



WORLD ORGANISATION FOR ANIMAL HEALTH
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SEACFMD Bulletin

Foot and Mouth Disease Situation
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Summary

The present issue summarises the Foot-and-mouth disease (FMD) outbreaks in the SEACFMD region in 2018 as well as the characterisation of detected FMD viruses (FMDVs). In total, 458 FMD outbreaks were reported in mainland South-East Asia countries, China, and Mongolia. Amongst the reported outbreaks, 211 were due to serotype O, 46 were due to serotype A, and the remaining 243 were not typed. The prevalent lineages of FMDV include O/SEA/Mya-98, O/ME-SA/Ind-2001, O/ME-SA/PanAsia, O/Cathay, and A/Asia/Sea-97. Significant epidemiological events in 2018 include: 1) detection of O/ME-SA/Ind2001 at endemic frequencies; 2) increased serotype A outbreak incidences in Thailand; 3) emergence of a genetic variant serotype A virus in Southern Lao PDR.

Introduction

1. Aims

Following the previous issues of SEACFMD Bulletin presenting the regional FMD situation in the years of 2015, 2016 and 2017, the current issue was developed to summarise the FMD situation in the entire year of 2018 in SEACFMD countries, including 10 ASEAN nations, China and Mongolia. The SEACFMD bulletins aim 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 - December 31st, 2018

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 24th OIE SEACFMD Subcommittee Meeting on 28-30 November 2018 in Ho Chi Minh City, Vietnam, and 22nd OIE SEACFMD National Coordinators Meeting held on 25-27 June 2019 in Ulaanbaatar, Mongolia.

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 2018

1. Overview of the regional situation in 2018

In 2018, FMD outbreaks have continued to affect traditionally endemic countries (China, Myanmar, Lao PDR, Vietnam, Thailand, Cambodia, and peninsular Malaysia) (Figure 1). Of the total 458 outbreaks reported, 211 were due to serotype O, 46 were due to serotype A, and the remaining 243 were not typed due to absence of or insufficient samples collected. Cattle were reported affected from 358 outbreaks, buffaloes from 25, goat and sheep from 34, and pigs from 40 outbreaks. Moreover, deer and camel were reported affected in one outbreak each (in Malaysia and Mongolia, respectively). Infection involving more than one species was commonly noted.

