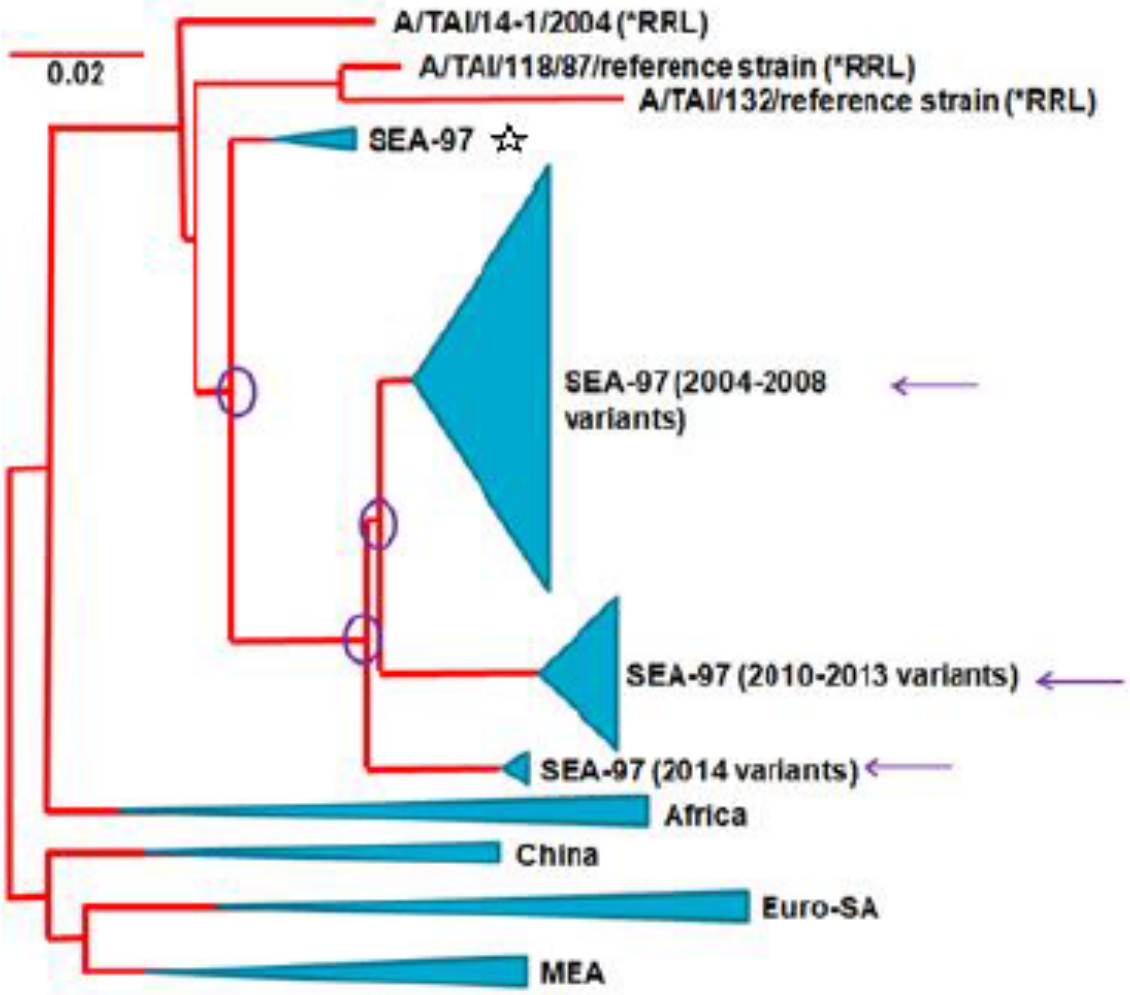
Phylogenetic tree of FMDV type A outbreak in South East Asia 2015

Indicates viruses in Thailand

Indicates viruses in Lao PDR

Indicates viruses in Vietnam




A/TAI/14-1/2004 (*RRL)
0.02
A/TAI/118/87/reference strain (*RRL)
A/TAI/132/reference strain (*RRL)
SEA-97
SEA-97 (2004-2008 variants)
SEA-97 (2010-2013 variants)
SEA-97 (2014 variants)
Africa
China
Euro-SA
MEA

