



WORLD ORGANISATION FOR ANIMAL HEALTH
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SEACFMD Bulletin

Foot and Mouth Disease Situation
January to December 2017



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Summary

The present issue summarises the Foot-and-mouth disease (FMD) outbreaks in SEACFMD region in 2017 as well as the characterisation of detected FMD viruses (FMDVs). In total, 330 FMD outbreaks were reported in mainland South-East Asia countries, China, and Mongolia. Amongst the reported outbreaks, 169 were due to serotype O, 15 were due to serotype A, 2 were due to serotype Asia-1 and the remaining 144 were not typed. The prevalent lineages of FMDV include O/SEA/Mya-98, O/ME-SA/Ind-2001, O/ME-SA/PanAsia, O/Cathay, A/Asia/Sea-97 and Asia 1/Asia/G-VIII. Significant epidemiological changes in 2017 include: 1) the detection of serotype Asia-1 in Rakhine state of Myanmar, which represents the 1st detection of this serotype in the SEACFMD region since 2009; 2) the continuous geographic expansion of O/ME-SA/Ind2001 which has been reported from almost all the endemic SEACFMD countries; 3) the 1st reported FMD field outbreaks in Northern Lao PDR since May 2013.

Introduction

1. Aims

Following the previous issues of SEACFMD Bulletin presenting the regional FMD situation in the years of 2015 and 2016, the current issue was developed to summarise the FMD situation in the entire year of 2017 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, 2017

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 21st OIE SEACFMD National Coordinators Meeting held on 17-19 July 2018, in Penang, Malaysia.

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 2017

1. Overview of the regional situation in 2017

In 2017, FMD outbreaks have continued to affect traditionally endemic countries (China, Myanmar, Lao PDR, Vietnam, Thailand, Cambodia, and peninsular Malaysia) (Figure 1). Of the total 330 outbreaks reported, 169 were due to serotype O, 15 were due to serotype A, 2 were due to serotype Asia-1 and the remaining 144 were not typed due to absence of or insufficient samples collected. Cattle were reported affected from 311 outbreaks, buffaloes from 53, goat and sheep from 20, and pigs from 8 outbreaks. Infection involving more than one species was commonly noted.

