Assessment of FMD virus serotype Asia 1 status in SEACFMD countries

Final Report

October 2024

Masako Wada, Jun Hee Han, Art Subharat

EpiCentre, School of Veterinary Science, Massey University

Contents

Abbreviations

FAO	Food and Agriculture Organisation of the United Nations
FMD	Foot-and-Mouth Disease
FMDV	Foot-and-Mouth Disease Virus
LHS	Latin Hypercube Sampling
PRCC	Partial Rank Correlation Coefficient
SEA	Southeast Asia
SEACFMD	Southeast Asia, China and Mongolia Foot and Mouth Disease program
WOAH	World Organisation for Animal Health
WRLFMD	World Reference Laboratory for Foot and Mouth Disease

Executive summary

Initiated in 2023 at the request of the World Organisation for Animal Health (WOAH), this project aimed to assess whether the absence of foot-and-mouth disease virus (FMDV) serotype Asia 1 reports within the Southeast Asia (SEA) region since 2017 indicates regional freedom from Asia 1 or reflects gaps in the existing surveillance systems. Given the reliance on passive surveillance in the region, a key question was identified regarding the sensitivity of passive surveillance in detecting FMDV in the population. To address this, scenario tree models were developed to estimate the probability of detecting FMDV or serotype Asia 1 specifically, based on the data from the World Reference Laboratory for FMD (WRLFMD) and country expert opinions, under an assumed design incidence rate.

The findings indicated notable variations in surveillance sensitivity across countries. Under a design annual incidence of 10% at the village level and 20% at the animal level, Mongolia and China demonstrated nearly 100% surveillance sensitivity for foot-and-mouth disease (FMD), due to extensive sampling and high probabilities of detection claimed by the country experts. Thailand showed moderately high detection sensitivity (71%), while Malaysia had a much lower detection probability (16%). In contrast, Cambodia, Lao PDR, Myanmar, and Vietnam exhibited extremely low sensitivities (below 4%), indicating that FMD in these countries is likely to go undetected at the assumed incidence rates.

When focusing specifically on FMDV serotype Asia 1, the detection probability was lower compared to all FMDV serotypes combined due to the near-zero incidence of this serotype in this region. Mongolia and China still showed higher detection probabilities for Asia 1 (12% and 7%, respectively), while other countries had near-zero detection probabilities. Combined surveillance efforts across all SEACFMD countries resulted in a 20% overall detection probability for Asia 1, suggesting that the likelihood of regional freedom from this serotype is around 56% in the absence of reports for a year. This confidence would increase with consecutive years of no reports, provided the risk of reintroduction remains below 10% each year. In other words, serotype Asia 1 has not been detected in the past 7 years, because of the combination of (1) low surveillance sensitivity, (2) less frequent introduction, and (3) the past strains or introduced strains of Asia 1 did not establish in the area at the detectable threshold like O or A. It is possible that reintroduction occurred and caused sporadic outbreaks, but it has not exceeded the threshold. In summary, Asia 1 is not circulating at the level that could be detected by the current passive surveillance system.

The study's limitations include a lack of empirical data on the risk of FMDV reintroduction from neighbouring regions, particularly Pool 2 (South Asia), where Asia 1 is endemic, and limited expert input. The low response rate, especially from China and Mongolia, may have influenced the accuracy of the model's estimates. Further refinement of input parameters and more comprehensive engagement with local experts could enhance the reliability of future assessments.

It is recommended to increase surveillance efforts and conduct additional sampling to better estimate the confidence level for freedom from Asia 1 in the Region. Recommended activities for the next phase include:

- Active surveillance for Asia 1, with a focus on key countries such as Myanmar, China or Cambodia

- Estimating the annual risk of virus introduction from Pool 2 to Pool 1 based on available data

- Refining passive surveillance parameters

- Identifying areas with low surveillance efficiency, and implementing awareness campaigns and training programmes for farmers, veterinarians and laboratory workers in targeted areas.

In conclusion, the results provide a preliminary understanding of passive surveillance sensitivity for FMDV in SEACFMD countries, including that of serotype Asia 1. Further data collection and model refinement are recommended to improve confidence in regional disease freedom and understand the risk of virus reintroduction from neighbouring regions.

Introduction

FMD is a highly contagious disease affecting many livestock species, including cattle, buffaloes, pigs, sheep and goats. FMD poses significant economic problems by reducing animal productivity, affecting the socioeconomic well-being of livestock owners, and restricting access to export markets. While FMD vaccines have historically played a key role in eradicating the disease in Europe, North and South America (Moura et al., 2024), FMD continues to circulate in the Southeast Asia for decades due to various challenges in control efforts. These include the dominance of smallholders with limited resources, low awareness and low biosecurity, short life of vaccine-induced immunity, growing demand for animal products, frequency of unofficial animal movements, inadequate border control, shortages in veterinary professionals, insufficient diagnostic laboratory capacity, constrained government budgets and the presence of other priority livestock diseases (Blacksell et al., 2019).

FMD endemic areas are grouped into seven geographical FMDV pools that share similar viruses. Southeast Asia (SEA), China and Mongolia are part of Pool 1 (Brito et al., 2017). Of the seven FMD virus serotypes, O and A have consistently been reported in this region, whereas Asia 1 has been only sporadically reported, particularly after the outbreaks of FMDV serotype Asia 1 across Asia in 2003 – 2007 (Brito et al., 2017; Tum et al., 2015; Valarcher et al., 2009). Based on the samples submitted to WRLFMD, there have been only two reports of Asia 1 in the region since 2010: one in Cambodia (2015) and another in Myanmar (2017). The Myanmar outbreak in 2017 marked the first detection of Asia 1 in the country in 12 years since 2005, with molecular analysis suggesting an imported strain (Bo et al., 2019). From the WRLFMD records, two samples from Cambodia were serologically positive to Asia 1 in 2015. However, these results were not confirmed by sequencing, and the possibility of cross-reaction in the ELISA test due to the high homogeneity between FMDV serotypes O and Asia 1 cannot be ruled out.