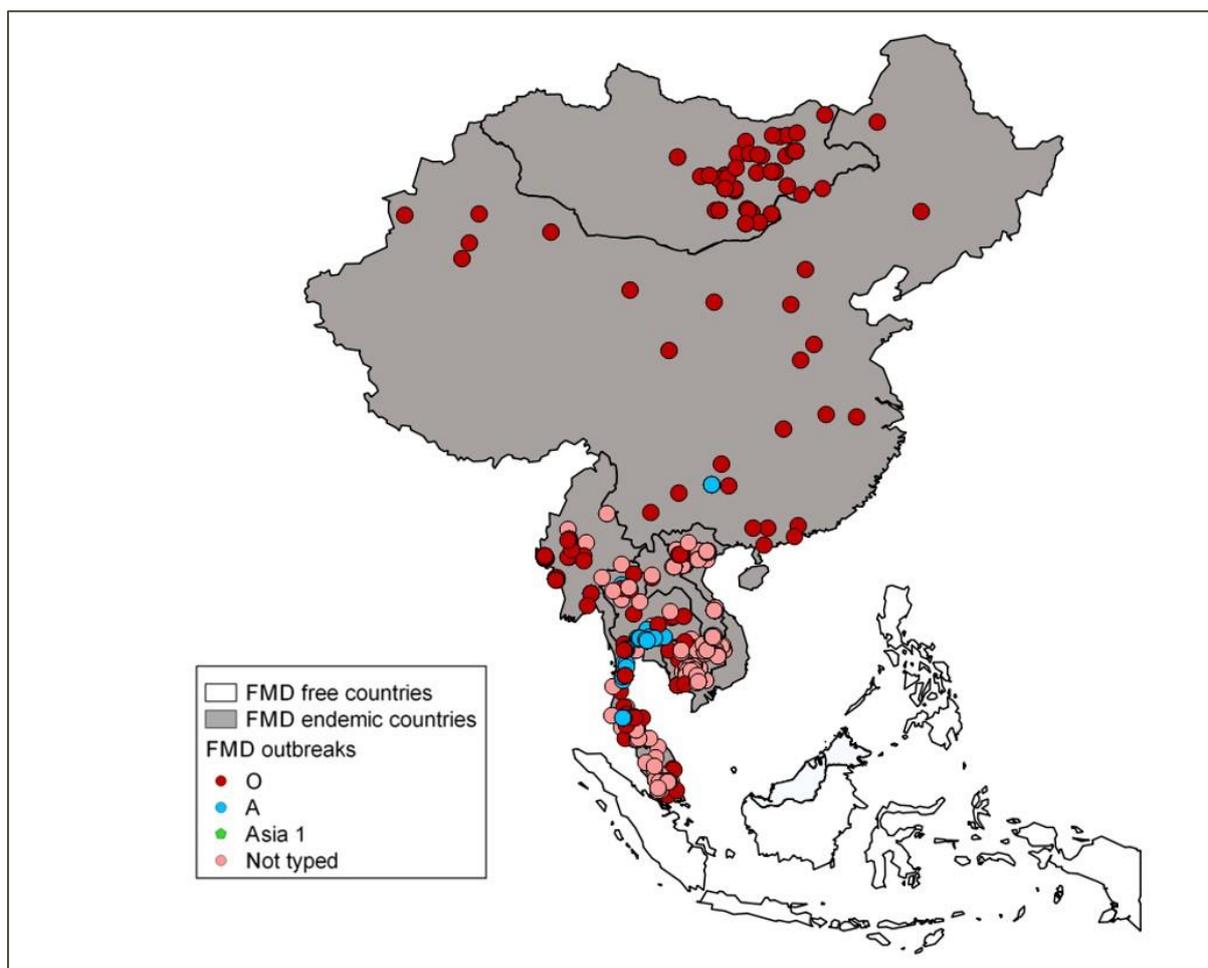


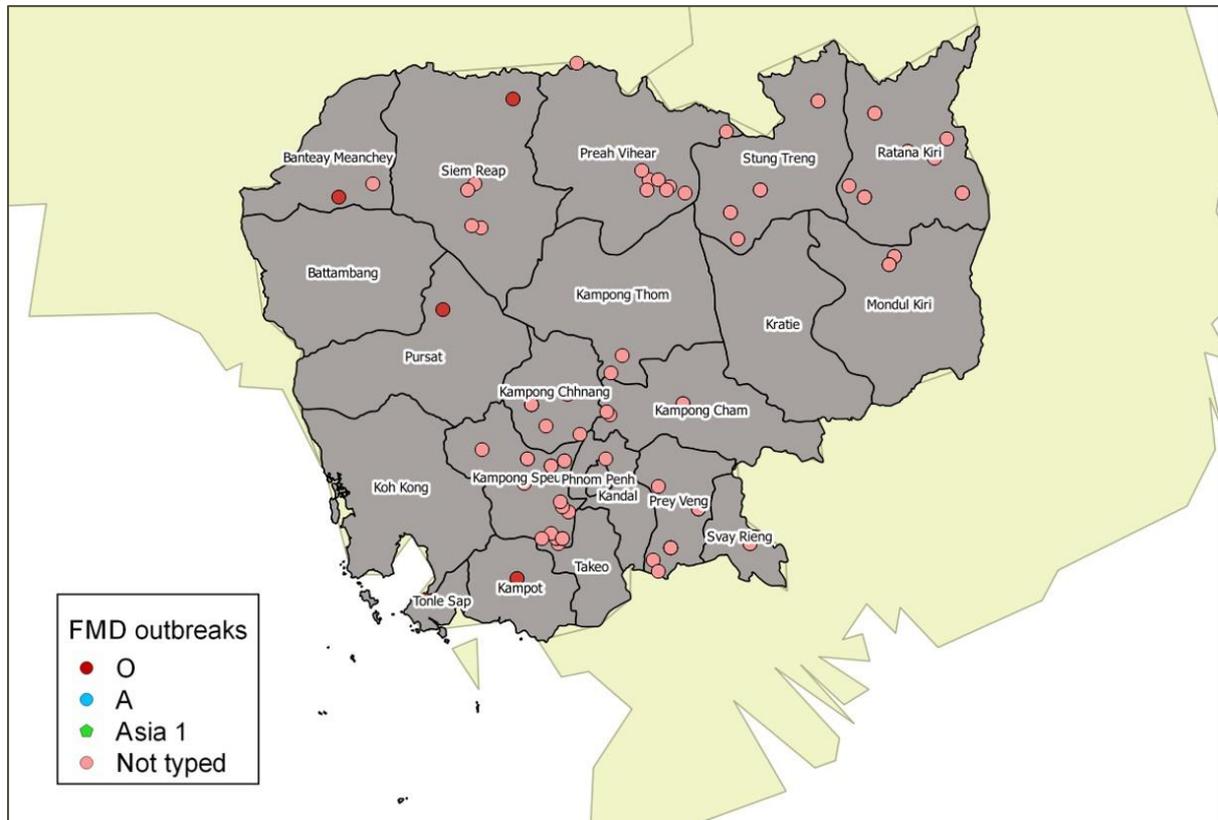
Figure 1. Distribution of FMD outbreaks in SEACFMD countries, 2018.

