Vaccine matching strain characterisation of FMDV in SEA region

<u>Wilai Linchongsubongkoch^{*1}</u> Kingkarn Boonsuya Seeyo^{*2} Janya Samanit^{*2}

- *1 OIE Expert for Foot and Mouth Disease, DLD's consultant
- *2 Regional Reference Laboratory for FMD in South East Asia National Institute of Animal Health, Department of Livestock Development Pakchong, THAILAND

To serve as an OIE Reference Laboratory for FMD

To serve as national laboratory for FMD diagnosis within the country (8 Veterinary Diagnostic Center

> ศูนย์อ้างอิ่งโรดปากและเท้าเปื้อย ภูมิกาดเอเชียตะวันออกเฉียงใต้ ได้รับการรับรอง ISO/IEC17025 : 2005

Regional Reference Laboratory for Foot and Mouth Disease in Southeast Asia Accredited by ISO/IEC 17025 : 2005

OIE Reference Laboratory for Foot and Mouth Disease Designated by World Organisation for Animal Health

OP

FMD Status in South East Asia



- FMD Diagnosis of specimen submission from OIE member countries by ELISA typing, Virus isolation, RT-PCR
- LP ELISA , NSP test







Procedure for vaccine matching investigation (r-value) by LP ELISA method





Initial ELISA typing test



virus isolation to get high viral titer



antigen titration to select an optimal dilution

Vaccine matching test

FMDV Strain differentiation

Objective:

To study antigenic and genomic variation between

strains within serotype for epidemiological

investigation and immunophophylaxis campaign.

Investigation method:

1) r-value = to determine serological relationship between virus vaccine strain and field outbreak strain for seed vaccine selection.

2) nucleotide sequencing = to analyze genetic relationship among viruses from field outbreak strains.

Material need for r-value investigation

Homologous virus : Seed vaccine strain such as O, A or Asia1

Heterologous virus: Isolation viruses from field outbreak

Homologous serum: Bovine serum, 21 post vaccinated with homologous vaccine strain

Serological methods for r-value

- Complement Fixation (CF) Test
- Virus Neutralization (VN) Test
- Liquid phase blocking ELISA (LP ELISA)



Plate layout and diagram for r-value investigation by LP ELISA



Antigen control of heterologous filed strain Bovine serum against heterologous field strain Bovine serum against homologous vaccine strain Antigen control of homologous vaccine strain



ELISA plate



Calculation of r-value and criteria for interpretation

r-value = Serum titer against heterologous field strain Serum titer against homologous vaccine strain

In the case of VNT:

 $r_1 = \geq 0.3$. Suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.

 $r_1 = < 0.3$. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protec

In the case of LPB ELISA:

 $r_1 = 0.4$ -1.0. Suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.

 $r_1 = 0.2-0.39$, Suggests that the field isolate is antigenically related to the vaccine strain. The vaccine strain might be suitable for use if no closer match can be found provided that a potent vaccine is used and animals are preferably immunised more than once.

 $r_1 = <0.2$. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect

Table 1.Vaccine matching of FMDV type O in SEA regionduring 2006-2008 (using O189/87 Thai vaccine Strain)

Country	Year	Total	Range of r-value by LP ELISA			
		sample	0-0.19	0.2-0.39	0.4-1.0	
			Poor Matching	moderate matching	Good Matching	
Vietnam	2006	6	-	-	6	
Cambodia		4	-	-	4	
LAO PDR		3	- Not done	-	3	
Thailand			Not done			
Lao PDR	2007	4	-	-	4	
Thailand		5	-	-	5	
Lao PDR	2008	2	-	-	2	
Cambodia		3	-	-	3	
Myanmar		2	-	-	2	
Thailand		5	-	-	5	
					34 (100%)	

Table 2.Vaccine matching of FMDV type O in SEA regionduring 2009-2010 (using O189/87 Thai vaccine Strain)

Country	Year	Total	Total Range of r-value by LP ELISA				
		sample	0-0.19 Poor Matching	0.2-0.39 moderate matching	0.4-1.0 Good Matching		
Myanmar Thailand	2009	3 4	-	-	3 4		
Cambodia	2010	3	-	-	3		
Vietnam	2010	11	-	-	11		
Thailand	2010	7	-	-	7		
					28 (100%)		

Table 3.Vaccine matching of FMDV type O in SEA regionin 2011 (using O189/87 Thai vaccine Strain)

Country	Year	Total	Range of r-value by LP ELISA				
		sample	0-0.19 Poor Matching	0.2-0.39 moderate matching	0.4-1.0 Good Matching		
Cambodia	2011	2	-	-	2		
Loa PDR	2011	3	-	-	3		
Thailand	2011	13	-	-	13		
					18 (100%)		

Table 4. Vaccine matching strain differentiation by VN test (2010)

Report no:		VNT					
Vaccine:		0	0	0	0	O TNN	
Field Isolate:		3039	4625	Manisa	Taw98	24/82	
O Cam 06/2010	Mean	0.56	0.65	0.25	>0.99	0.38	
O Cam 08/2010	Mean	0.44	0.67	0.25	>0.89	0.48	

Report no:		VNT					
Vaccine:	a	0	0	0	0	O TNN	O Tur
Field Isolate:	VNT	3039	4625	Manisa	Taw98	24/82	5/09
O Vit 18/2010	Mean	0.76	0.76	0.30	>0.83	0.20	>0.65
O Vit 23/2010	Mean	0.70	0.62	0.18	0.87	0.10	0.51