The FMD virus serotype C has not been reported globally since 2004, despite many countries discontinuing the use of vaccines against serotype C, and its potential extinction is currently under assessment (Paton et al., 2021). On the other hand, the absence of reports of serotype Asia 1 in Pool 1 raises questions whether this serotype has been eliminated from the region or it is due to surveillance gaps. Understanding the status of Asia 1 and the risk of its reintroduction is important for informing surveillance strategies, selecting appropriate FMD vaccines and efficiently allocating resources for FMD control in this area. However, assessing the FMDV Asia 1 status requires knowledge on the effectiveness of existing

surveillance systems, the potential for subclinical infections due to vaccine-induced immunity, and routine vaccination practices – all of which are currently limited.

To address this knowledge gap, the aim of this study was to identify, collect and collate available data, and evaluate the current status of FMDV serotype Asia 1 in SEA countries by developing a stochastic scenario tree model.

Materials and methods

Target countries

This study targeted eight member countries of the Southeast Asia, China and Mongolia Foot and Mouth Disease program (SEACFMD), where FMD was known to be endemic during 2010 – 2022: Cambodia, China, Lao People's Democratic Republic (PDR), Malaysia, Mongolia, Myanmar, Thailand, and Vietnam. Indonesia was included in the questionnaire survey, but excluded from the further analysis because it was FMD free until 2022. We specifically targeted cattle populations in these countries, because cattle were the most common livestock species susceptible to FMD based on the questionnaire survey.

WRLFMD data

We obtained the WOAH/FAO FMD Reference Laboratories Network Annual Reports between 2010 and 2022 from their website (King et al., 2010-2022). The number of clinical samples submitted to WRLFMD for FMD diagnosis, vaccine matching and sequencing for each year, along with the number of samples positive for FMD virus serotype Asia 1 were manually extracted from the annual reports by the authors. The study period was restricted to 2010 onwards due to the minimal relevance of earlier data to the current analysis and insufficient information on sample submissions from most target countries before 2010.

Questionnaire survey

A questionnaire was developed by the EpiCentre to gather information on FMD surveillance systems, sampling protocols, diagnostic capacities and vaccination practices in the country, with a focus on the robustness of passive surveillance (see Appendix 1). As exact information or data were likely absent, the questionnaire employed Likert methods, asking participants to indicate possible ranges (e.g., <10%, 10-40%, 40-60%, 60-90%, >90%) based on their knowledge instead of requesting specific estimates.

The survey was delivered to the targeted participants in June 2024 via Qualtrics, a cloud-based platform for administering online surveys. The targeted participants were identified by the coordinators from WOAH Sub-Regional Representation for Southeast Asia, including National Coordinators, EpiNet focal points, LabNetwork focal points, and Upper Mekong Working Group Member by WOAH.

For the scenario tree models, responses to the relevant questions were summarised at the country level by averaging the likely, minimum, and maximum values.

Asia 1 positivity

The proportion of FMD clinical samples positive for serotype Asia 1 was estimated using a Bayesian approach. The number of samples positive for Asia 1 from country i in year t ($k_{i,t}$) was assumed to follow a binomial distribution that:

$$k_{i,t} \sim Binomial(n_{i,t}, \rho_{i,t})$$
<div align="right">Eq. 1</div>

where $n_{i,t}$ is the number of clinical samples submitted from country i in year t, and $\rho_{i,t}$ is the proportion of clinical samples positive to FMD Asia 1 in country i in year t. We assumed that the prior distribution of $\rho_{i,t}$ ($\pi(\rho_{i,t})$) was a beta distribution that:

$$\pi(\rho_{i,t}) \sim Beta(1 + A, 1 + B)$$
<div align="right">Eq. 2</div>

$$A = \sum_{j=1}^{J} k_{t-j} e^{-j}$$

$$B = \sum_{j=1}^{J} (n_{t-j} - k_{t-j}) e^{-j}$$

Equation 2 indicates that the prior information of $\rho_{i,t}$ was based on the total number of clinical samples submitted (n_{t-j}) and the total number of FMD Asia 1-positive samples (k_{t-j}) from all the target countries in J previous years, with the effect of previous data on the prior distribution being exponentially reduced over the years. The mathematical structure of the prior distribution implies that all the target countries were exposed to the equivalent level of FMD Asia 1 virus introduction given the geographical proximity and animal movements between the countries. In this study, we also assumed that $\pi(\rho_{i,t})$ was based on the previous data of up to five years (i.e. $J = 5$). A five-year period was considered sufficient to encompass the likely duration of virus circulation within the region. Inclusion of periods beyond five years would have minimal impact on the analysis, as the effects would be discounted to e^{-6} = 0.002, e^{-7} = 0.0009, etc. Because of the conjugacy between the beta

and binomial distributions, Equations 1 and 2 thus indicate that the posterior distribution of $\rho_{i,t}$ ($P(\rho_{i,t}|k_t n_t)$) is:

$$P\left(\rho_{i,t}\middle|k_t n_t\right) = Beta\left(1 + \sum_{j=0}^{5} k_{t-j}e^{-j}, 1 + \sum_{j=0}^{5}(n_{t-j} - k_{t-j})e^{-j}\right).$$

Scenario tree model

We applied the stochastic scenario tree approach described by Martin et al. (2007) to estimate the probability of freedom from serotype Asia 1 in the target population. This approach was chosen as it is the current reference method for proving freedom from disease, widely used for various diseases and countries (Meletis et al., 2024).

Two scenario tree models were developed: one for FMD in general (including all serotypes), and the other specifically for serotype Asia 1. These models incorporated passive surveillance components for each of the eight countries, accounting for differences in vaccination practice and surveillance intensity by country (Figure 1). While the two models followed the similar structure, the Asia 1 model incorporated two additional parameters to adjust the incidence and susceptibility (Table 1). Parameters were estimated for each country based on data gathered from WRLFMD and the questionnaire survey. Due to the lack of data, active surveillance components were not included in the models; however, passive surveillance remained the primary method for detecting FMD in the target populations.

