



WORLD ORGANISATION FOR ANIMAL HEALTH
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SEACFMD Bulletin

Foot and Mouth Disease Situation
January to December 2016



OIE SUB-REGIONAL REPRESENTATION FOR SOUTH-EAST ASIA (SRR-SEA)
C/o Department of Livestock Development, Phaya Thai 10400, Bangkok, Thailand
Tel.: (+66-2) 6534864 * Fax (+66-2) 6534904 Email: srr.seasia@oie.int

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Summary

The present issue summarises the Foot and mouth disease (FMD) outbreaks in SEACFMD region in 2016 as well as the characterisation of isolated Foot and mouth disease viruses (FMDVs). In total, 518 FMD outbreaks were reported in mainland South-East Asia countries and China, of which 35% were caused by serotype O viruses and 5% by serotype A viruses and the remaining 60% were untyped. The prevalent lineages of FMDV were O/SEA/Mya-98, O/ME-SA/PanAsia, O/ME-SA/Ind-2001d, O/Cathay, and A/Asia/Sea-97. Significant epidemiological changes in 2016 include the incursion of the O/ME-SA/Ind-2001d strain in Thailand and the re-introduction of serotype A viruses in Malaysia.

Introduction

1. Aims

Following the previous issues of SEACFMD Bulletin presenting the regional FMD situation in the year of 2015 and the first half year of 2016, the current issue was developed to summarise the FMD situation in the entire year of 2016 in SEACFMD countries, including South-East Asia nations, China and Mongolia. The SEACFMD bulletins aimed to update countries, partners and stakeholders of the regional FMD situation on a regular basis and to facilitate the formulation of risk-based strategies and more effective FMD control and prevention measures.

2. Reporting period

January 1st 2016 - 31st December 2016

3. Data source

Sources of information in this report include data submitted by members to OIE through the World Animal Health Information Systems (WAHIS), the WAHIS Regional Core for South-East Asia/ASEAN Regional Animal Health Information System (ARAHIS), reports from OIE FMD Reference Laboratories in Pirbright (UK), Pakchong (Thailand) and Lanzhou (China), and country reports presented at the 23rd Meeting of the OIE Sub-Commission for FMD in South-East Asia and China held on March 8-10, 2017 in Siem Reap, Cambodia.

A FMD outbreak is defined as the occurrence of FMD in one or more animals in an epidemiological unit (*refer to a commune in Vietnam, a sub-district in Cambodia, or village/farm in the other SEACFMD countries*). All cases within 2 weeks from the previous case are considered as part of the same outbreak.

Outbreaks of FMD in SEACFMD Countries in 2016

1. Overview of the regional situation in 2016

In 2016, FMD outbreaks have continued to affect traditionally endemic countries (China, Myanmar, Lao PDR, Vietnam, Thailand, Cambodia, and peninsular Malaysia) (Figure 1). Of the total 518 outbreaks reported, 179 were due to serotype O, 26 were due to serotype A and 313 were not typed due to absence of or insufficient samples collected. Cattle were the main affected animal, followed by buffalo, pig and goat (Figure 2). The majority of outbreaks were reported during August to December, which accounted for 58% of the total outbreaks (Figure 3).