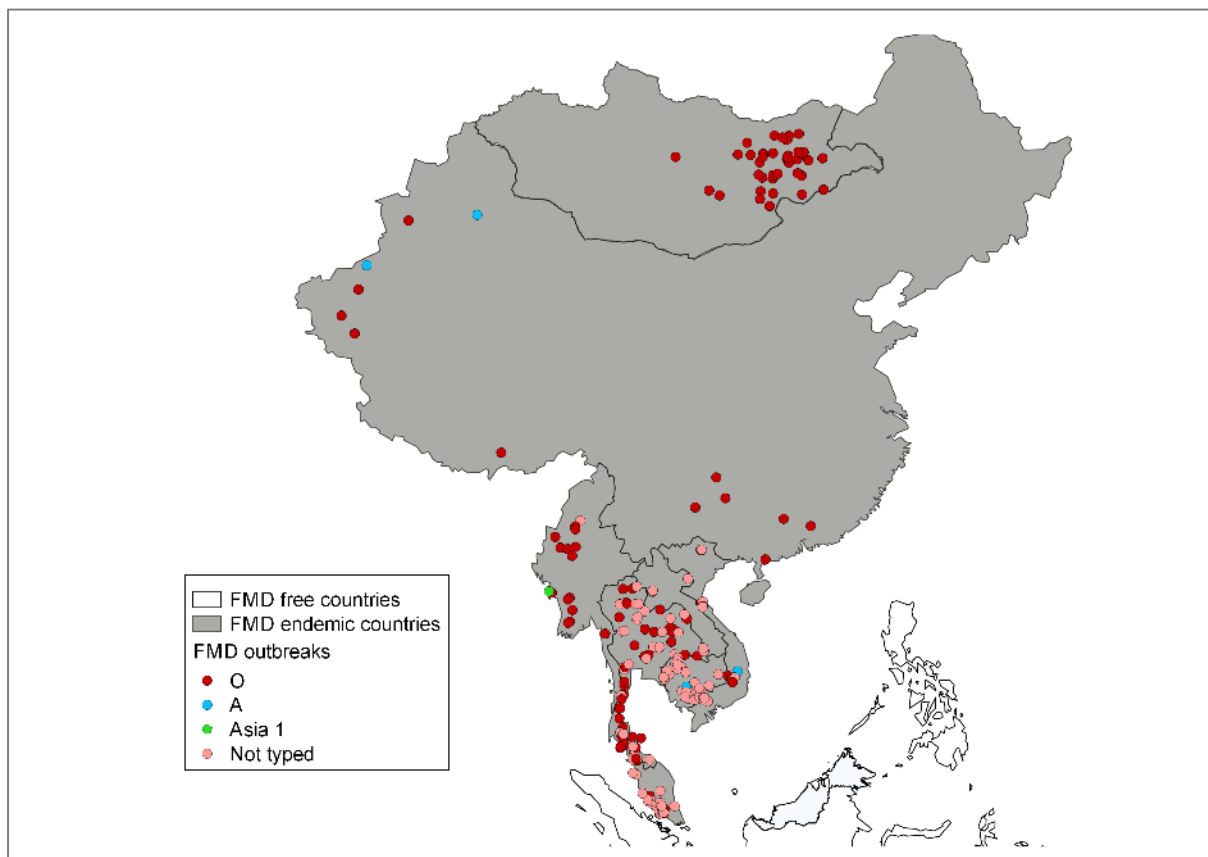


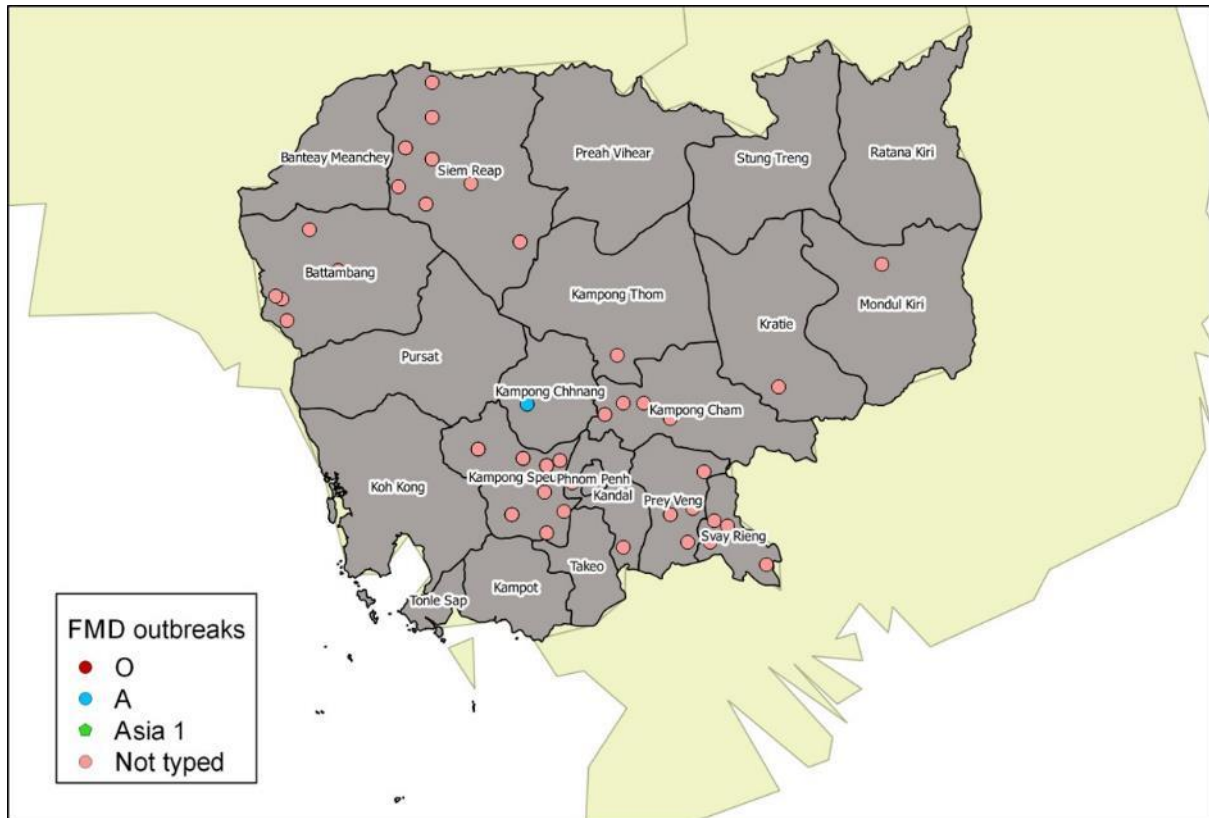
Figure 1. Distribution of FMD outbreaks in SEACFMD countries, 2017.

2. FMD situation in SEACFMD countries

The Brunei, Indonesia, Philippines, and Singapore did not report any FMD outbreaks in 2017 and maintained their official status of FMD free without vaccination.