For the demonstration of disease freedom, a design prevalence is required. This is a hypothetical prevalence typically set at a low value (e.g. 1%) to represent the level of undetected disease, if present, in the population (Cannon, 2002). Considering the high turnover rate of FMD, we used a design annual incidence rate[1] of 10% at the village level and 20% at the animal level to reflect the level of FMD circulation among the target populations. These incidence rates align with field observations in the region, while maintaining a conservative approach. For the Asia 1 model, the estimated posterior Asia 1

---

[1] For example, if there were 100 animals per village and a total of 1,000 villages in the region, each year 100 villages (1,000 villages x 10%) and 2,000 animals (100 animals/village x 20% x 100 villages) would be infected. Of these infected animals, *p.Asia1* (approximately 0.04), or 80 animals (2,000 animals x 0.04) would be specifically infected with serotype Asia 1. The estimated sensitivity is a probability that the current passive surveillance detects any of these animals assumed to be positive.

positivity was applied to these FMD design incidence rates to estimate the likely incidence of Asia 1 circulating in this region, if present.
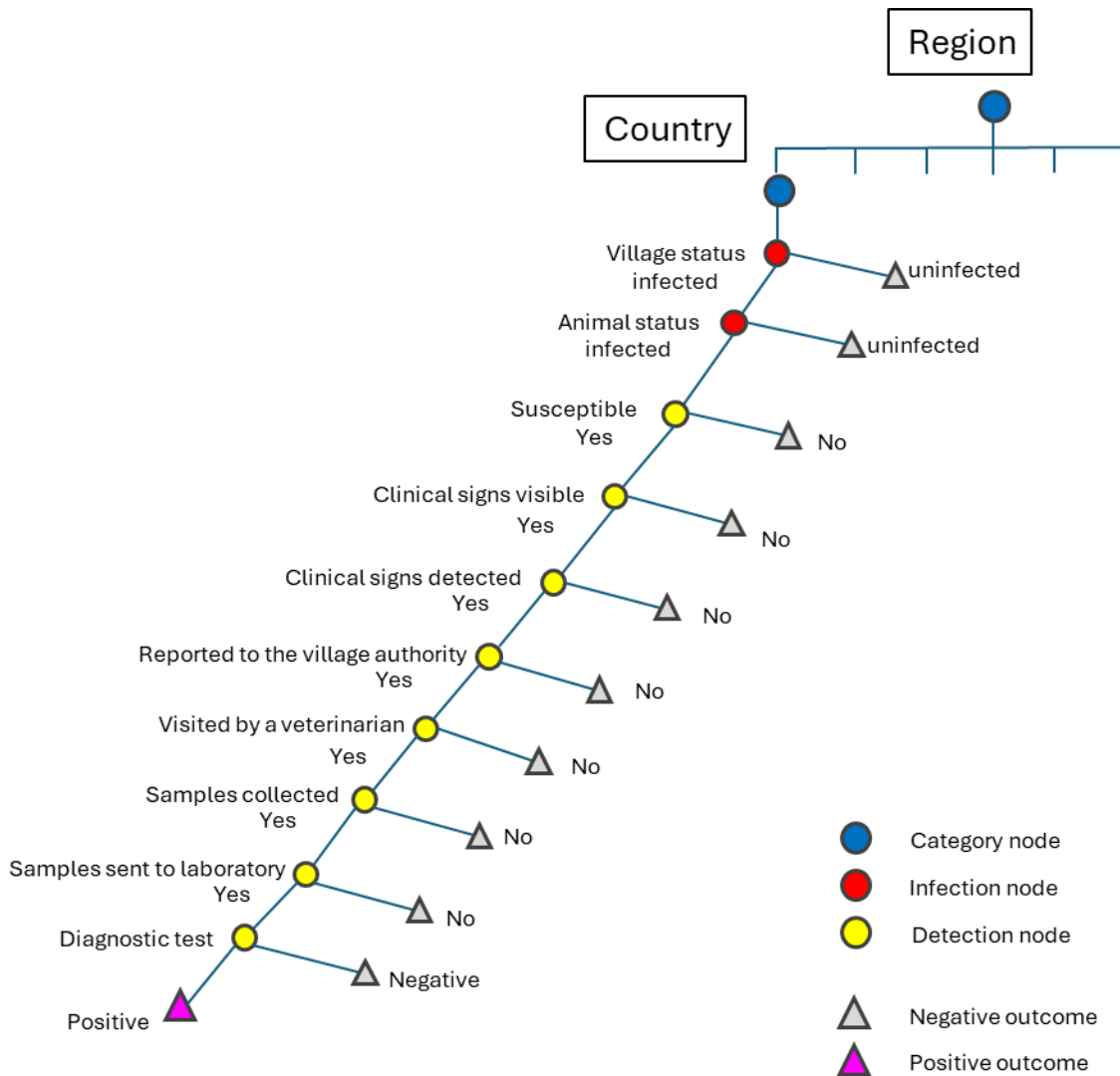

Figure 1. Scenario tree for detecting foot-and-mouth disease (FMD) by passive surveillance in the region encompassing Southeast Asia, China and Mongolia. Only one county's branch is shown, and all other country branches are identical.

Table 1. Parameters for scenario tree models for foot-and-mouth disease (FMD) and FMD virus serotype Asia 1 (indicated with *). Country-specific parameters are indicated as country _i_.

Parameter	Definition
_Ph_	Design incidence rate of FMD (any serotypes) at the village level (% village per year)
_Pu_	Design incidence rate of FMD (any serotypes) at the animal level within an infected village (% animal per year)
p.Asia1$_i$	*Serotype Asia 1 positivity (country _i_)
p.vac$_i$	Probability of animals vaccinated against FMD (country _i_)
p.triv$_i$	*Probability of using trivalent vaccines (vaccines against Asia 1) (country _i_)
p.clin	Probability of animals presenting clinical signs if animals were susceptible and infected
p.det$_i$	Probability of farmers detecting clinical signs if animals presented clinical signs (country _i_)
p.rep$_i$	Probability of farmers contacting the village authority if clinical signs were detected (country _i_)
p.vet$_i$	Probability of veterinarians visiting the village if the village was detected with FMD (country _i_)
p.smp$_i$	Probability of veterinarians collecting samples if the veterinarians visited the village (country _i_)
p.test$_i$	Probability of samples sent to FMD reference laboratories (country _i_)
SeT	Diagnostic test sensitivity
n.smp$_i$	Number of animals sampled per village in the village reported with clinical FMD (country _i_)
n.vil$_i$	Number of clinical villages tested in a year (country _i_)

Outcomes

The two stochastic scenario tree models (FMD model and Asia 1 model) were run for 100 iterations, each time randomly selecting parameter values from the assigned parameter distributions to generate the following outcome distributions.