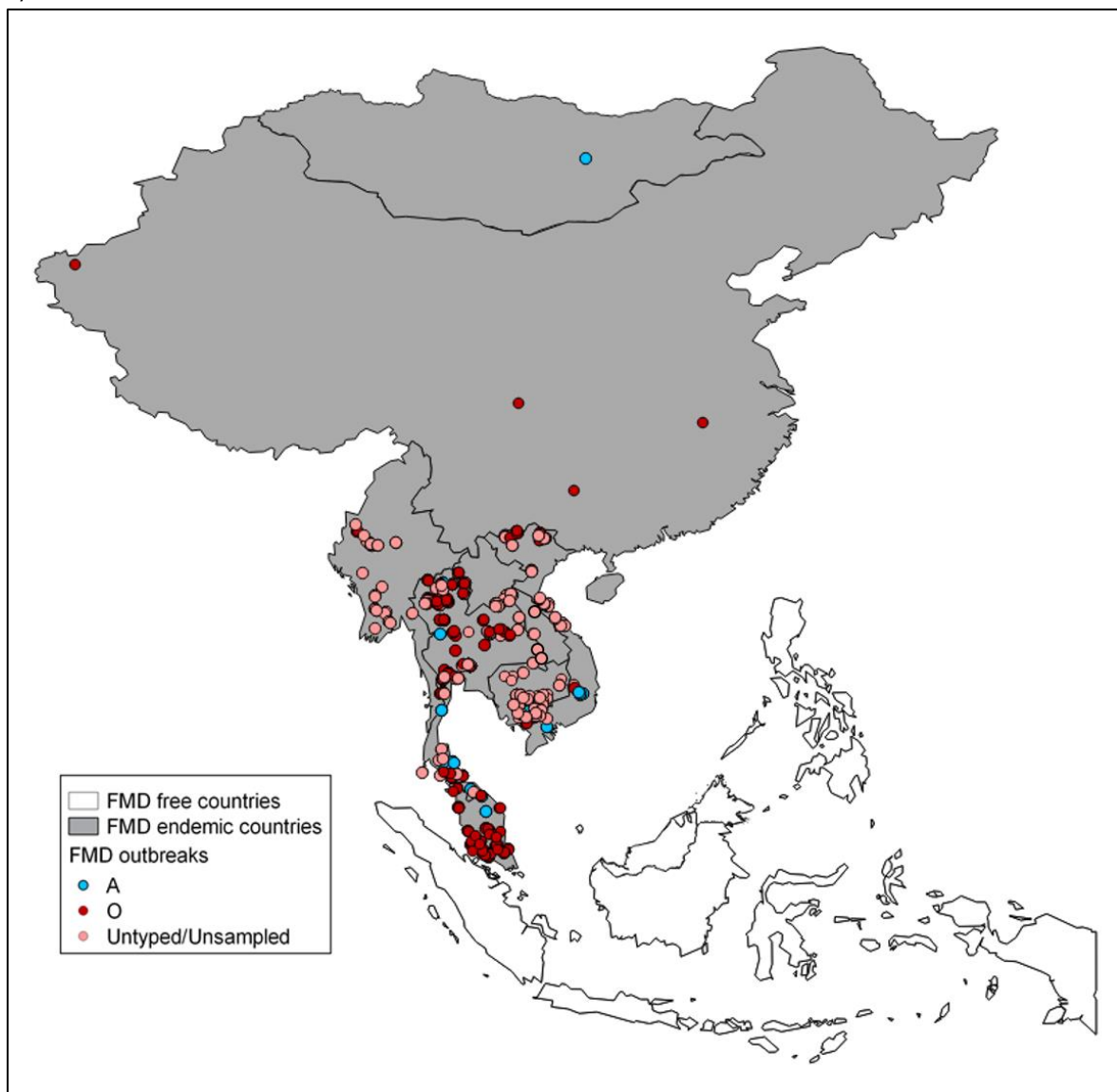


Figure 1. Distribution of FMD outbreaks in SEACFMD countries, 2016.

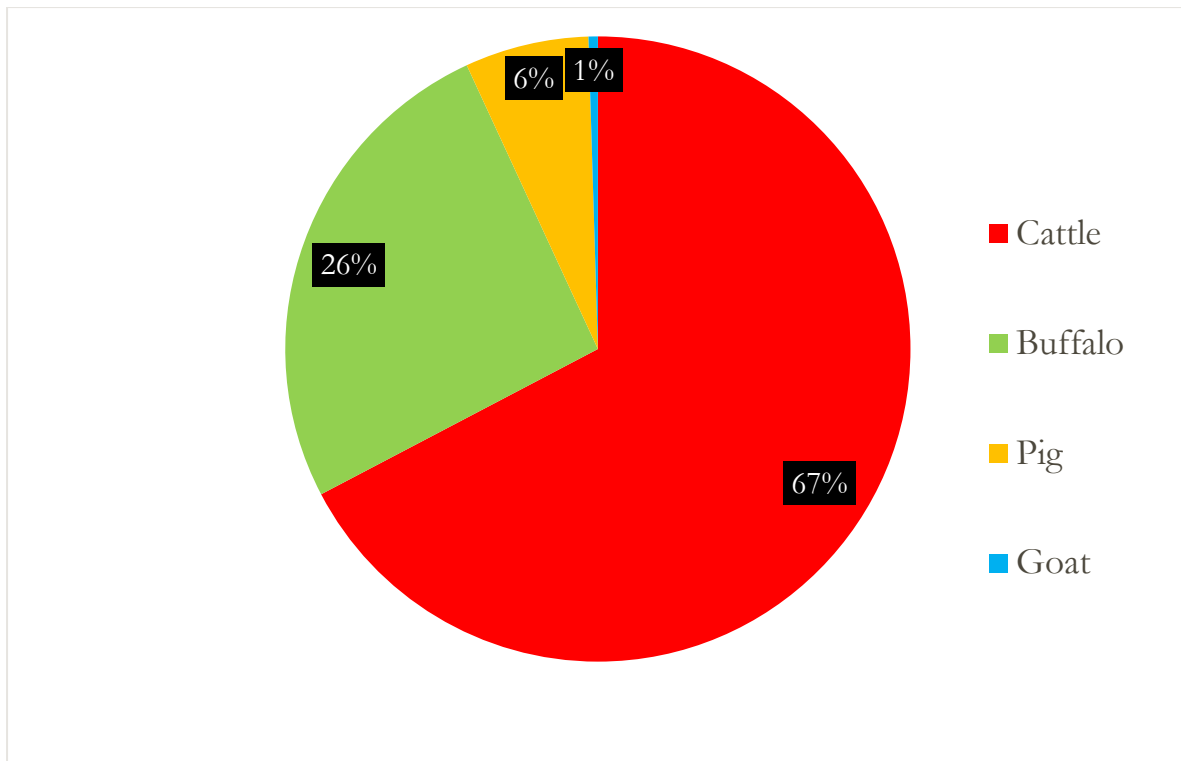


Figure 2. Distribution of FMD outbreaks in various animal species, 2016.