Nucleotide sequencing results 2014-2015 in Thailand and South East Asia

FMDV	2014	2015
Type O	SEA topotype (Mya-98 strain)	SEA topotype (Mya-98 strain)
		ME-SA topotype (PanAsia strain)
Type A	ASIA topotype (Sea-97 strain)	ASIA topotype (Sea-97 strain)

Vaccine matching of FMDV type O in SEA region in 2013-2015

(Homologous using O Udornthani 189/87 Thai vaccine strain)

Country	Year	Total sample	Range of r-value by LP ELISA		
			0-0.19 Poor Matching	0.2-0.39 moderate matching	0.4-1.0 Good Matching
Cambodia	2013	5	-	-	5
	2014	1	-	-	1
Thailand	2013	17	-	-	17
	2014	16	-	1	15
	2015	13	-	-	13
Lao PDR	2015	4	-	-	4
Total		56	-	1 (1.79%)	55 (98.21%)

SUMMARY OF FMD VACCINE MATCHING

Vaccine matching or r-value of FMDV type A in SEA region in 2013-2015

Country	Year	Total Sample	Range of r – value by ELISA test					
			A/Sakolnakorn/97			A/Lopburi/2012		
			0 – 0.19	0.2 – 0.39	0.4 – 1.0	0 – 0.19	0.2 – 0.39	0.4 – 1.0
Thailand	2013	16	-	-	-	-	2	14
	2014	16	-	-	-	-	1	15
	2015	10	-	1	3	-	-	10
Lao PDR	2014	3	-	-	-	-	1	2
	2015	1	-	-	-	-	-	1
Vietnam	2013	3	-	-	-	-	-	3
	2015	15	2	-	13	4	1	10

Summary of work done at RRL, Pakchong – April 2015

Singanallur Nagendrakumar[1], Timothy Bowden[1], Kingkarn Bonsooya[2], Janya Samanit[2]