FMD model

The population sensitivity of passive surveillance for FMD (the probability of detecting FMD, if circulating in the population at the designed incidence rate), for a village (SeP_{vi}), country _i_ (SeP_i) and the whole region (SeP_r) were estimated as follows:

$$SeP_{vi} = 1 - (1 - Pu \times (1 - p.vac_i) \times p.clin \times p.det_i \times p.rep_i \times p.vet_i \times p.smp_i \times p.test_i \times SeT)^{n.smp_i}$$

$$SeP_i = 1 - (1 - Ph \times SeP_{vi})^{n.vil_i}$$

$$SeP_r = 1 - \prod_{i=1}^{8} (1 - SeP_i)$$

Asia 1 model

The population sensitivity of passive surveillance for serotype Asia 1 (the probability of detecting Asia 1 by passive surveillance at the designed FMD incidence rate and Asia 1 positivity) for a village ($SeP_{vi}*$), country i (SeP_i*) and the whole region (SeP_r*) were estimated as:

$$SeP_{vi}* = 1 - (1 - Pu \times p.Asia1_i \times (1 - p.vac_i \times p.triv_i) \times p.clin \times p.det_i \times p.rep_i \times p.vet_i \times p.smp_i \times p.test_i \times SeT)^{n.smp_i}$$

$$SeP_i* = 1 - (1 - Ph \times SeP_{vi}*)^{n.vil_i}$$

$$SeP_r* = 1 - \prod_{i=1}^{8} (1 - SeP_i*)$$

The probability of Asia 1 freedom, given there was no detection for one year, for the region (PF_1) was then calculated as:

$$PF_1 = \frac{1 - prior_1}{1 - SeP_r* \times prior_1}$$

Where $prior_1$ is the pre-surveillance estimate of the probability that the region is infected with Asia 1. A neutral prior, 50%, was used.

To assess multiple years of absence of report of Asia 1 in the region, the accumulated probability of freedom after t years (PF_t) was estimated as:

$$PF_t = \frac{1 - prior_t}{1 - SeP_r* \times prior_t}$$

where $prior_t$ is the probability that the region is infected with Asia 1 after $t-1$ years, calculated as:

$$prior_t = (1 - PF_{t-1}) + p.intro - ((1 - PF_{t-1}) \times p.intro)$$

Where *p.intro* is the risk of disease introduction from other regions each year. There is no data to estimate this, hence 0%, 5% and 10% were applied.

Sensitivity analysis

To assess the robustness of the conclusions, given the uncertainty in input parameters, a sensitivity analysis was performed using Latin Hypercube Sampling and Partial Rank Correlation Coefficient (LHS/PRCC) methods (Blower & Dowlatabadi, 1994). In this analysis, parameter values were simultaneously varied within the assigned distributions, and PRCC values were estimated, for the surveillance sensitivity for Asia 1 (SeP_r*). The most influential parameters were identified based on their PRCC values.

Result

WRLFMD data

The number of samples submitted to WRLFMD between 2010 and 2022 by year and country is shown in Table 2. In total, 4,602 samples were submitted from the region during the past 13 years. The median number of samples annually submitted by a country was 20.5 (range: 0 – 474), with the highest median of 130 (range: 58 - 474) by Thailand and the lowest median of 0 by Malaysia (range: 0 – 51) and Myanmar (range: 0 – 36).

Out of the 4,602 samples, 4 tested positive for serotype Asia 1: 2 in Cambodia in 2015 and 2 in Myanmar in 2017.

Table 2. The number of samples submitted to the World Reference Laboratory for foot-and-mouth disease (WRLFMD) between 2010 and 2022 for endemic countries of the Southeast Asia, China and Mongolia FMD program (SEACFMD). Samples including those positive for serotype Asia 1 are indicated with *.

Countries	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Cambodia	28	32	5	15	20	22*	0	5	0	0	100	35	12
China	34	53	84	52	36	38	34	58	139	76	27	17	14
Lao PDR	2	22	0	17	11	20	50	7	25	0	14	20	0
Malaysia	32	20	18	0	51	0	26	0	12	0	0	0	0
Mongolia	21	0	0	13	12	12	5	35	38	7	0	16	20
Myanmar	8	0	0	0	0	26	26	36*	0	15	0	0	0
Thailand	58	91	68	121	376	474	312	104	130	138	274	75	329
Vietnam	77	38	31	73	32	24	35	0	40	55	39	24	11

Questionnaire survey

Responses were obtained from 20 individuals across nine countries. The median number of responses per country was 2 (range: 1 – 7), with Thailand having the highest number of respondents (7) and China, Mongolia and Myanmar the lowest (1 each). All respondents had veterinary backgrounds, with 12 (60%) affiliated with central governments, and 6 (30%) with diagnostic laboratories. Most respondents (n = 15; 75%) were over 40 years old, and 12 (60%) were female.