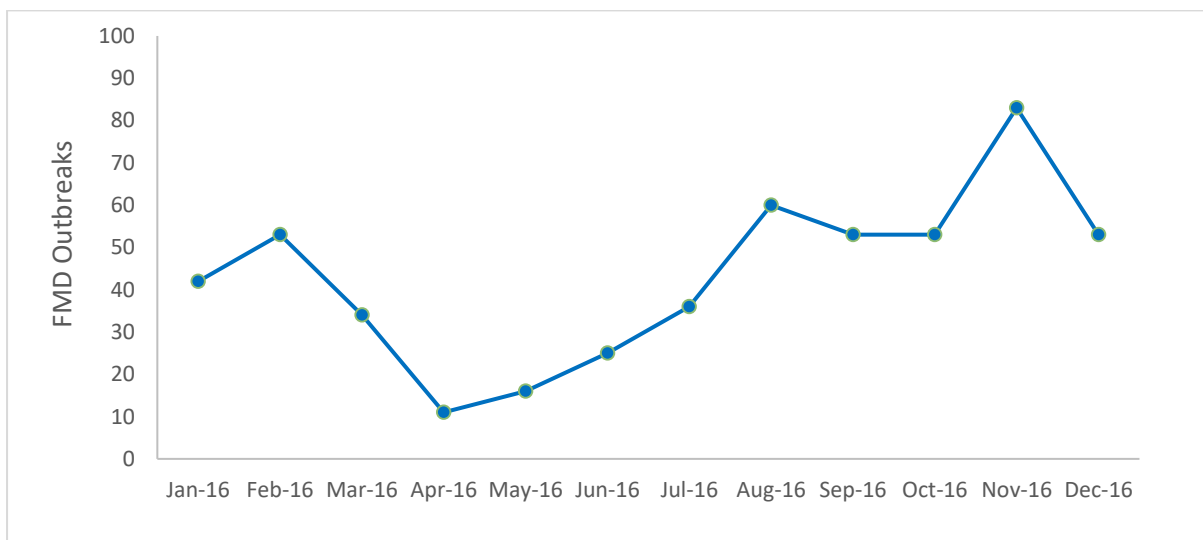


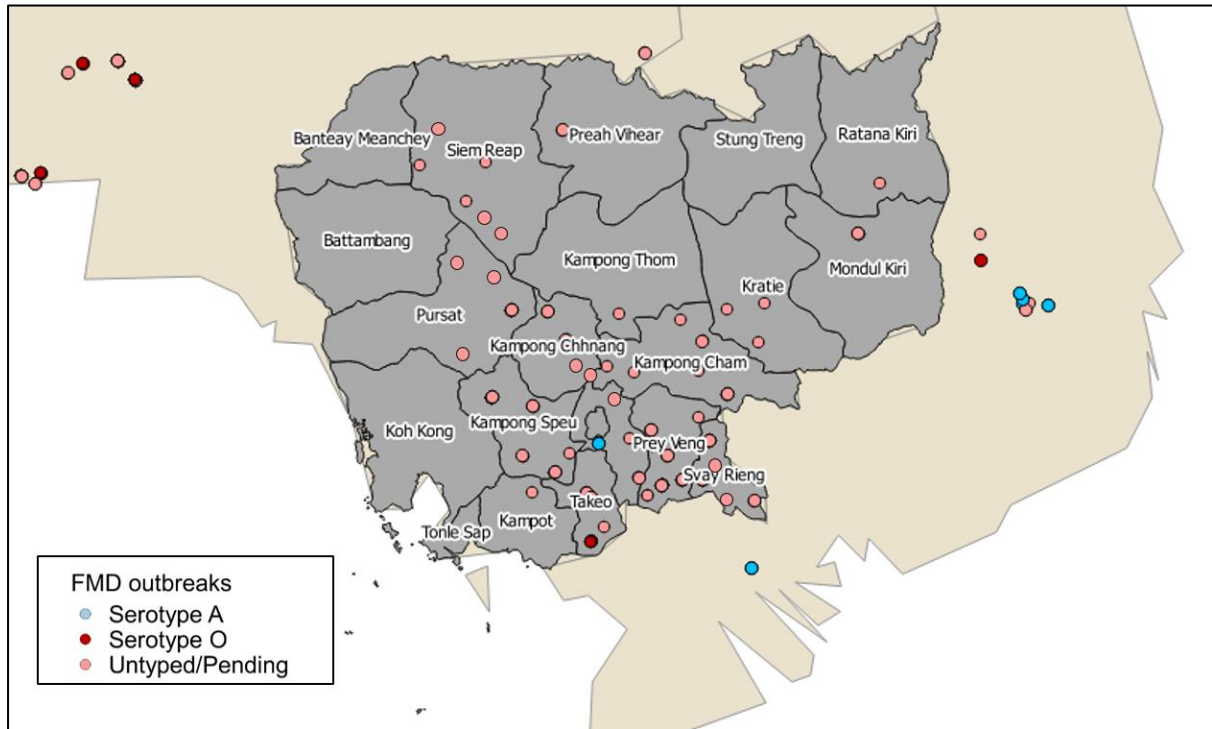
Figure 3. Monthly distribution of FMD outbreaks in SEACFMD countries, 2016.

2. FMD situation in SEACFMD countries

The Brunei, Indonesia, Philippines, and Singapore did not report any FMD outbreaks in 2016 and maintained their official status of FMD free without vaccination.

Cambodia

Cambodia reported 71 FMD outbreaks involving 17 provinces. Affected animals include cattle, buffaloes and pigs. Both serotype O and A viruses were confirmed, whilst the causative viruses of the majority of outbreaks remained unknown.