2. FMD situation in SEACFMD countries

The Brunei, Indonesia, Philippines, and Singapore did not report any FMD outbreaks in 2018 and maintained their official status of FMD free without vaccination.

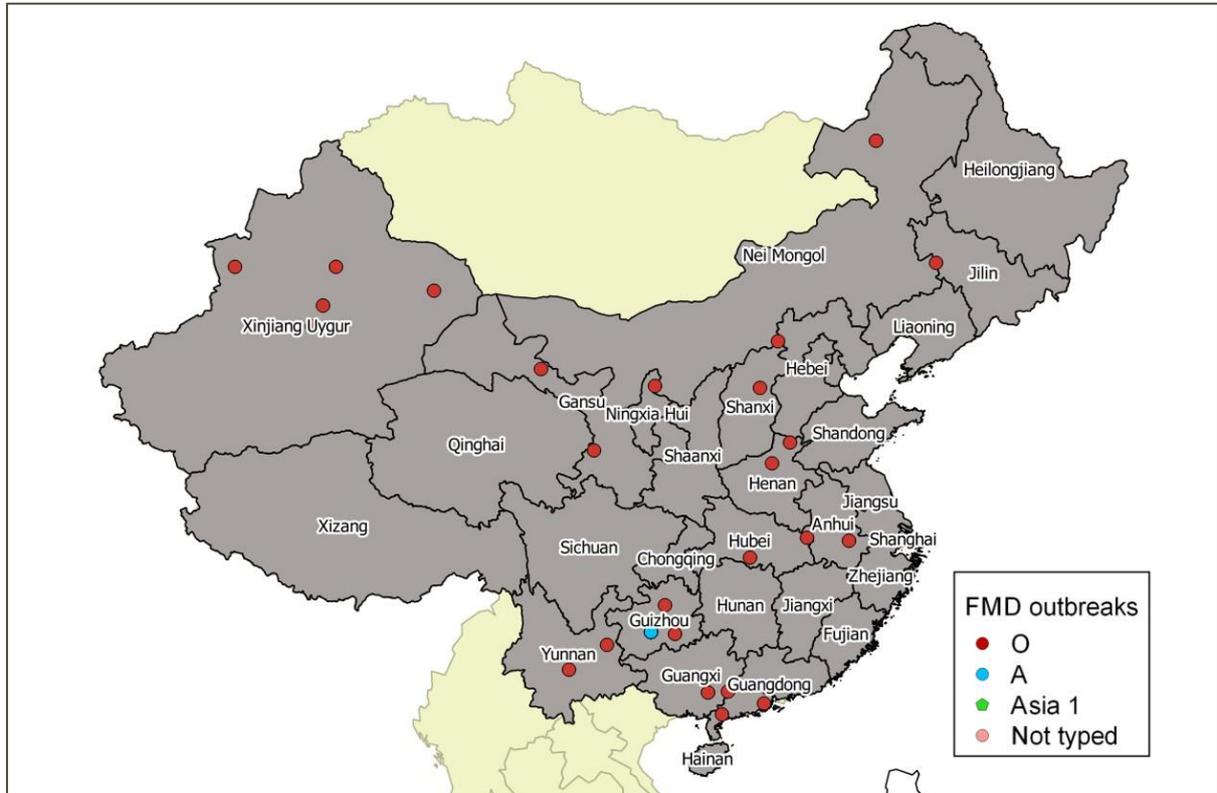
Cambodia

Cambodia reported 68 FMD outbreaks in 18 provinces. Affected animals include cattle, buffaloes and pigs. Five outbreaks were typed as due to serotype O virus, while the causative viruses of the majority outbreaks remained uncharacterised.