Figure 2 shows the summary results of the questionnaire survey. The detailed results of the questionnaire survey are provided in Appendix 2.
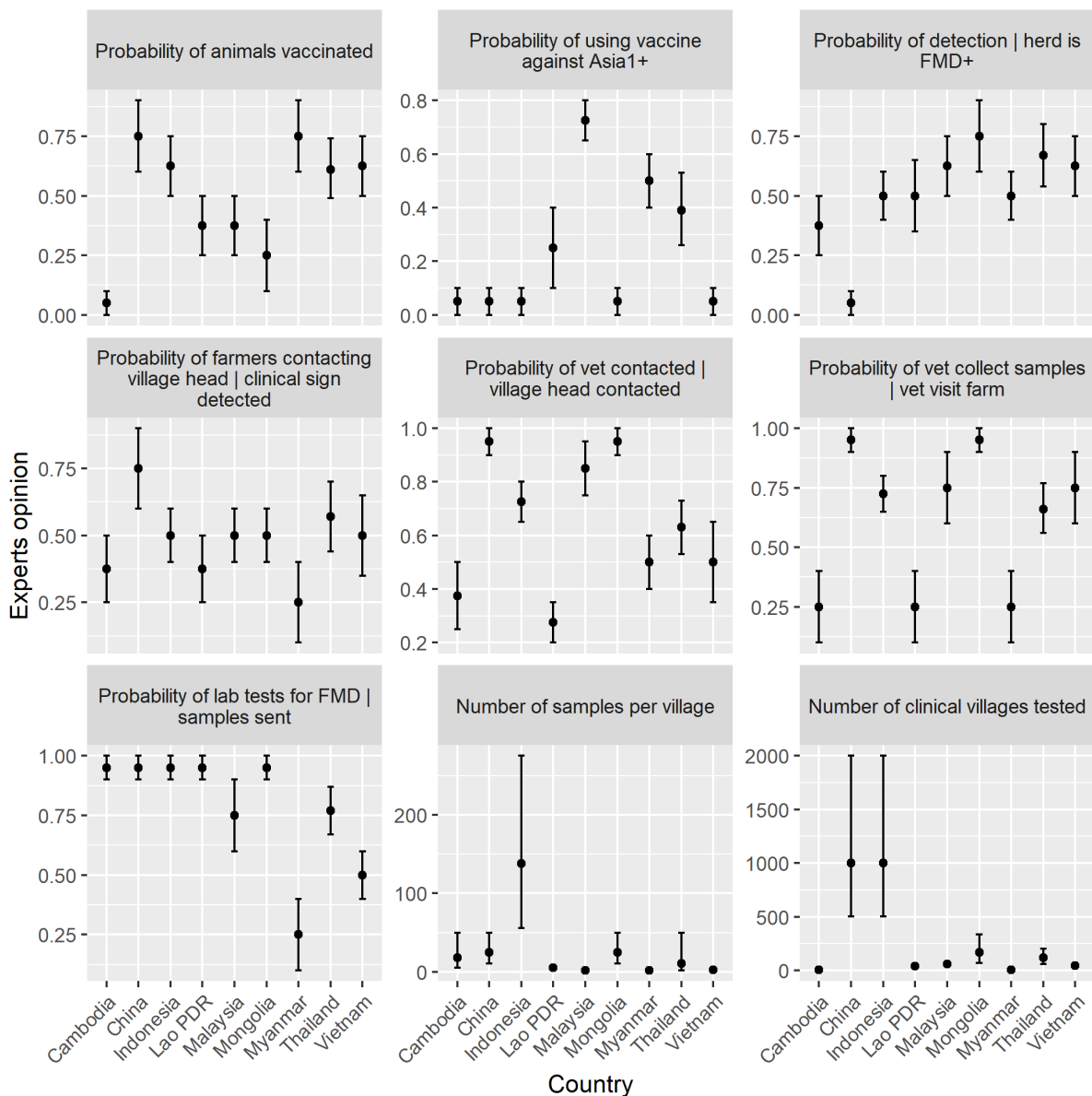
Figure 2. Summary results of the questionnaire survey regarding vaccination practice and passive surveillance for foot-and-mouth disease (FMD) by country in Southeast Asia, China and Mongolia.

Asia 1 positivity

The estimated Asia 1 positivity among the clinical FMD samples for each country from 2010 to 2022 is shown in Figure 3. The median estimated positivity ranged from 0.0010 to 0.0096, with an overall median of 0.0042. The highest positivity was estimated for Cambodia in 2015 (0.0096), followed by Myanmar in 2017 (0.0088). In 2022, the estimated median positivity ranged from 0.0015 in Thailand to 0.0046 in Lao PDR, Myanmar and Malaysia. Noting the small variation by year, we used the 2022 positivity estimates for the scenario tree model parameters.

13

Figure 3. Posterior positivity of foot-and-mouth disease (FMD) virus serotype Asia 1 among all clinical FMD samples sent to WRLFMD between 2010 and 2022 by countries in Southeast Asia, China and Mongolia.

Scenario tree parameters

The parameters estimated for use in the scenario tree models are summarised in Table 3.

Table 3. Estimated parameters for scenario tree model parameters for foot-and-mouth disease (FMD) serotype Asia 1 in Southeast Asia, China and Mongolia.