Cambodia

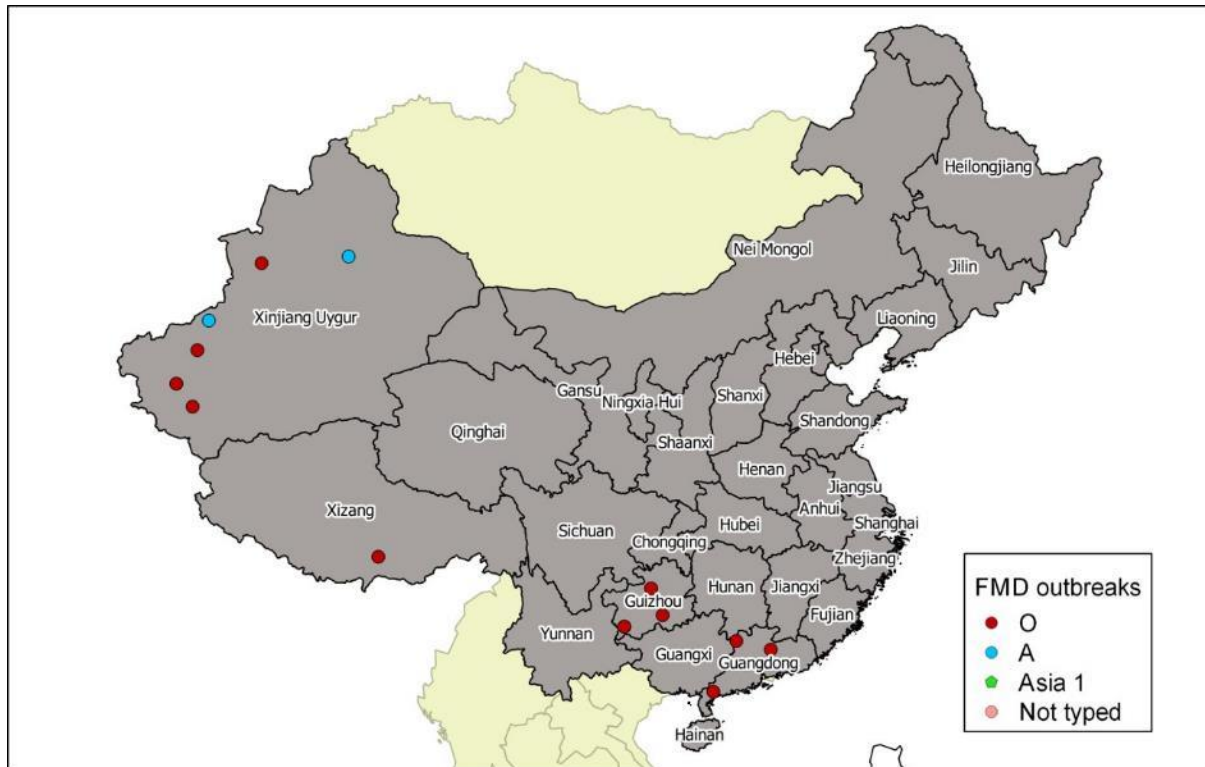
Cambodia reported 57 FMD outbreaks in 13 provinces. Affected animals include cattle and buffaloes. Only one outbreak was typed as due to serotype A virus, while the causative viruses of the majority of outbreaks remained uncharacterised.



China

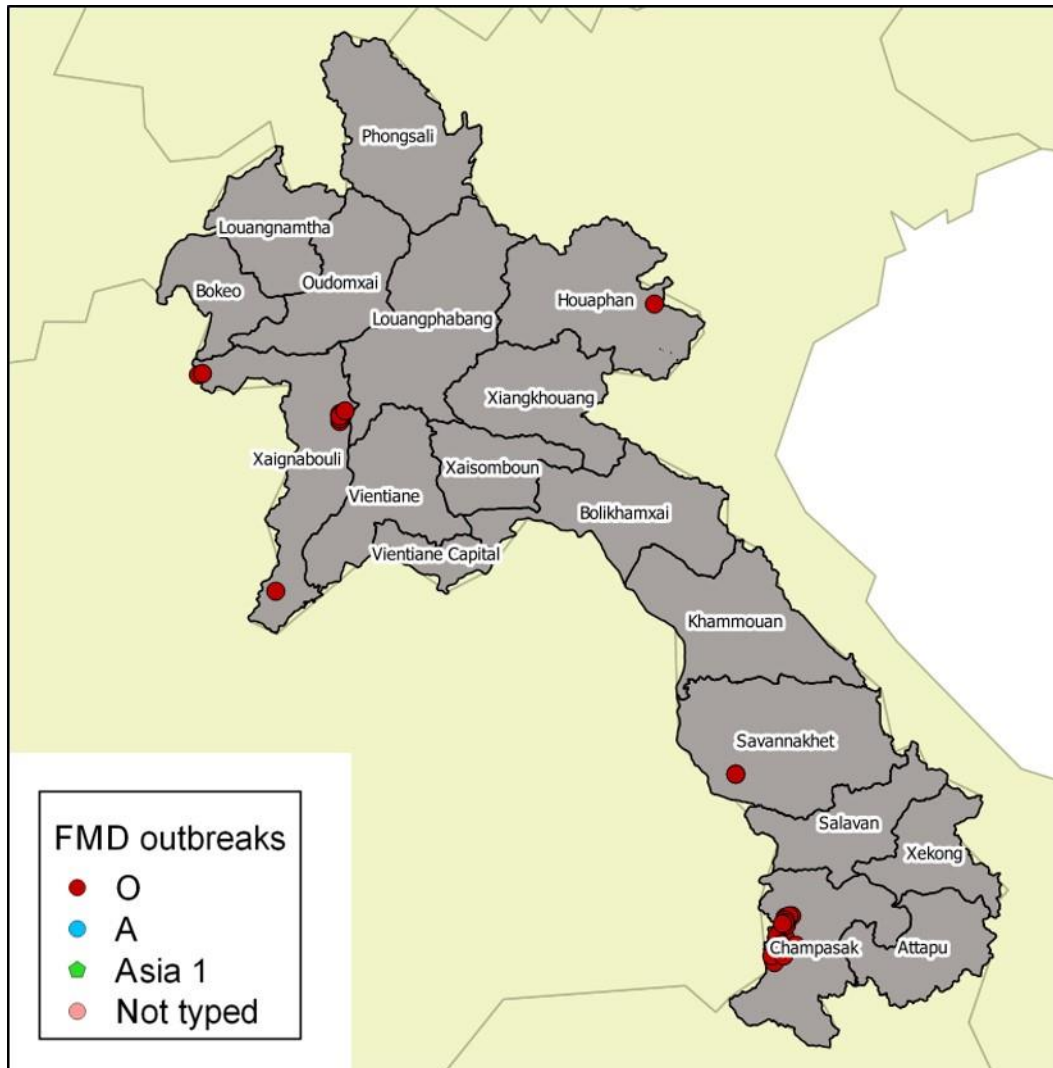
In 2017, China reported 14 FMD outbreaks in four provinces. All the outbreak viruses were characterised, amongst which 2 were due to serotype A viruses and all the remaining were caused by serotype O viruses. Cattle, buffaloes, goats and pigs were affected.