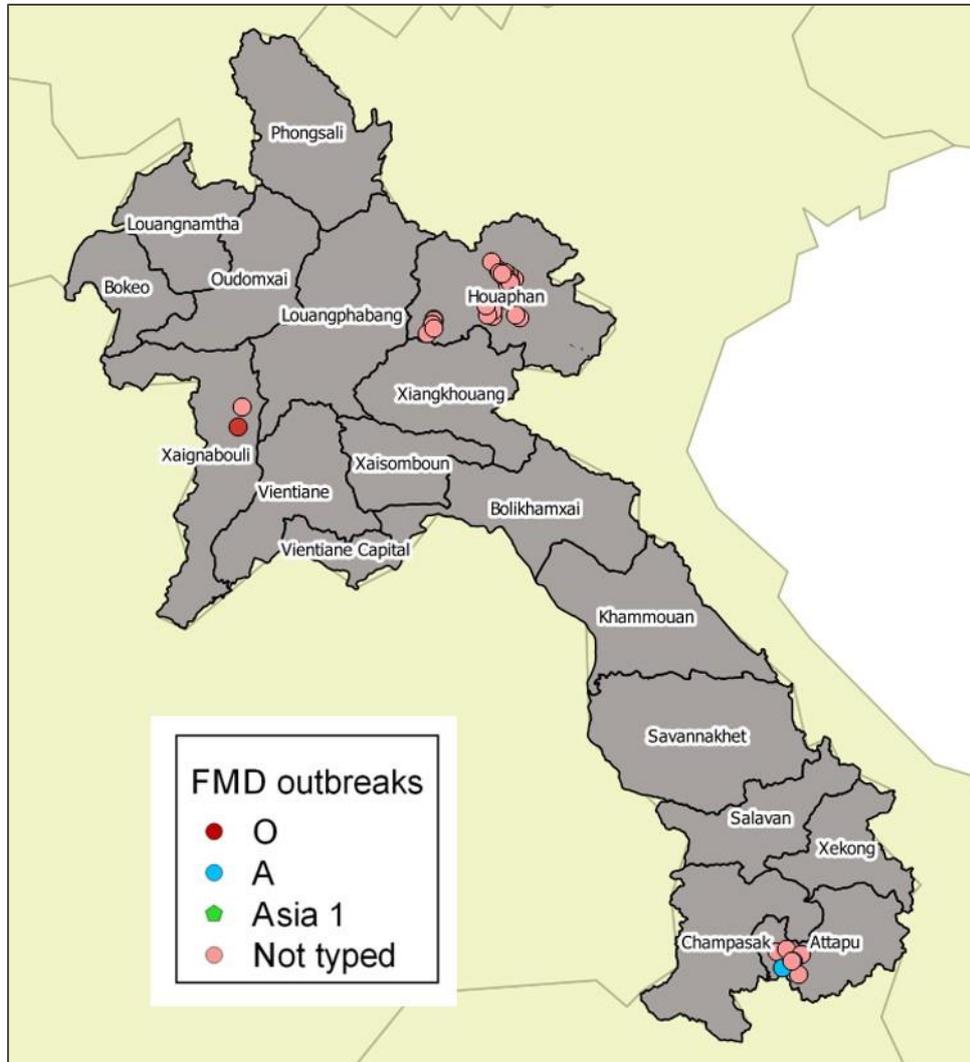
China

In 2018, China reported 27 FMD outbreaks in 12 provinces. All the outbreak viruses were characterised, amongst which only one was due to serotype A virus (in Guizhou Province) and all the remaining were caused by serotype O viruses. Cattle, sheep and pigs were affected.