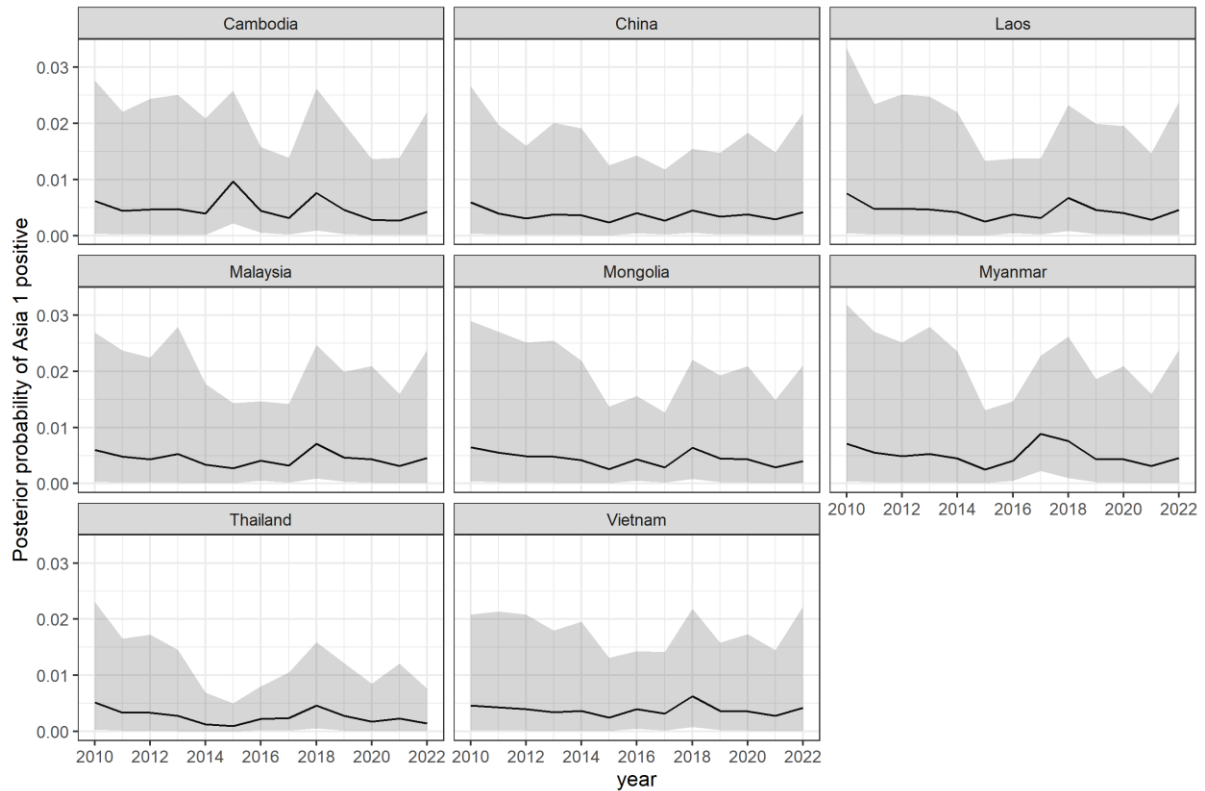| Parameter	
Ph	0.1
Pu	0.2
$p.Asia1_i$	Beta pert distribution; (min, likely, max) = KH (0.0002, 0.0042, 0.0221), CN (0.0002, 0.0042, 0.0218), LA (0.0002, 0.0046, 0.0238), MY (0.0002, 0.0046, 0.0238), MN (0.0002, 0.0040, 0.0211), MM (0.0002, 0.0046, 0.0238), TH (0.0001, 0.0015, 0.0077), VN (0.0002, 0.0043, 0.0222)
$p.vac_i$	Beta pert distribution; (min, likely, max) = KH (0, 0.05, 0.1), CN (0.6, 0.75, 0.9), LA (0.25, 0.375, 0.5), MY (0.25, 0.375, 0.5), MN (0.1, 0.25, 0.4), MM (0.6, 0.75, 0.9), TH (0.49, 0.61, 0.74), VN (0.5, 0.625, 0.75)
$p.triv_i$	Beta pert distribution; (min, likely, max) = KH (0, 0.05, 0.1), CN (0, 0.05, 0.1), LA (0.1, 0.25, 0.4), MY (0.65, 0.725, 0.8), MN (0, 0.05, 0.1), MM (0.4, 0.5, 0.6), TH (0.26, 0.39, 0.53), VN (0, 0.05, 0.1)
$p.clin$	Beta pert distribution; (min, likely, max) = (0.6, 0.9, 1)
$p.det_i$	Beta pert distribution; (min, likely, max) = KH (0.25, 0.375, 0.5), CN (0, 0.05, 0.1), LA (0.35, 0.5, 0.65), MY (0.5, 0.625, 0.75), MN (0.6, 0.75, 0.9), MM (0.4, 0.5, 0.6), TH (0.54, 0.67, 0.8), VN (0.5, 0.625, 0.75)
$p.rep_i$	Beta pert distribution; (min, likely, max) = KH (0.25, 0.375, 0.5), CN (0.6, 0.75, 0.9), LA (0.25, 0.375, 0.5), MY (0.4, 0.5, 0.6), MN (0.4, 0.5, 0.6), MM (0.1, 0.25, 0.4), TH (0.44, 0.57, 0.7), VN (0.35, 0.5, 0.65)
$p.vet_i$	Beta pert distribution; (min, likely, max) = KH (0.25, 0.375, 0.5), CN (0.9, 0.95, 1), LA (0.2, 0.275, 0.35), MY (0.75, 0.85, 0.95), MN (0.9, 0.95, 1), MM (0.4, 0.5, 0.6), TH (0.53, 0.63, 0.73), VN (0.35, 0.5, 0.65)
$p.smp_i$	Beta pert distribution; (min, likely, max) = KH (0.1, 0.25, 0.4), CN (0.9, 0.95, 1), LA (0.1, 0.25, 0.4), MY (0.6, 0.75, 0.9), MN (0.9, 0.95, 1), MM (0.1, 0.25, 0.4), TH (0.56, 0.66, 0.77), VN (0.6, 0.75, 0.9)
$p.test_i$	Beta pert distribution; (min, likely, max) = KH (0.9, 0.95, 1), CN (0.9, 0.95, 1), LA (0.9, 0.95, 1), MY (0.6, 0.75, 0.9), MN (0.9, 0.95, 1), MM (0.1, 0.25, 0.4), TH (0.67, 0.77, 0.87), VN (0.4, 0.5, 0.6)
SeT	Beta pert distribution; (min, likely, max) = (0.8, 0.95, 0.99)
$n.smp_i$	Beta pert distribution; (min, likely, max) = KH (5, 18, 50), CN (11, 25, 50), LA (3, 5, 6), MY (2, 2, 2), MN (11, 25, 50), MM (2, 2, 2), TH (2, 11, 50), VN (2, 2.5, 3)
$n.vil_i$	Beta pert distribution; (min, likely, max) = KH (0, 5, 10), CN (501, 1000, 2000), LA (26, 40, 55), MY (38, 60, 83), MN (67, 168, 337), MM (0, 5, 10), TH (60, 118, 203), VN (24, 42, 67)

KH: Cambodia; CN: China; LA: Lao PDR; MY: Malaysia; MN: Mongolia; MM: Myanmar; TH: Thailand; VN: Vietnam

Outcomes

The estimated population sensitivity of passive surveillance for FMD detection, assuming a design annual incidence of 10% at the village level and 20% at the animal level, varied significantly across countries (Table 4). Mongolia had the highest population sensitivity with a median of 100%, followed by China (median: 96%) and Thailand (median: 71%). Malaysia showed a lower population sensitivity of 16%, while the remaining countries had extremely low population sensitivities of below 4%.

Given the historically low Asia 1 positivity in the region, the probability of detecting serotype Asia 1 by passive surveillance alone was estimated to be 0 – 12%, with the highest in Mongolia (median: 12%), followed by China (median: 7%). When all the countries were combined, the population sensitivity for detecting Asia 1 for the whole region was 20%.