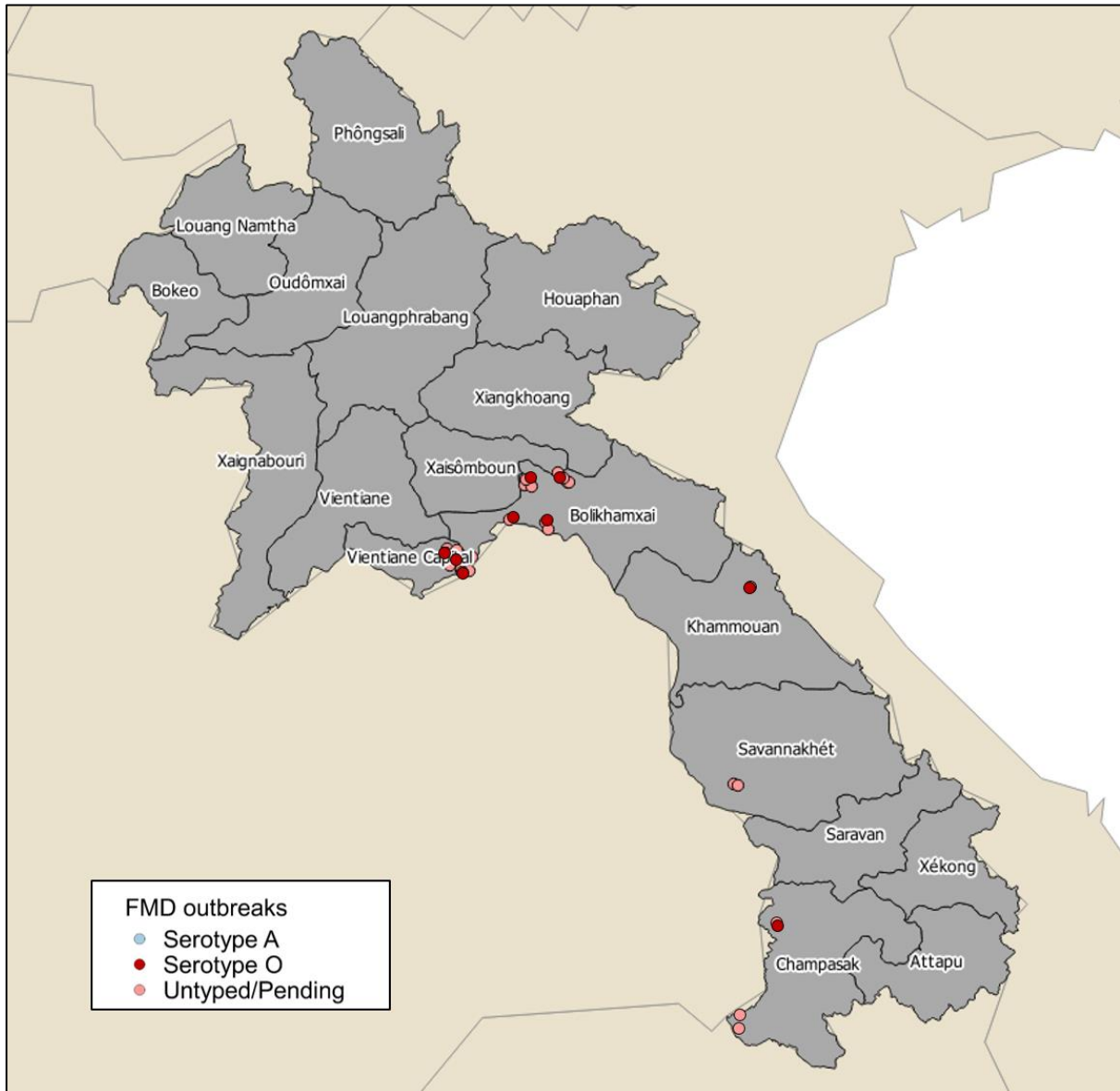
China

In 2016, China reported four FMD outbreaks in four provinces, all due to serotype O viruses. Cattle and pigs were affected.