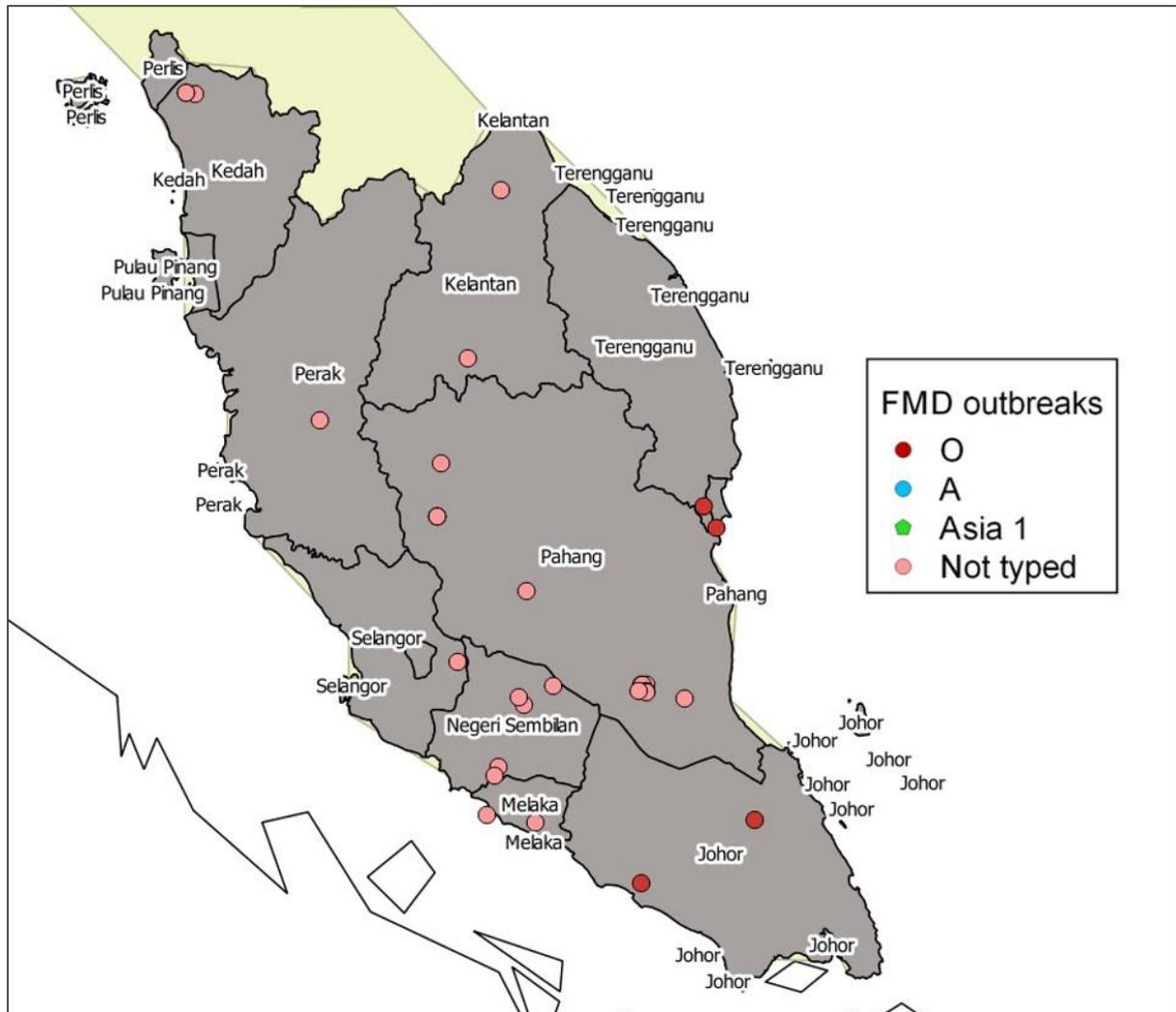
Lao PDR

Lao PDR reported 56 FMD outbreaks in 3 provinces in 2018, affecting cattle, buffaloes and pigs. Following the FMD outbreaks in 2017 as the 1st report in the recent 5 years, new FMD outbreaks were continuously reported in Houaphan and Xayabouli Provinces, from which the O/ME-SA/PanAsia strain was identified. In addition, outbreaks were reported in the Southern (Attapu province) in 2018, from which A/Asia/SEA-97 was identified. Interestingly, genetic divergent A/Asia/SEA-97 variants were found co-circulating in the affected villages (WRLFMD 2018).