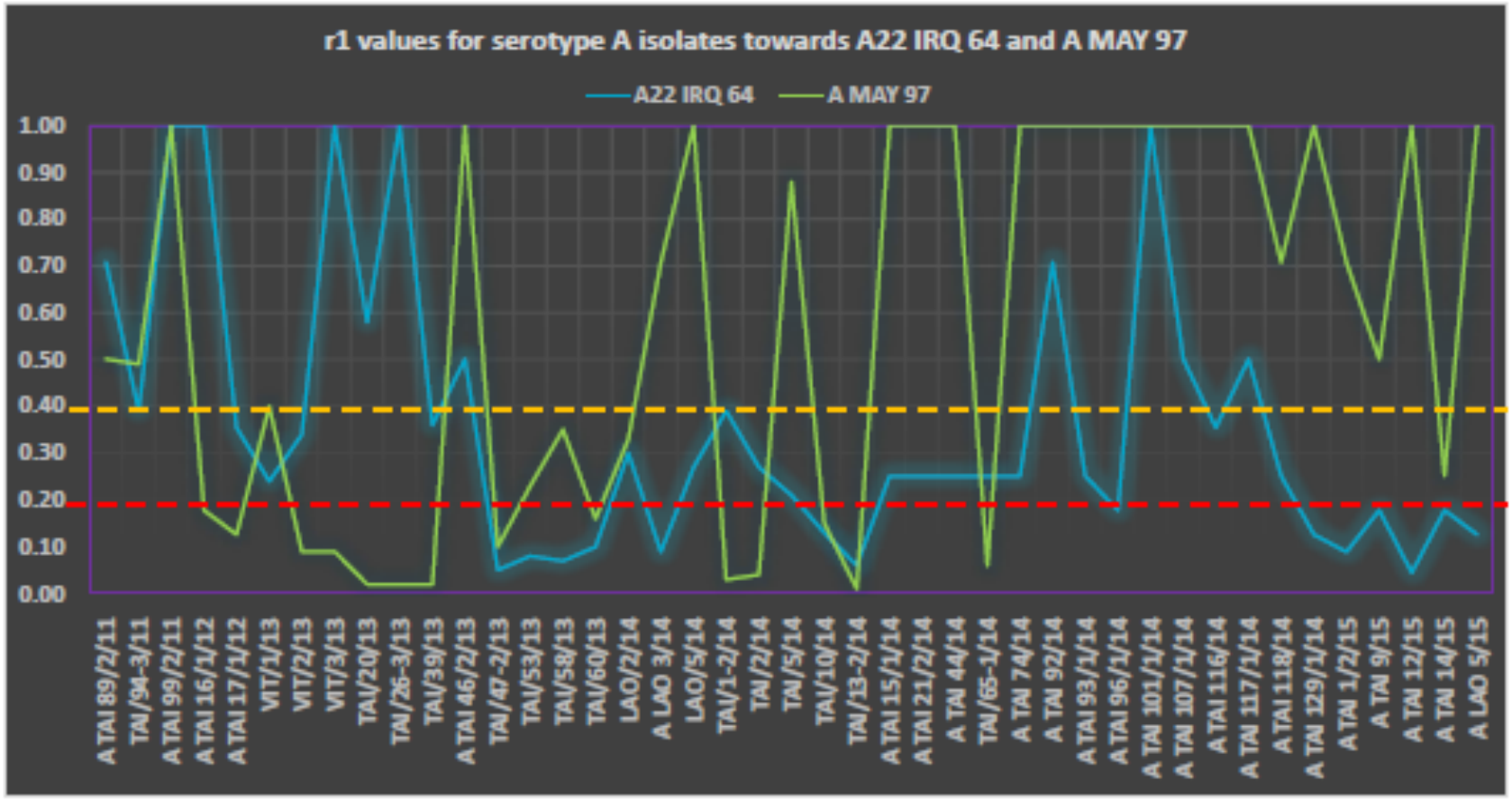
[1]Foot-and-Mouth Disease Risk Management Project, CSIRO Biosecurity Flagship, AAHL, Geelong, Australia
[2]Regional Reference Laboratory for FMD in SEA, Pakchong, Thailand.