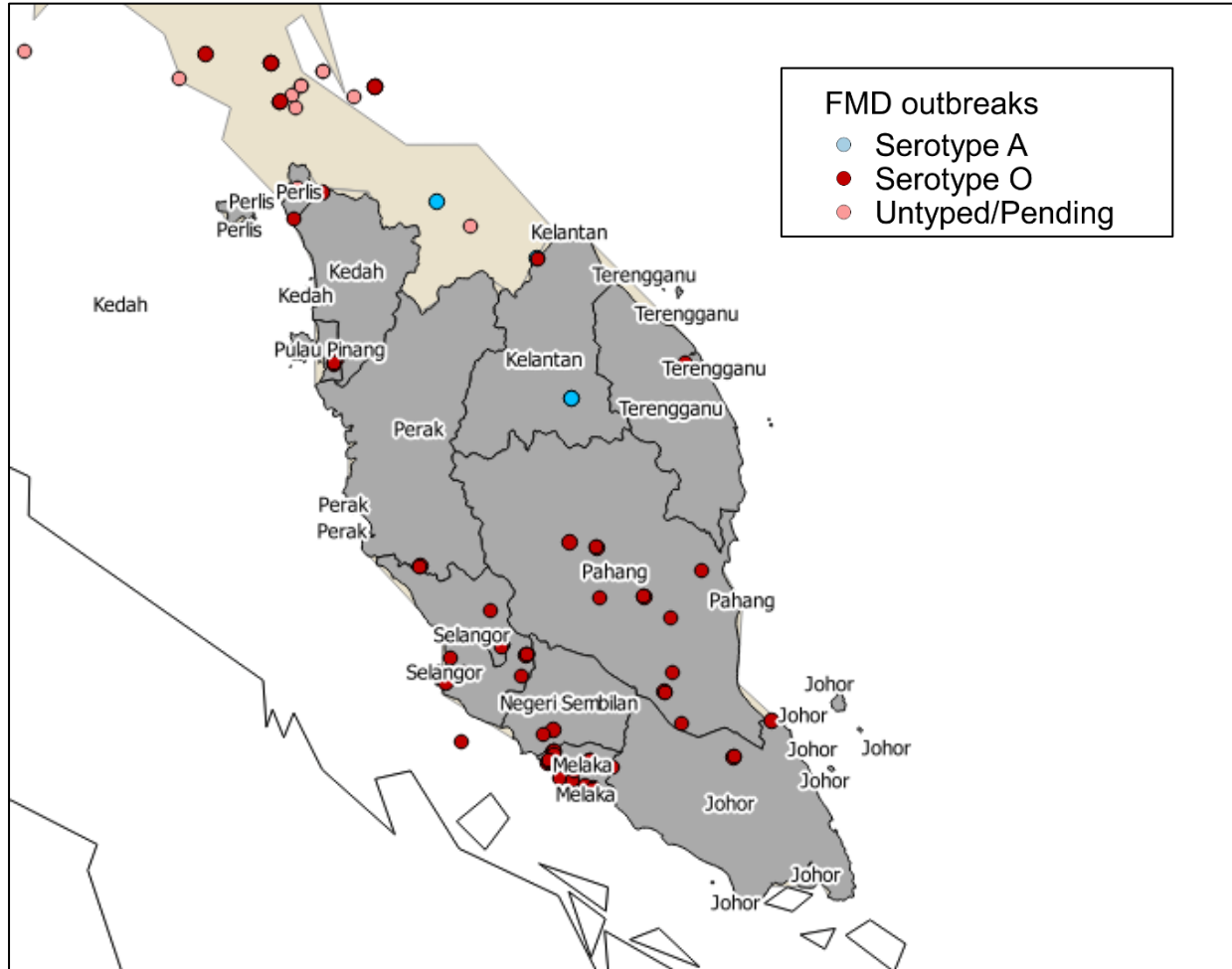
Lao PDR

Lao PDR reported 45 FMD outbreaks in 5 provinces, affecting cattle, buffaloes, and goats. Serotype O viruses were confirmed in 13 outbreaks in all affected provinces except Savannakhet.



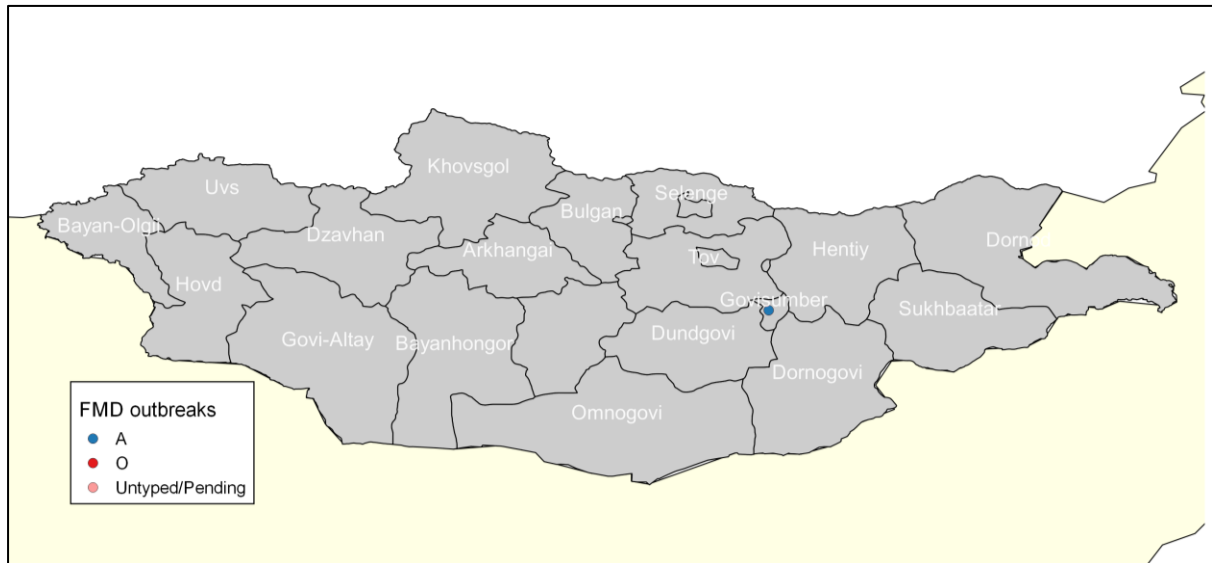
Malaysia

Malaysia reported 71 FMD outbreaks in 12 provinces in the peninsular region, affecting cattle, buffaloes and pigs. Of these outbreaks, 56% were caused by serotype O virus and 3.5% were caused by serotype A viruses. Malaysia reported the re-introduction of Serotype A virus in May 2016, which was likely associated with the substantial cross-border livestock movements prior to the religious festivals. East Malaysia retained its FMD free status.