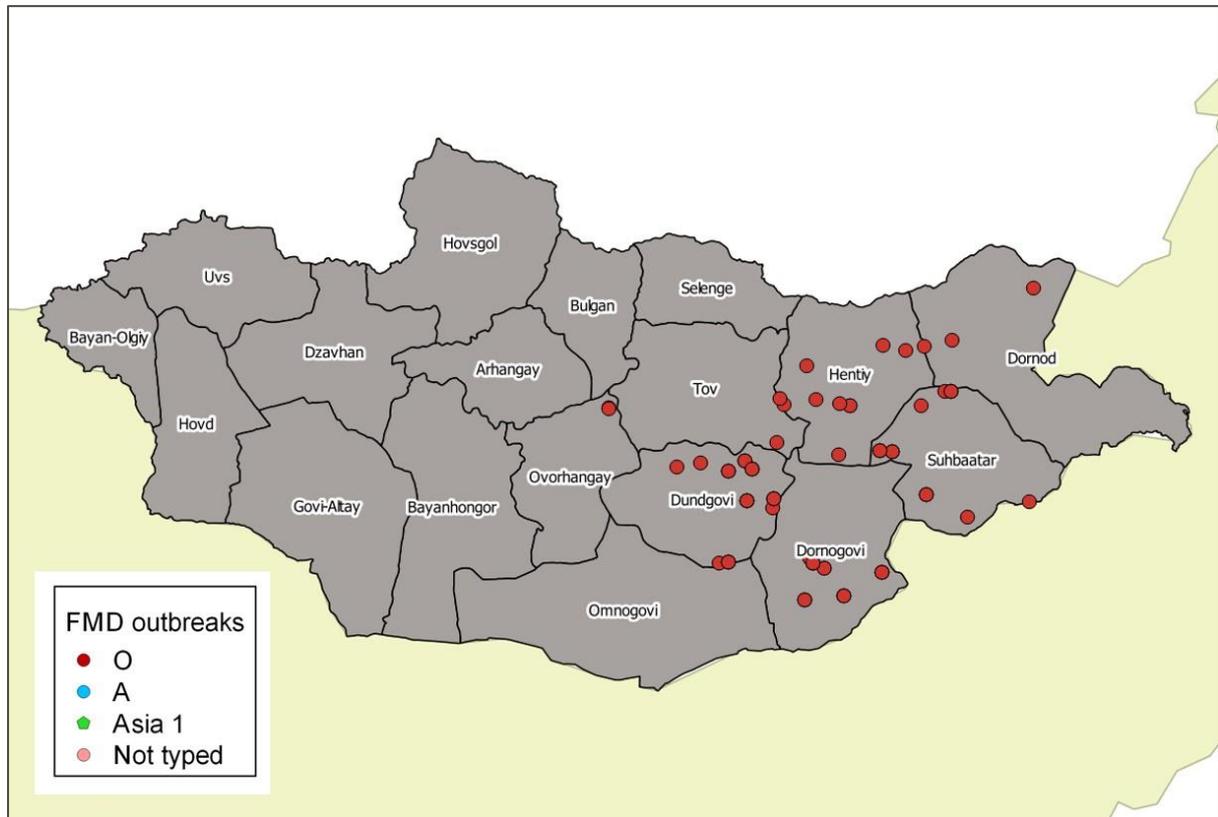
Malaysia

Malaysia reported 33 FMD outbreaks in 10 provinces in the peninsular region, affecting cattle, buffaloes and deer. Four outbreaks were typed as due to the O/ME-SA/Ind2001 strain and the remaining majority were not characterised.



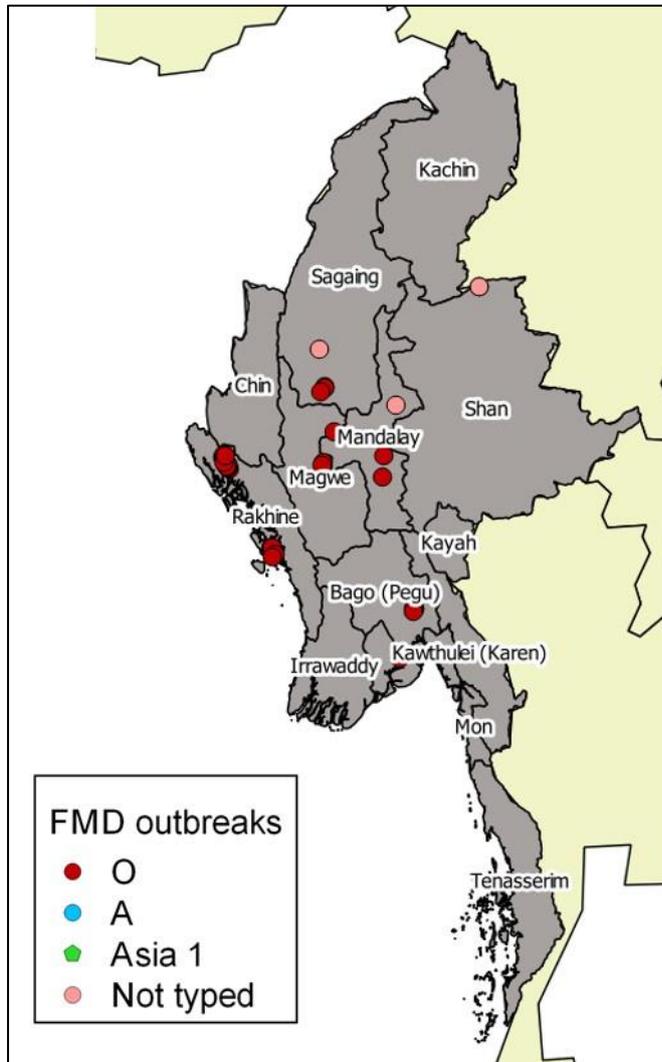
Mongolia

Mongolia reported 71 FMD outbreaks in 2018. All the outbreaks were due to serotype O viruses (O/ME-SA/PanAsia or O/ME-SA/Ind2001 strains), and the majority were concentrated in the Eastern Region of the country. Affected animals include cattle, goat, sheep and camel.