For the 1st time, China reported the O/ME-SA/Ind2001 strain as detected from field FMD outbreaks in Xinjiang Province during January- February 2017. Sequencing and phylogenetic analysis of VP1 sequences show that the virus is closely related to viruses detected from Nepal, Myanmar, Russia and South Korea (Zhu *et al.* 2018).



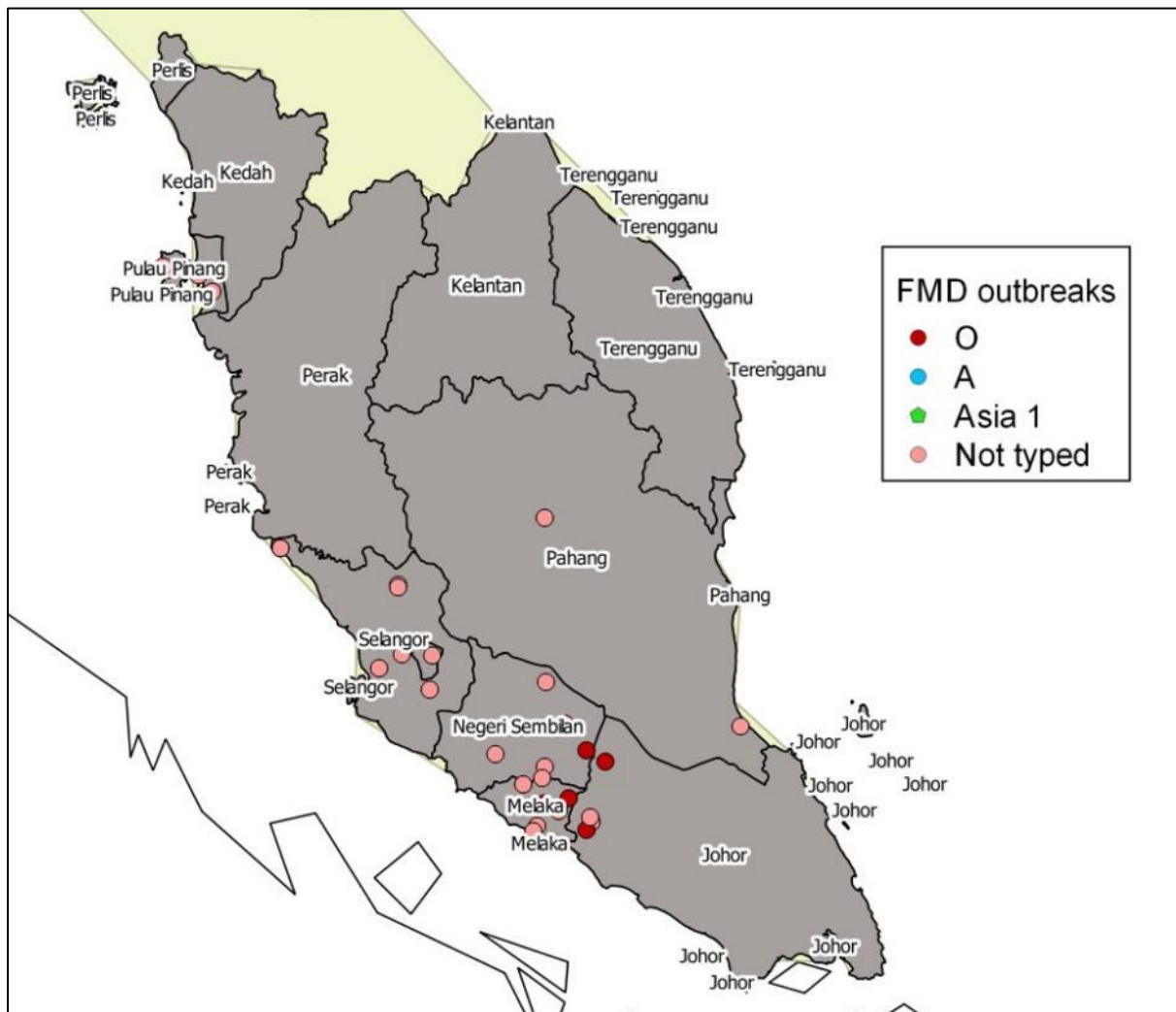
Lao PDR

Lao PDR reported 27 FMD outbreaks in 4 provinces, all due to serotype O viruses. Cattle, buffaloes and pigs were affected. Notably, the field outbreaks in Houaphan and Xayabouli Provinces represent the 1st FMD field outbreaks in Northern Lao PDR since May 2017. The causative viruses from both provinces were characterised as the O/ME-SA/PanAsia strain. It is expected that the population