The regional population sensitivity of 20% indicates that, in the absence of prior information regarding Asia 1 status before surveillance, one year of absence of Asia 1 reporting provides a 56% confidence that the region is free from Asia 1.

The confidence in regional Asia 1 freedom by passive surveillance was shown to accumulate over time, depending on the risk of introduction from other regions (Figure 4). The confidence of freedom increased with a prolonged absence of reports, provided the risk of reintroduction remains below ~10%. After seven years without Asia 1 detection, the median confidence of regional freedom from Asia 1 reached 83%, 69%, and 56%, if the annual risk of reintroduction were 0%, 5% and 10%, respectively.

Table 4. Estimated population sensitivity (SeP) of passive surveillance for foot-and-mouth disease (FMD) and Asia 1 specifically, and probability of Asia 1 freedom (PF) given the absence of report for one year, for each country and for all countries combined (region). Median and 5th and 95th percentile range are presented.

	SeP (FMD)			SeP (Asia 1)			PF (Asia 1)		
	Median	5%	95%	Median	5%	95%	Median	5%	95%
Mongolia	100.00	99.69	100.00	11.57	2.37	32.94	53.07	50.60	59.86
China	95.88	64.62	99.97	6.91	1.37	21.70	51.79	50.35	56.09
Thailand	71.49	32.19	94.90	0.49	0.09	2.03	50.12	50.02	50.51
Malaysia	16.26	10.64	22.59	0.14	0.03	0.32	50.03	50.01	50.08
Vietnam	3.60	2.12	5.98	0.05	0.01	0.15	50.01	50.00	50.04
Lao PDR	2.26	1.20	3.95	0.02	0.00	0.06	50.01	50.00	50.02
Cambodia	1.67	0.51	4.43	0.01	0.00	0.04	50.00	50.00	50.01
Myanmar	0.01	0.00	0.03	0.00	0.00	0.00	50.00	50.00	50.00
Region	100.00	100.00	100.00	20.01	7.80	41.21	55.56	52.03	62.98
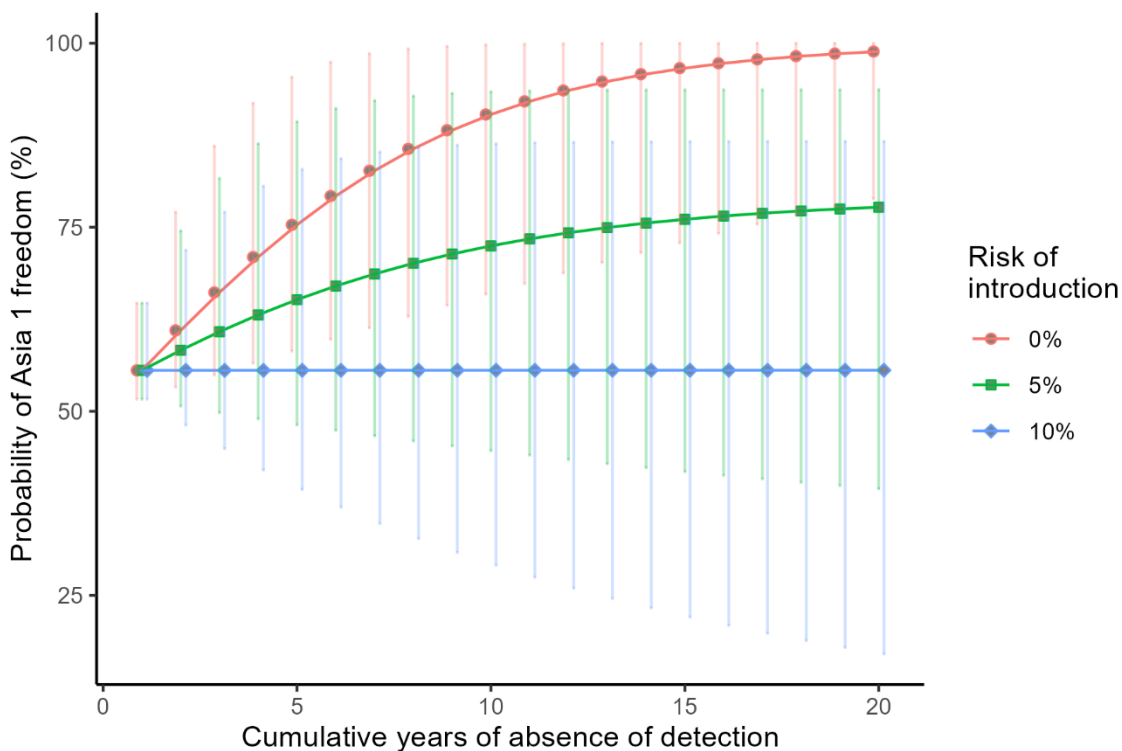
Figure 4. Probability of regional freedom from foot-and-mouth disease (FMD) serotype Asia 1 at the assumed design incidence, given negative surveillance findings over 20 year period, with varying risk of introduction (0%, 5% and 10%). The estimated median values (points) with 5th and 95th percentile ranges (error bars) are shown.

Sensitivity analysis

Figure 5 shows the estimated PRCC values, illustrating the magnitude of influence that parameter uncertainty has on the model outcomes. The key parameters identified as important, were those from countries with higher surveillance sensitivity, notably Mongolia and China. Particularly, the number of villages tested per year, the number of animals sampled per village, and the probability of farmers' detection for Mongolia and China had PRCC values ranging from 0.31 to 0.69, indicating a strong correlation with the model outcomes.