Mongolia

Mongolia reported only one FMD outbreak in 2016. The outbreak occurred in cattle in Govisumber province in July, and was caused by a serotype A virus.



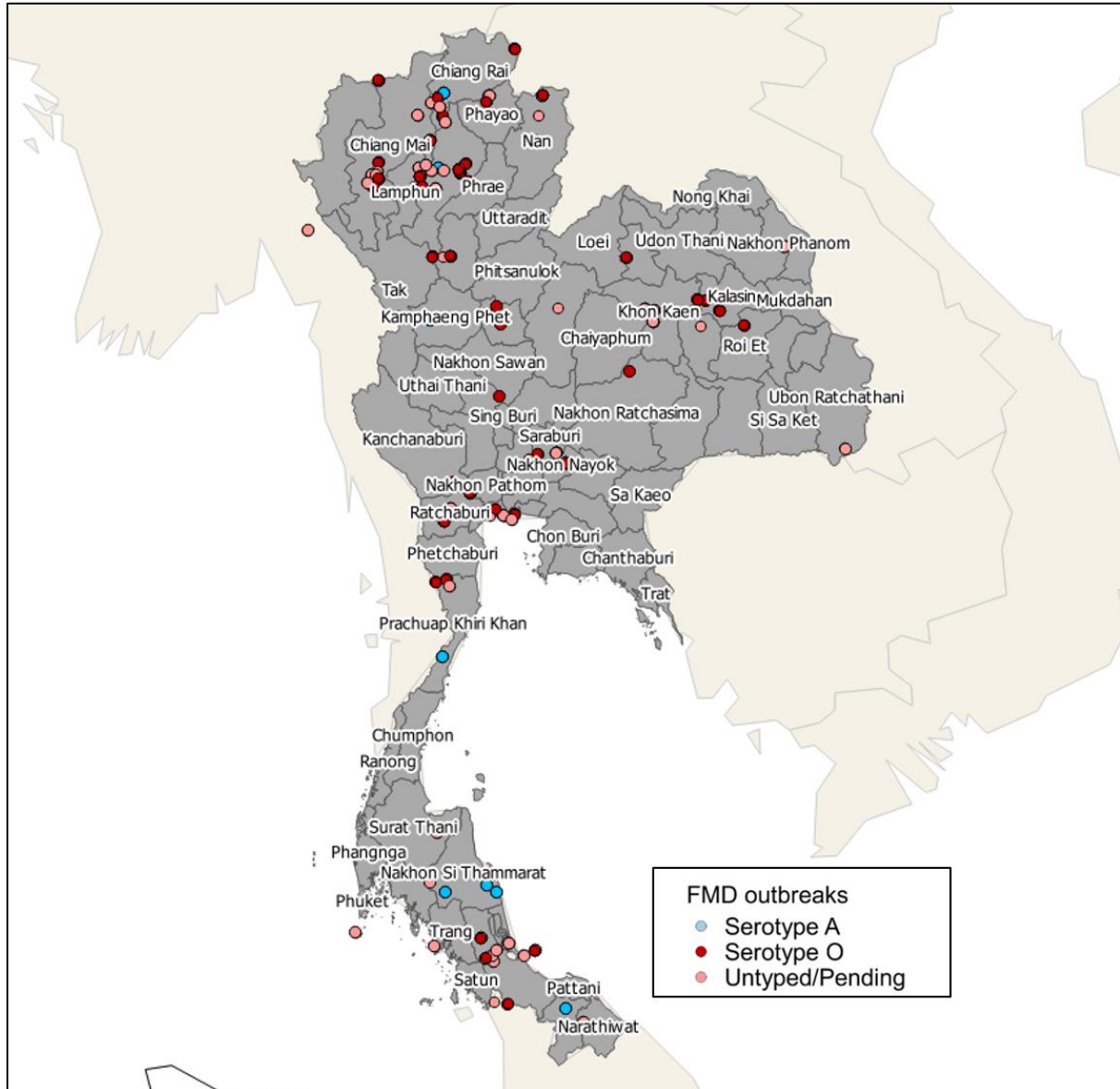
Myanmar

Myanmar reported 27 FMD outbreaks, all in cattle. Six states were affected. Serotype O viruses were confirmed in 4 outbreaks in 3 states.