immunity in Northern Lao PDR has declined significantly since the cease of the OIE-supported mass FMD vaccination campaign in December 2016.



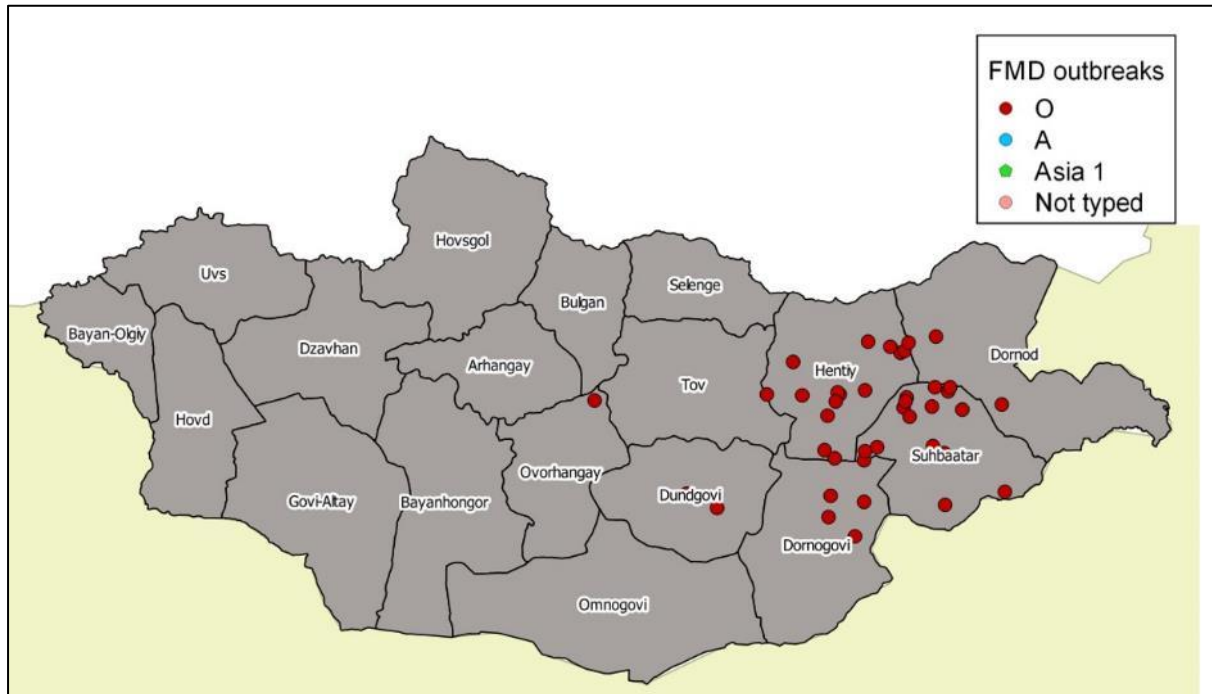
Malaysia

Malaysia reported 32 FMD outbreaks in 7 provinces in the peninsular region, affecting cattle, and buffaloes. Five outbreaks were typed as due to O viruses and the remaining majority were not characterised. For the first time the O/ME-SA/Ind2001 strain was detected from samples collected from gaur in Kuala Krau in November 2016, and it was further reported from field outbreaks in Negeri Sembilan and Melaka Provinces during June-July 2017. Genotyping report from WRLFMD shows these viruses are most closely related to Russia, Sri Lanka and China (WRLFMD 2017).