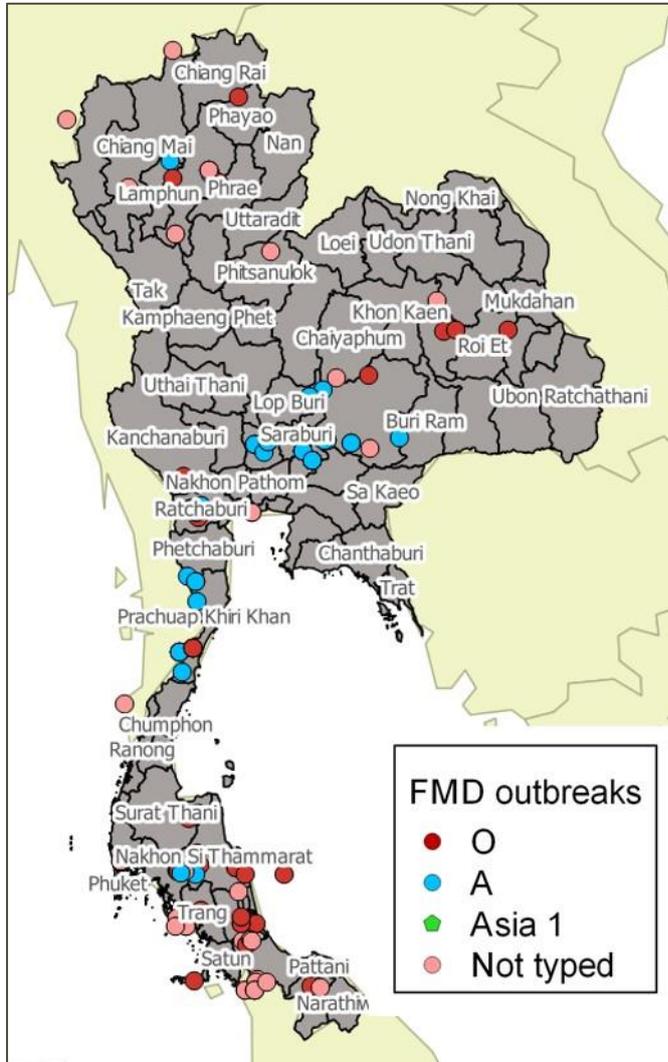
Myanmar

Myanmar reported 39 FMD outbreaks in 7 provinces, and only cattle were reported affected. Serotype O was reported as the cause of 35 outbreaks; the remaining 4 outbreaks were not characterised. Serotype Asia-1 was no longer detected in any clinical outbreaks following its detection in 2017.



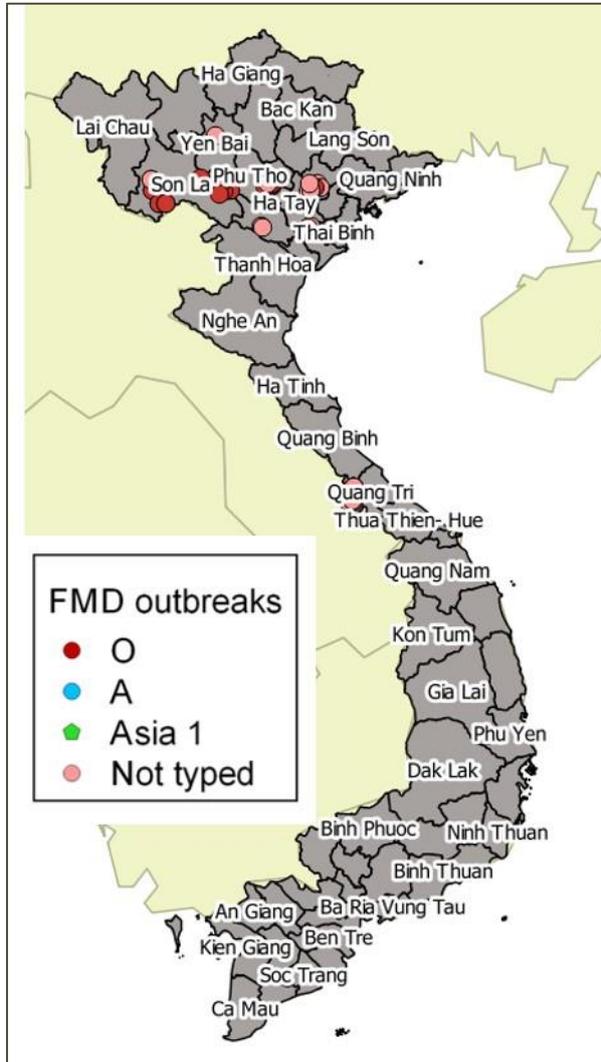
Thailand

Thailand reported 131 FMD outbreaks distributed throughout the country except for Region 2 in East Thailand. Affected animals include cattle, buffaloes and pigs. Of these outbreaks, 12 were caused by serotype O and 41 were caused by serotype A viruses. This flags that serotype A has become predominant in Thailand for the 1st time since 2015.



Viet Nam

Viet Nam reported 33 FMD outbreaks in 7 provinces, mainly concentrated in the North. Cattle, buffaloes, pigs and goats were reported affected. Causative viruses were characterized in 15 outbreaks, all due to serotype O viruses.