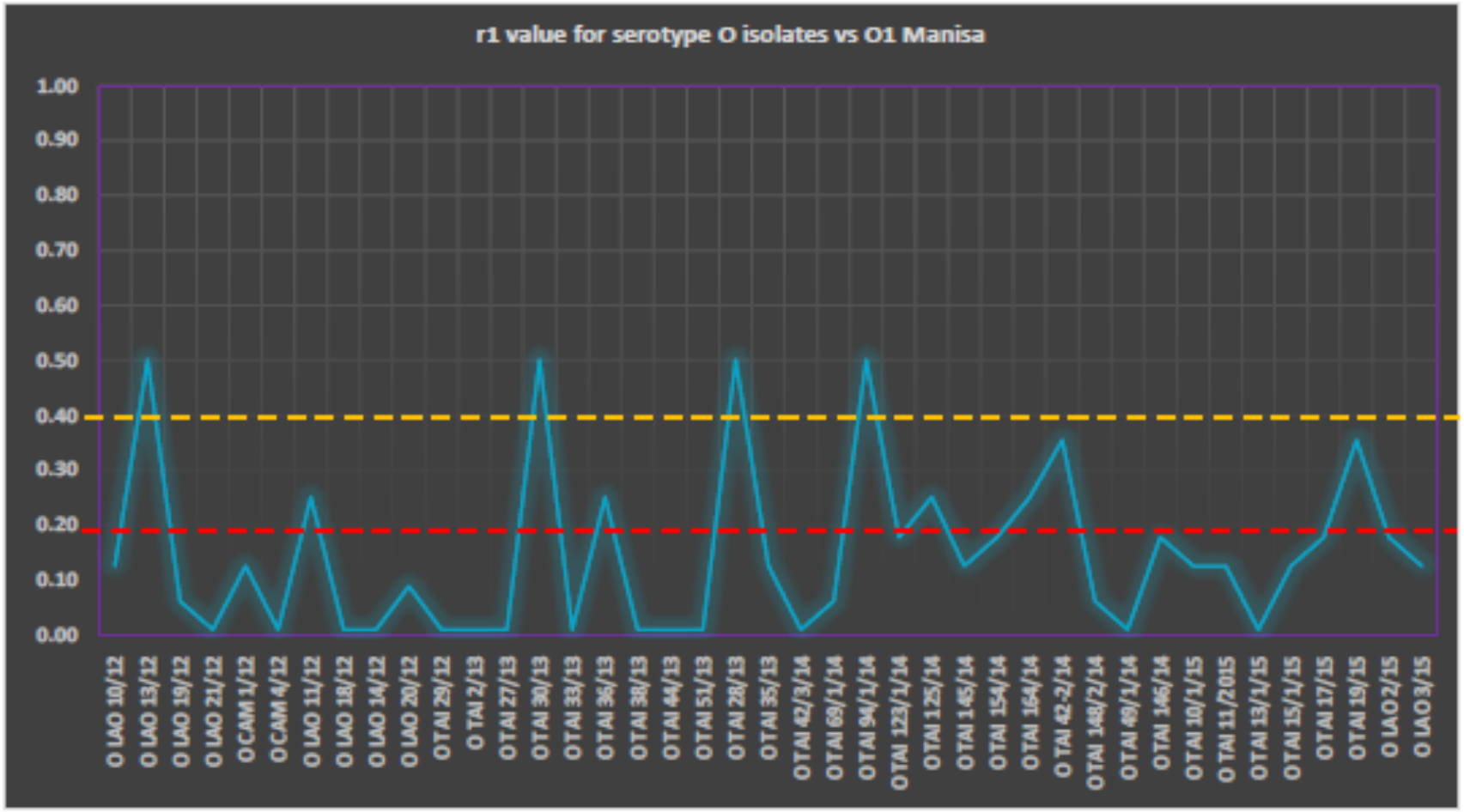
‘r’ value estimates

Sample IDs	A Lop Buri 2012			A22 IRQ 64			A MAY 97		
	Homo	Hetero	‘r’ value	Homo	Hetero	‘r’ value	Homo	Hetero	‘r’ value
VIT/1/13 B3	3.16	3.16	1.00	3.37	2.75	0.24	3.78	3.38	0.40
VIT/2/13 B3	3.16	2.86	0.50	3.59	3.11	0.34	4.08	3.02	0.09
VIT/3/13 B3	3.46	3.16	0.50	3.14	3.18	>1.00	4.38	3.34	0.09
TAI/20/13 R3B3	3.76	3.46	0.50	3.12	2.88	0.58	4.05	2.32	0.02
TAI/26-3/13 R3B2	3.76	3.46	0.50	3.39	4.08	>1.00	4.69	2.33	0.00
TAI/39/13 R1B2	3.16	2.98	0.66	3.22	2.78	0.36	4.20	2.58	0.02
TAI/47-2/13 R1B2	3.16	2.98	0.66	3.78	2.47	0.05	4.00	3.02	0.10
TAI/53/13 R2B2	3.16	2.98	0.66	3.80	2.72	0.08	3.72	3.08	0.23
TAI/58/13 R3B2	3.16	2.98	0.66	3.61	2.45	0.07	3.60	3.15	0.35
TAI/60/13 R1B2	3.46	3.58	>1.00	3.47	2.46	0.10	4.12	3.33	0.16