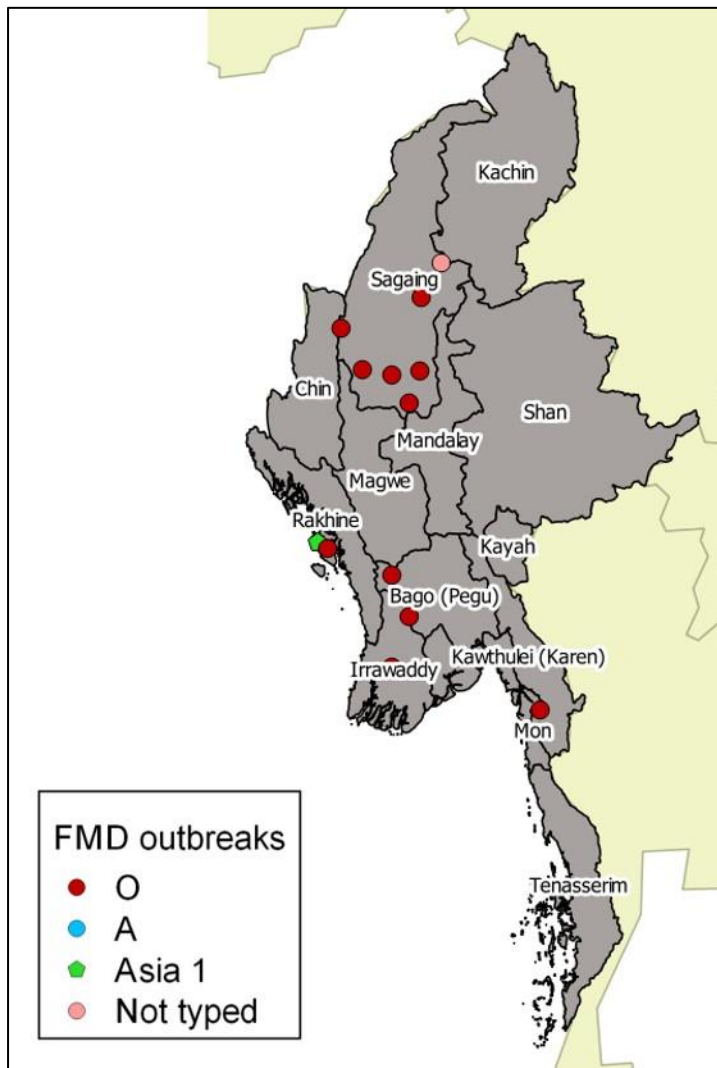
Mongolia

Mongolia reported 44 FMD outbreaks in 2017, significantly increased as compared to only 1 outbreak recorded in 2016. All the outbreaks were due to serotype O viruses, and the majority were concentrated in the Eastern Region of the country. Affected animals include cattle, goat and sheep.