Characterisation of FMDVs in SEACFMD Countries in 2018

In 2018, some FMDVs were sequenced for the VP1 coding region for strain identification, by which the following strains were detected:

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

Table 1. FMDV strains detected in SEACFMD Member Countries in 2018, as characterised by the World and/or Regional Laboratory for FMD.

Country	Serotype O	Topotype...				Serotype A	Serotype Asia-1
		SEA/Mya-98	ME-SA/PanAsia	ME-SA/Ind-2001	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 World Reference Laboratory for FMD (WRL)

<http://www.wrlfmd.org/country-reports> and RRL-Pakchong, and country reports presented at the 24th OIE SEACFMD Subcommission Meeting on 28-30 November 2018, in Ho Chi Minh City, Vietnam, and 22nd OIE SEACFMD National Coordinators Meeting held on 25-27 June 2019, in Ulaanbaatar, Mongolia.

Serotype O continued to be the most prevailing serotype in 2018, with several lineages co-circulating. The Ind-2001 strain (e sublineage) was continuously reported in China, Malaysia, Mongolia, Myanmar and Thailand. As till the end of 2018, the Ind-2001 strain has been reported in all endemic SEACFMD countries except for Cambodia. Unfortunately, the traditional antigen ELISA typing technique used in Cambodia does not allow strain identification, and its inability to submit samples to the World/Regional Reference Laboratories in the past 2 years prevents in-depth viral characterisation.

Similar to previous years, all the detected serotype A viruses belong to the A/Asia/Sea-97 lineage. Importantly, a genetic drift Sea-97 was detected in the field outbreaks in Attapu province of Lao PDR. This variant shows <95% identity to any known Sea-97 viruses, however, the inability to isolate "live" FMDV for these cases excludes the possibility to characterise its antigenic property.

Following the single detection of serotype Asia-1 FMDV in Rakhine State of Myanmar in early 2017, this serotype was no longer detected in any clinical outbreaks in the SEACFMD region. The Myanmar virus was found to be genetically similar to those found from the Indian sub-continent but very different from the Asia-1 FMDVs previously detected in Myanmar and other parts of South-East Asia in 1990s and early 2000s. With support from the OIE SRR-SEA, cattle sera collected from Mandalay and Sagaing Regions during Dec 2016 – Jan 2017 were tested against the Asia-1/Shamir virus by virus-neutralisation test (VNT) at WRL. The results show that 6 out of the 51 sera samples tested positive, suggesting the possibility of silent circulation of serotype Asia-1 in at least in some parts of Myanmar. However, a prevailing question is raised why the South-East Asia lineage of Asia-1 FMDV couldn't be detected from FMD outbreaks in Myanmar or elsewhere in the SEACFMD endemic countries during the past 10 years; whereas in the 1990s and early 2000s, the South-East Asia lineage of Asia-1 FMDV was reported every year. Further epidemiological investigation is needed to verify and characterize the circulating Asia-1 FMDVs in this region.

Conclusions and discussions

In 2018, a total of 458 FMD outbreaks were reported in the SEACFMD countries, which was increased when compared to the 330 FMD outbreaks reported in 2017. Although the majority of characterised outbreaks in the whole region were due to serotype O, the predominance of serotype A was obviously noted in Thailand.

The Ind2001 strain of serotype O continued to spread in the region and laboratory evidence shows that it has been detected at endemic frequencies. Vaccine matching studies at the OIE reference laboratories in UK, Thailand and China show that the commonly used vaccine strains (i.e. O/3039, O/189/87 and O/MYA98/BY/2010) in the region can confer effective protection against this strain. However, the insufficient vaccination coverage resulted in the continued field Ind2001 outbreaks, as similar to other endemic FMDVs.

The upsurge of serotype A outbreaks in Thailand was noted in late 2017 and became more obvious in 2018. Vaccine matching studies in the OIE reference laboratory in Thailand show a good antigenic match between field isolates and the vaccine strain A/Lopburi/2012. A genetic variant Sea-97 virus was detected from field outbreaks in Southern Lao PDR but its antigenicity was not characterised due to failure in live virus isolation.

Serotype Asia-1 was no longer reported in any field outbreaks in the region since the single outbreaks in Myanmar in 2017. However, serological evidence indicates that the possibility of its silent circulation at low frequencies cannot be excluded. More vigilant virological surveillance, through clinical and probang sampling, is highly needed to help us better understand the virus and its risks. This is especially true in high-risk areas, including Western Myanmar where share borders with South Asia that is still endemic with serotype Asia-1.

References

WRLFMD (2018) *Genotyping report, serotype A, Lao PDR* [online], available: https://www.wrlfmd.org/sites/world/files/quick_media/WRLMEG-2019-00008-LAO-GTR-O-A_001.pdf [accessed July 1st].



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