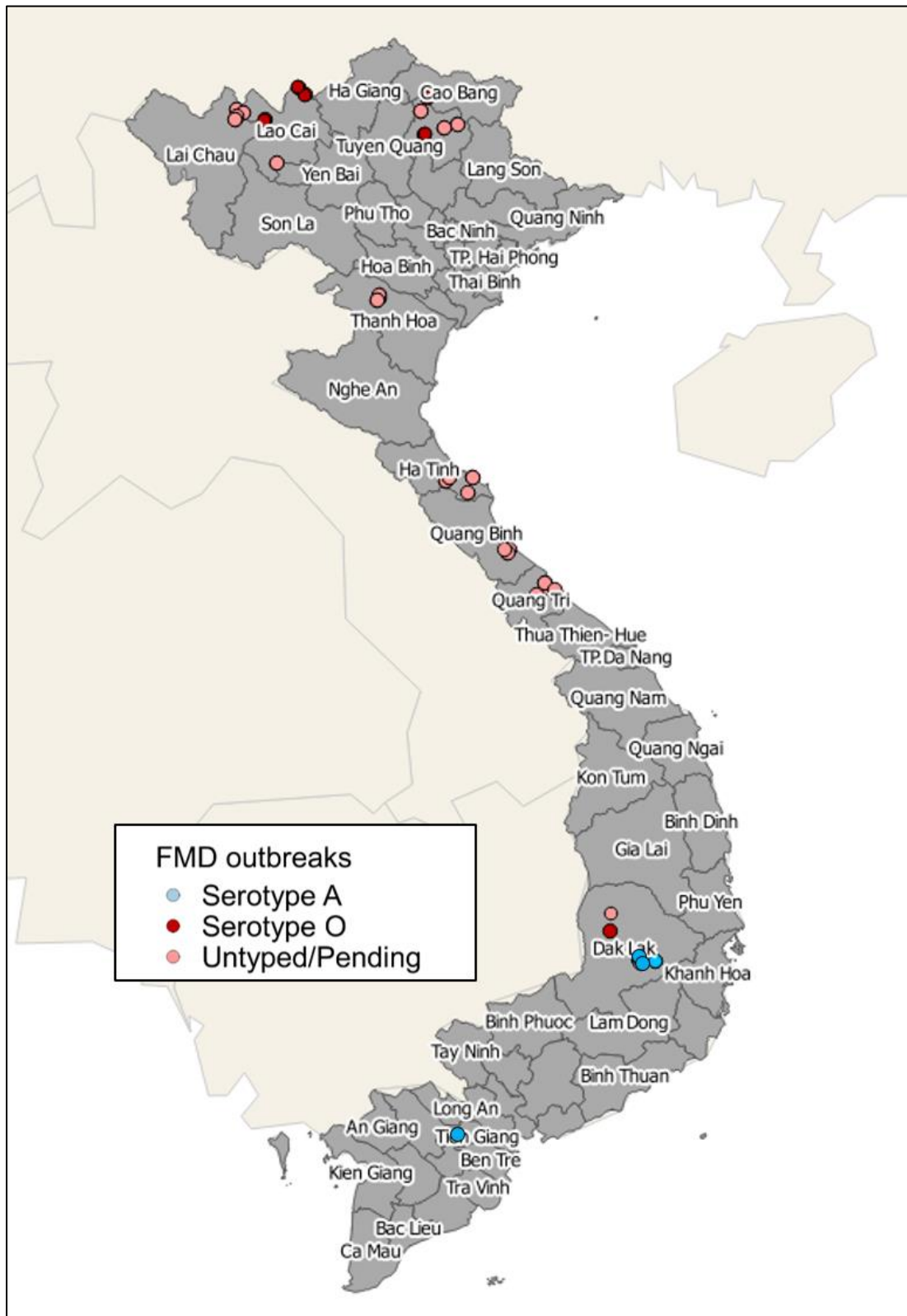
Thailand

Thailand reported 262 FMD outbreaks distributed throughout the country except Region 2 in East Thailand. Affected animals include cattle, buffaloes and pigs. Of these outbreaks, 59% were caused by serotype O and 12% were caused by serotype A viruses. Importantly, a new strain – O/ME-SA/Ind-2001d – was detected in Nonthaburi Province of Thailand in September 2016 and afterwards it quickly spread to another 11 provinces.



Viet Nam

Viet Nam reported 37 FMD outbreaks in 2016, affecting cattle, buffaloes, and pigs. Causative viruses were characterized in 11 outbreaks, belonging to serotype O (6 outbreaks) or serotype A (5 outbreaks).



Characterisation of FMDVs in SEACFMD Countries in 2016

Two serotypes - A and O – FMDVs were endemic in the SEACFMD region in 2016 (Table 1). A collection of FMD field samples have been characterised by genotyping. Based on the current available VP1 sequence data, circulating FMDV lineages in mainland SEA and China include:

- Serotype O: O/SEA/Mya-98, O/ME-SA/PanAsia, O/ME-SA/Ind-2001d and O/Cathay
- Serotype A: A/ASIA/Sea-97

Table 1. FMDV strains detected in SEACFMD Member Countries in 2016, as characterised by World and/or Regional Laboratory for FMD.

Country	Serotype O	Topotype...				Serotype A	Topotype
		SEA/ Mya-98	ME-SA/ PanAsia	ME-SA/ Ind- 2001d	Cathay		
Cambodia	+	+	+			+	+
China	+	+			+		
Lao PDR	+						
Myanmar	+	+					
Malaysia	+	+				+	+
Mongolia						+	+
Thailand	+	+		+		+	+
Viet Nam	+					+	

+: the FMDV lineage present in the country.

Note: data were based on the genotyping reports of the Pirbright Institute (http://www.wrlfmd.org/fmd_genotyping/asia.html) and RRL-Pakchong, and country reports presented at the 22nd Meeting of the OIE Sub-Commission for FMD in South-East Asia and China held on March 8-11, 2016 in Chiang Rai, Thailand.