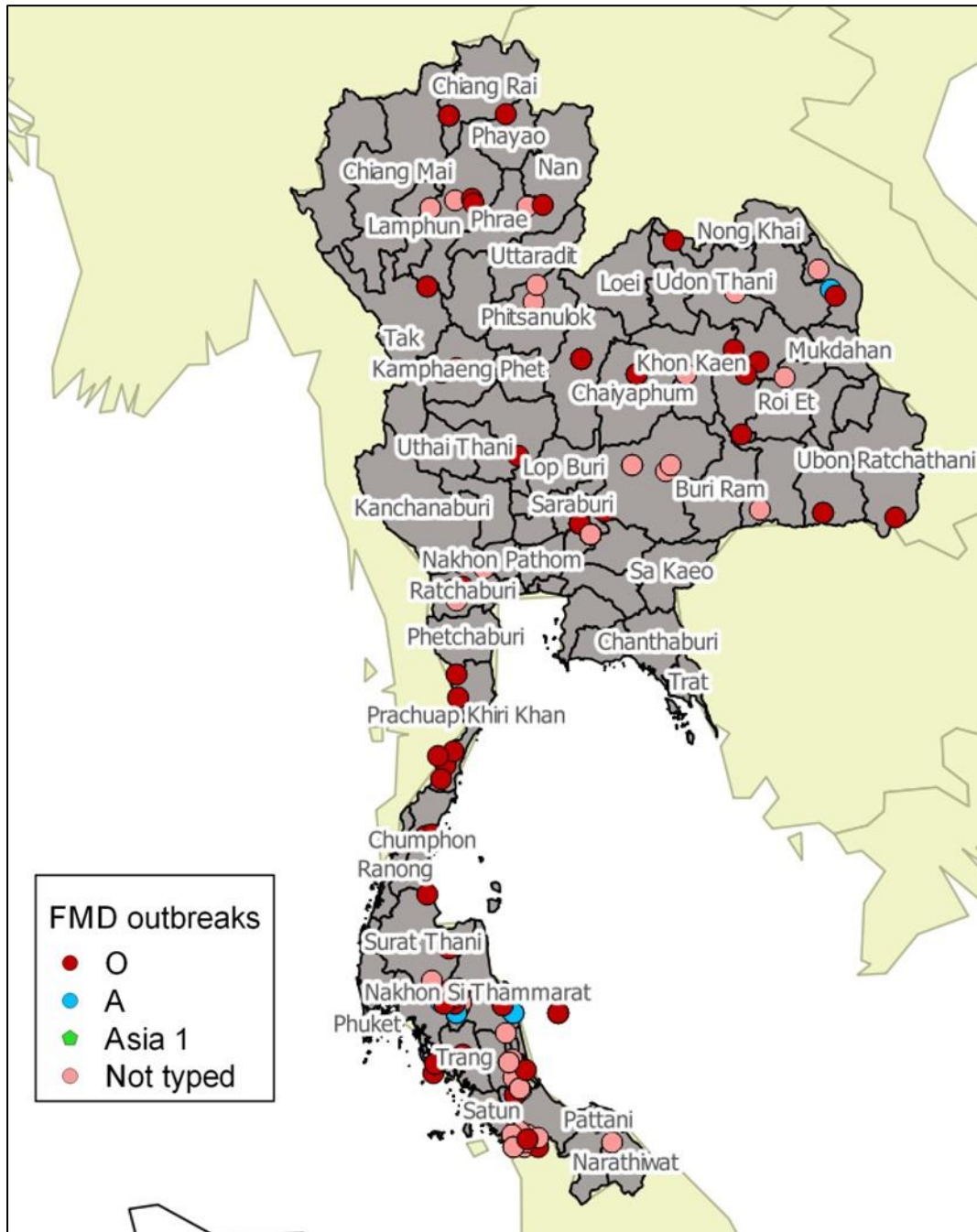
Myanmar

Myanmar reported 16 FMD outbreaks, affecting cattle and buffaloes. Serotype O continued to dominate as being the cause of 13 outbreaks; surprisingly, serotype Asia-1 was detected for the 1st time since the last detection in Myanmar in 2005, as the cause of two outbreaks in Rakhine State during January-February 2017. Viral genetic analysis revealed that the Myanmar Asia-1 virus is different from historical viruses from South-East Asia but very closely related to viruses circulating in Bangladesh and India during 2012–2013, indicating the occurrence of a novel viral introduction (Bo *et al.* 2019). The precise origin of the outbreaks was not clear, but frequent informal livestock trade with South Asia was reported at Rakhine state. No further clinical Asia-1 outbreaks were noted in Myanmar or any other SEACFMD countries.



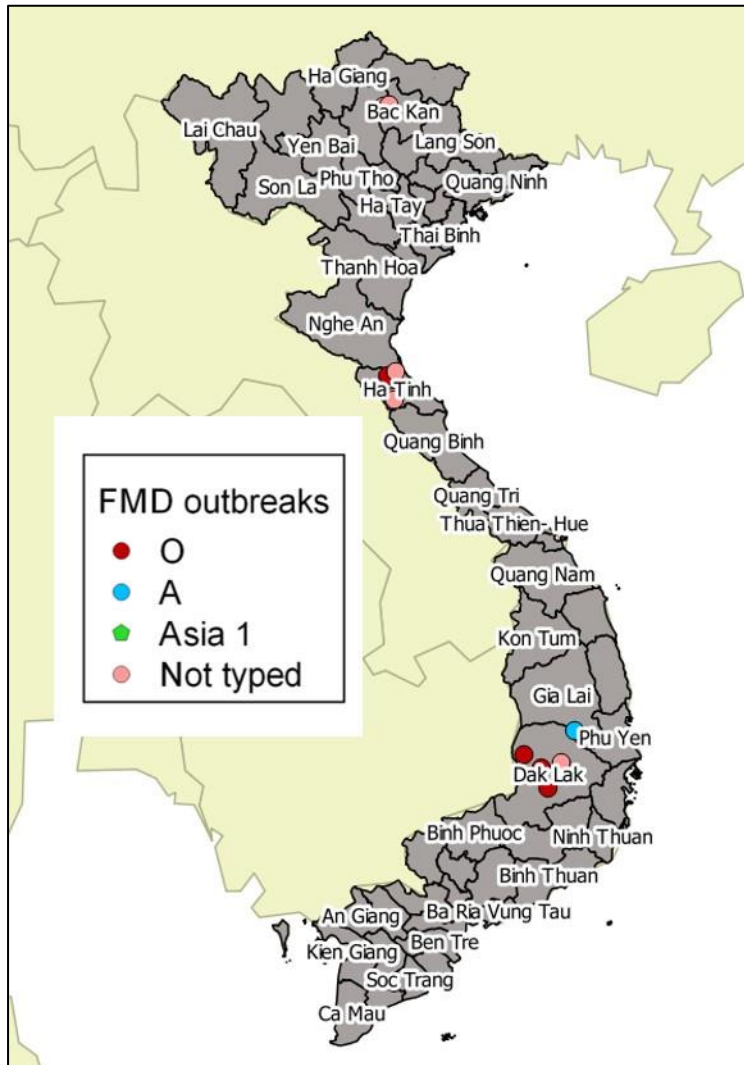
Thailand

Thailand reported 127 FMD outbreaks distributed throughout the country except for Region 2 in East Thailand. Affected animals include cattle, buffaloes and pigs. Of these outbreaks, 63 were caused by serotype O and 11 were caused by serotype A viruses.