‘r’ value estimates

Sample IDs	A Lop Buri 2012			A22 IRQ 64			A MAY 97		
	Homo	Hetero	‘r’ value	Homo	Hetero	‘r’ value	Homo	Hetero	‘r’ value
LAO/2/14 B4	2.56	2.68	>1.00	3.01	2.49	0.30	4.16	3.67	0.33
LAO/5/14 B3	2.56	2.68	>1.00	3.14	2.57	0.27	3.66	3.98	>1.00
TAI/1-2/14 B3	2.56	2.68	>1.00	3.35	2.95	0.39	4.52	2.98	0.03
TAI/2/14 B3	2.56	2.68	>1.00	3.13	2.57	0.27	4.56	3.20	0.04
TAI/5/14 B1	2.56	2.68	>1.00	3.19	2.52	0.21	3.88	3.82	0.88
TAI/10/14 R2B3	2.56	2.68	>1.00	3.57	2.69	0.13	3.83	3.01	0.15
TAI/13-2/14 B4	2.56	2.68	>1.00	3.58	2.38	0.06	4.81	2.74	0.01
TAI /21-2/14 B4	3.46	3.58	>1.00	2.99	2.85	0.73	4.67	3.04	0.02
TAI/44/14 B4	3.16	2.98	0.66	4.00	2.58	0.04	3.60	2.90	0.20
TAI/65-1/14 R1B2	-	-	-	3.35	2.75	0.25	3.95	2.74	0.06


r1 values for serotype A isolates towards A22 IRQ 64 and A MAY 97
A22 IRQ 64
A MAY 97
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
A TAI 89/2/11
TAI/94-3/11
A TAI 99/2/11
A TAI 16/1/12
A TAI 17/1/12
VIT/1/13
VIT/2/13
VIT/3/13
TAI/20/13
TAI/26-3/13
TAI/39/13
A TAI 46/2/13
TAI/47-2/13
TAI/53/13
TAI/58/13
TAI/60/13
LAO/2/14
A LAO 3/14
LAO/5/14
TAI/1-2/14
TAI/2/14
TAI/5/14
TAI/10/14
TAI/13-2/14
A TAI 15/1/14
A TAI 21/2/14
A TAI 44/14
TAI/65-1/14
A TAI 74/14
A TAI 92/14
A TAI 93/1/14
A TAI 96/1/14
A TAI 101/1/14
A TAI 107/1/14
A TAI 116/14
A TAI 117/1/14
A TAI 118/14
A TAI 129/1/14
A TAI 1/2/15
A TAI 9/15
A TAI 12/15
A TAI 14/15
A LAO 5/15


r1 value for serotype O isolates vs O1 Manisa
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
O IAO 10/12
O IAO 13/12
O IAO 19/12
O IAO 21/12
O CAM 1/12
O CAM 4/12
O IAO 11/12
O IAO 18/12
O IAO 14/12
O IAO 20/12
O TAI 29/12
O TAI 2/13
O TAI 27/13
O TAI 30/13
O TAI 33/13
O TAI 36/13
O TAI 38/13
O TAI 44/13
O TAI 51/13
O TAI 28/13
O TAI 35/13
O TAI 42/3/14
O TAI 69/1/14
O TAI 94/1/14
O TAI 123/1/14
O TAI 125/14
O TAI 145/14
O TAI 154/14
O TAI 164/14
O TAI 42-2/14
O TAI 168/2/14
O TAI 49/1/14
O TAI 146/14
O TAI 10/1/15
O TAI 11/2015
O TAI 13/1/15
O TAI 15/1/15
O TAI 17/15
O TAI 19/15
O IAO2/15
O IAO3/15

Conclusions

- O1 Manisa has poor match with the strain in SEA.

- Type A : 2014 and 2015 strains are turning to be intermediary or heterologous to A22 IRQ 64 while becoming homologous to intermediary to A MAY 97.

- New sublineage of type A has been observed since 2014.

- Phylogenetic tree data and epidemiological data required to make any meaningful conclusions.

(Vaccine Matching and Genetic Characterization of FMDV Serotype O and A isolates in South East Asia : RRL and AAHL; FMD Risk Management collaboration project.)

Thank you for your attention

Acknowledgements:

- **RRL staff**
- **OIE-SRR SEA**

Vaccine suitable for SEA region

Circulating Serotype	*Internationally available vaccines*	*Locally produced vaccine*
O	O TAW 98 O 3039 O1 Manisa	Thailand, O Udornthani 189/87
A	A22 Iraq A Malaysia 97	Thailand, A Lopburi/12 A Sakolnakorn/97
Asia 1	Asia1 Shamir	Thailand Asia1/85