Genetic analysis of viral VP1 shows the majority of serotype O viruses characterised in 2016 are the SEA indigenous Mya-98 strain, followed by the PanAsia strain and the Cathay strain. No further outbreaks due to the Ind-2001d strain were reported in Lao PDR, Viet Nam and Myanmar, following its first detections in these countries in 2015. However, for the first time this exotic FMDV strain was detected in Thailand in September 2016 and has become widespread nationally since then. Genetic analysis of the VP1 gene revealed that the Thai isolates are closely related to previous Ind2001d viruses isolated in Myanmar and Bangladesh (98% identity) but are distantly related to the Ind2001d viruses isolated in Laos and Vietnam (91-92% identity). This agrees with the report that the Thai viruses were first isolated from cattle smuggled from Myanmar or Bangladesh.

All serotype A viruses isolated in mainland SEA and Mongolia belong to the A/Asia/Sea-97 G2 lineage (*also called as the Lopburi strain*). Serotype Asia 1 FMDVs have not been reported in the SEACFMD region since 2009.

Table 2 summarises the prevailing FMDV lineages in individual SEACFMD countries during 2011-2016. In some cases, viruses were not sequenced following serotyping and thus the genotypes remained unidentified.

Table 2. FMDV strains detected in SEACFMD Member Countries during 2011–2016, as characterised by World and/or Regional Laboratory for FMD.

Country	Virus Lineage	2011	2012	2013	2014	2015	2016
Cambodia	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98					+	+
	O/ME-SA/PanAsia		+	+		+	+
	O/ME-SA/Ind2001 d						
	O/Cathay						
	Serotype A				+	+	+
A/Asia/Sea97					+	+	
China	Serotype O	+	+	+	+		+
	O/SEA/Mya98	+	+	+	+		+
	O/ME-SA/PanAsia	+	+	+			
	O/ME-SA/Ind2001 d						
	O/Cathay						+
	Serotype A			+	+	+	
A/Asia/Sea97			+	+	+		
Lao PDR	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98	+	+	+	+	+	
	O/ME-SA/PanAsia	+	+				
	O/ME-SA/Ind2001 d					+	
	O/Cathay						
	Serotype A				+	+	
A/Asia/Sea97				+	+		
Malaysia	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98	+	+	+	+		+
	O/ME-SA/PanAsia						
	O/ME-SA/Ind2001 d						
	O/Cathay						
	Serotype A	+	+	+	+		+
A/Asia/Sea97	+	+	+	+		+	
Myanmar	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98					+	+
	O/ME-SA/PanAsia						
	O/ME-SA/Ind2001 d						
	O/Cathay						
	Serotype A					+	
A/Asia/Sea97					+		
Mongolia	Serotype O				+	+	
	O/SEA/Mya98					+	
	O/ME-SA/PanAsia				+	+	
	O/ME-SA/Ind2001 d						
	O/Cathay						
	Serotype A			+			+
A/Asia/Sea97			+			+	
Thailand	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98	+	+	+	+	+	+
	O/ME-SA/PanAsia	+	+			+	+
	O/ME-SA/Ind2001 d						
	O/Cathay		+				
	Serotype A	+	+	+	+	+	+
A/Asia/Sea97	+	+	+	+	+	+	
Viet Nam	Serotype O	+	+	+	+	+	+
	O/SEA/Mya98				+	+	
	O/ME-SA/PanAsia	+	+	+	+	+	
	O/ME-SA/Ind2001 d					+	
	O/Cathay					+	
	Serotype A		+	+	+	+	+
A/Asia/Sea97		+	+	+	+	+	

+: the FMDV lineage present in the country.

Note: data were based on the genotyping results from the Pirbright Institute

(http://www.wrlfmd.org/fmd_genotyping/asia.html) and country reports presented at the 18th – 23rd Meetings of the OIE Sub-Commission for FMD in South-East Asia and China.

Conclusions

In 2016, a total of 518 FMD outbreaks were reported in SEACFMD countries, which was increased when compared to the 348 outbreaks in 2015 and the 303 outbreaks in 2014. Similar to 2015, serotype O remained to be the dominant serotype in 2016, but it was different from the situation in 2013 and 2014 when serotype O and A were detected at similar frequencies. Following its detections in Lao PDR in April 2015, in Viet Nam in May 2015, and in Myanmar in October 2015, the O/ME-SA/Ind-2001d lineage was again reported in Thailand and has become widespread in this country. The Thai isolates were found sourced from Bangladesh or Myanmar and introduced via cross-border movements of infected cattle. These viruses are distinct from the Ind2001d isolates detected in Lao PDR and Vietnam, representing at least two independent incursions of Ind2001d from the Indian Sub-continent to South-East Asia have occurred recently. A regional risk assessment study organised by the OIE SRR-SEA has been initiated to examine the risks of exotic FMDV strain incursion and its spread within the SEACFMD region. The assessment will investigate the risk pathways and consider risk reduction measures along these pathways. The study findings will help SEACFMD Member Countries to formulate risk-based control/prevention measures to mitigate the potential risks. Meanwhile, SEACFMD Member Countries are recommended to actively monitor the incursion/spread of this exotic FMDV strain, including report and share outbreak information timely, collect more clinical samples and submit them to Regional Reference Laboratories for analysis as early as possible.



OIE Sub-Regional Representation for South-East Asia
c/o DLD, 69/1 Phayathai Road, Rachathewi, 10400 Bangkok, THAILAND
tel (+662) 653-4864 ; fax (+662) 653-4904 ; srr.seasia@oie.int