Source: World Reference Laboratory for FMD (WRL), UK

Table 5. Vaccine matching strain differentiation by VN test (2011)

Report no:		VNT					
Vaccine:	-	0		0	0		O Tur
Field Isolate:	VNT	3039	O 4625	Manisa	Taw98	24/82	5/09
O Tai 02/2011	Mean	0.51	>0.76	0.29	>0.85	0.21	>0.67
O Tai 07/2011	Mean	0.49	0.52	0.21	>1.0	0.17	>0.68

Report no:	VNT					
Vaccine: Field Isolate:		O 3039	0 4625	O Manisa	O Taw98	O TNN 24/82
O Lao 01/2011	Mean	>0.67	>0.88	0.25	0.93	0.24

Source: World Reference Laboratory for FMD (WRL), UK

Table 6. Vaccine matching of FMDV type Asia 1 in SEA during 2005- 2006(using Asia 1/85 Thai vaccine Strain)

Country	Year	Total	Range of r-value by LP ELISA				
		sample	0-0.19 Poor Matching	0.2-0.39 moderate matching	0.4-1.0 Good Matching		
Myanmar	2005	1	-	-	1		
Vietnam	2006	4	-	-	4		
					5(100%)		

Thailand: no type Asia 1 outbreak since 1998

Table 7. Vaccine matching of FMDV type A in SEA during 2006- 2008(using A118/87 Thai vaccine Strain)

Country	Country Year Total		Range of r-value by LP ELISA				
		sample	0-0.19 Poor Matching	0.2-0.39 moderate matching	0.4-1.0 Good Matching		
Cambodia	2006	2	-	-	2		
LAO PDR		4	-	-	4		
Thailand		16	-	1	15		
LAO PDR	2007	16			16		
Thailand		10	-	-	10		
Cambodia	2008	1	-	-	1		
Lao PDR		1	-		1		
Vietnam		1	-	-	1		
Thailand		14	-	-	14		
				1 (1.54%	64(98 . 46%)		
					10		

Table 8. Vaccine matching or r-value of FMDV type A (A118/87) and A/Sakolnakorn/97 in SEA region (specimens received in 2009-2012)

Country	Year	Total	Ra	nge of r-valu	e by LP ELISA t	est
		sample	A118/87		A/Sakoln	akorn/97
			0.2-0.39	0.4-1.0	0.2-0.39	0.4-1.0
Lao PDR Vietnam Thailand	2009	1 6 9	- 1	1 5 9	ND ND ND	
Thailand Vietnam	2010	3 1	No binding r by antigen t	eaction itration		3* 1*
Thailand	2011 2012	39 2	No binding ı by antigen ti	reaction tration		39* 2*

Supporting investigation on FMD profiling test

by antigen titration of field virus type A in 2011 (No. 1-11) indicating the high binding reaction to A/sakol/97 system



A/sakol/97 system

A118/87 system

FMD profiling test of FMD viruses in 2011





Purpose:

1. to calculate % antigenic binding reaction of field isolate viruses and compare to several reference vaccine strains

2. To select the appropriate reagent system used in vaccine matching test or other research



vaccine matching (r-value) using several reference vaccine strain ; A132 , A118/87 and A/sakol/97 system



A132

A118/87

A/sakol/97

Figure 1. ELISA Profile test of field isolate viruses from Thailand during 2005-2007 react with reference viruses: A132/87, A22/Iraq, A/Sakolnakorn/97 and A118/87



Sample Name:				
No.1 = THA 2/07	NO.6 = THA 16/06			
No.2 = THA 87/06	No.7 = THA 46-1/05			
No.3 = THA 31-1/05	No.8 = THA 80/05			
No.4 = THA 76/06	No. 9 = THA 50/06			
No.5 = THA 84/06	No.10 = THA 78/06			
No. 11 = Reference homologous virus				

Figure 2. ELISA Profile test of isolate viruses from LAO in 2007 react with reference viruses: A132/87, A22/Iraq, A/Sakolnakorn/97 and A118/87



Sample Name:				
No.1 = LAO 1/07	NO.6 = LAO11/07			
No.2 = LAO2/07	No.7 = LAO14/07			
No.3 = LAO3/07	No.8 = LAO15/07			
No.4 = LAO4/07	No. 9 = LAO17/07			
No.5 = LAO10/07	No.10 = LAO 7/07			
No.11 = Reference homologous virus				

Conclusion

- 1. r-value of type O viruses causing outbreak in SEA region during 2006-2011 demonstrated that no antigenic change from recent vaccine strain.
- 2. r-value of type A viruses causing outbreak in Thailand during 2010 -2012 has antigenically varied from A118/87 to A/sakol/97 vaccine strain. Therefore, an additional of A/sakol/97 vaccine in the current vaccine was recommended.
- 3. History of A/sakol /97 vaccine strain was used in late 1997 to 2001, then changed to 118/87 in beginning of 2001 up to 2009, furthermore by end of 2010, A/sakol/97 was recommended to use again.

Priority vaccines recommendation in SEA region

Serotype	Internationally available vaccines	Locally produced vaccine
0	O Taiwan 98, O/ 3039 O /4625	Thailand 189/87
A	A/MAY 97/ A22 Iraq	Thailand 118/87, A Sakolnakorn/97 (equivalent to A/MAY/97)
Asia 1	Asia1/Shamir	Thailand/85