Viet Nam

Viet Nam reported 13 FMD outbreaks in 2017, affecting cattle, buffaloes and pigs. Causative viruses were characterized in 6 outbreaks, belonging to serotype O (5 outbreaks) or serotype A (1 outbreak). Virological evidence shows that co-circulation of O/ME-SA/PanAsia and O/Cathay occurred in Ea Nuol village, Dak Lak Province in August 2017.



Characterisation of FMDVs in SEACFMD Countries in 2017

In 2017, 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
- Serotype Asia-1: Asia/G-VIII

Table 1. FMDV strains detected in SEACFMD Member Countries in 2017, as characterised by 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 21st OIE SEACFMD National Coordinators Meeting held on 17-19 July 2018, in Penang, Malaysia.

Serotype O continued to be the dominant serotype in 2017. Genetic analysis of viral VP1 shows the majority of serotype O viruses characterised in 2017 were the SEA indigenous Mya-98 strain, followed by the Ind-2001, PanAsia and Cathay strains. The Ind-2001 strain was continuously detected in Myanmar, Thailand and Vietnam, from field outbreaks or active surveillance. In addition, it has further spread to China and Malaysia. It was also found in Mongolia in clinical samples dated back to 2015 (Nishi *et al.* 2017) and from field outbreaks in 2017. The 'absence' of this strain in Lao PDR and Cambodia in 2017 may be a result of under-detection given the limited number of outbreaks reported (Lao PDR) or characterised (Cambodia).

Similar to previous years, all the detected serotype A viruses belong to the A/Asia/Sea-97 lineage. After almost 10 years absence, serotype Asia 1 FMDV was once again detected in the SEACFMD region, from field outbreaks in Rakhine State of Myanmar. The viral VP1 coding sequence was retrieved from only one clinical sample (GenBank accession number MG603266), and was categorised as belonging to the G-VIII lineage of serotype Asia 1.

Genetic analysis of the VP1 coding sequence showed that this virus shared the closest sequence identity (97.1%-97.6%) to viruses present in India and Bangladesh during 2012-2013, and only 82.9-83.7% identity with historical viruses of this serotype detected in Myanmar in 2005. These results indicate that the recent Myanmar outbreaks are due to a novel introduction of Asia 1 virus that likely originated from a South Asian country, rather than a continual viral circulation within Myanmar. Unfortunately, the inability to isolate "live" FMDV for these cases from Myanmar excludes the possibility for vaccine matching tests.

Conclusions and discussions

In 2017, a total of 330 FMD outbreaks were reported in the SEACFMD countries, which was decreased when compared to the 518 FMD outbreaks reported in 2016. Similar to the previous two years, serotype O remained to be the dominant serotype, but it was different from the situation in 2013 and 2014 when serotype O and A were detected at similar frequencies.

Within serotype O, Mya-98 continued to be predominant strain in 2017 but an upsurge in outbreaks due to Ind-2001 has been noted. The Ind-2001 strain was initially classified by WRL into four sub-lineages named a, b, c and d. By 2009, the 'd' sublineage of the O/ME-SA/Ind-2001 lineage (Ind-2001d) has outcompeted the long-established O/ME-SA/PanAsia strain and became the predominant serotype O virus in South Asia (Bachanek-Bankowska *et al.* 2018), and later on it has evolved to acquire sequence heterogeneity within the sub-lineage. The Ind-2001d sub-lineage has become widely known due to its ability to cause extensive epidemics in North Africa and the Middle East during 2013-2014 (Valdazo-Gonzalez *et al.* 2014) and in South-East Asia and East Asia since 2015. The Ind-2001d sub-lineage was first reported from field outbreaks in Lao PDR and Vietnam in 2015 (Qiu *et al.* 2018); its genetic variant was detected in Myanmar in the same year and several months later re-named by WRL as O/ME-SA/Ind-2001 sub-lineage e (Ind-2001e). The later was subsequently detected in Thailand, Vietnam and Malaysia in 2016 and in China in 2017.

The detection of the serotype Asia-1 virus in Myanmar in 2017 once again highlights the vulnerability of the region to the incursions of exotic viruses. Indeed, a regional qualitative risk assessment study organised by the OIE concludes a high likelihood of future incursions of exotic strains of FMDV into South-East Asia. Such incursions may result from a number of risk pathways including imports of live animals and animal products, movements of humans and vehicles, etc, all which are associated with significant consequences in terms of production losses, costs of control and trade implications (Bartels *et al.* 2017).

To better support countries to prevent and better manage incursion of an exotic FMDV, the OIE organised a regional workshop on 15 August 2017, facilitated by Dr Chris Bartels, the OIE consultant for the risk assessment study. The workshop discussed and identified a selection of key recommendations on risk-mitigation measures, such as facilitating legal animal transport and trading across SEA and into China. It is expected that when such transport becomes more transparent, it will be easier to monitor cross-border movements and even to minimise contacts between traded and local livestock. In addition, strengthening passive surveillance, including farmers' and community animal health workers' willingness to report, in-depth outbreak investigation, proper sampling, and swift and complete diagnostics were stressed as critical for early detection and rapid responses of outbreaks due to either an exotic or endemic strain.

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