In contrast, parameters from the remaining countries, which had lower surveillance sensitivity, showed PRCC values close to 0, indicating that their uncertainty was relatively less important on the overall model conclusions.
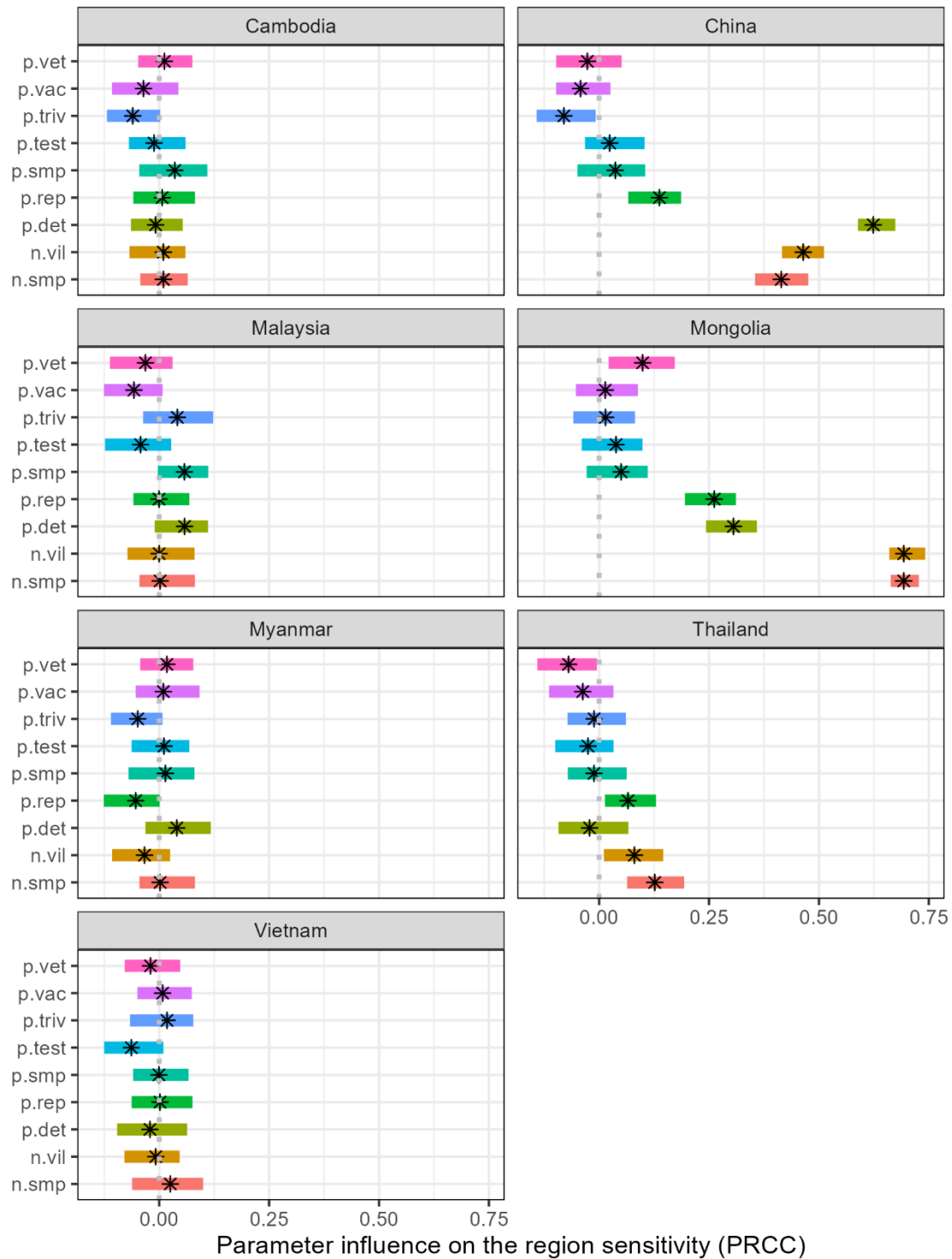
Figure 5. Estimated partial rank correlation coefficient (PRCC) for parameters used for scenario tree models for foot-and-mouth disease (FMD) detection.

Discussion

This project, initiated in 2023 at the request of WOAH, aimed to assess whether the absence of FMDV serotype Asia 1 reports within SEACFMD since 2017 indicates regional freedom from Asia 1, or if it has been missed by the current surveillance scheme. This raised another question regarding the sensitivity of passive surveillance, which has been the primary method for detecting FMD in this region. To address these problems, we developed scenario tree models using the gathered data to estimate the probability of detecting FMDV of any serotypes or specifically serotype Asia 1 by passive surveillance, given the assumed design incidence rate.

Based on our scenario tree models, Mongolia and China demonstrated the highest surveillance sensitivity of approximately 100%. This indicates that if FMD were circulating at the assumed annual incidence rate of 10% at the village level and 20% at the animal level, it would almost always be detected in these countries. These results were contributed by a combination of factors, such as a high number of animals tested (11-50 animals/village) and a high probability of detection (60 – 90%) for Mongolia, or a high number of animals (11-50 animals/village) and villages (>500 villages per year) tested for China, as claimed by in-country experts. Thailand was estimated to have a moderately high detection probability of 71%, followed by Malaysia at 16%. In contrast, Cambodia, Lao PDR, Myanmar and Vietnam had low surveillance sensitivities of below 4%, suggesting that FMD in these countries would likely go unreported at the assumed incidence rates. This aligns with the previous study estimating the official reporting rate of 5% for Cambodia in 2009 (Vergne et al., 2012).

For FMDV serotype Asia 1 specifically, the detection probability was notably lower compared to that of all FMDV serotypes combined, reflecting its historically low occurrence in this region. The probability of detecting Asia 1 dropped to 12% for Mongolia and 7% for China, while it was almost 0% for other countries. When combining the surveillance efforts of all the countries, the overall probability of detecting serotype Asia 1 in the region was estimated to be 20%. This suggests that if there were no report of Asia 1 in the region for a year, the likelihood of regional freedom from serotype Asia 1 (i.e., no circulation above the detection threshold) would be just over 50% (56%). Confidence in regional freedom from Asia 1 would increase with consecutive years of no reports, only if the annual risk of reintroduction from other regions remained below 10%.

We lacked data on the actual risk of FMDV introduction from neighbouring regions. Although we considered an annual reintroduction risk of 0%, 5% and 10%, these assumptions are not supported by empirical data. Myanmar and China share a border with Pool 2 (South Asia), where Asia 1 is historically endemic (Aslam & Alkheraije, 2023; Brito et al., 2017). While there are border checkpoints, unofficial movements of animals may occur with unknown frequency due to porous border security. The reintroduction risk likely varies across countries by year due to differences in policies, border security and market demands, as well as distance. This warrants future research to investigate the risk of virus introduction from Pool 2 to Pool 1.

The design incidence rate of 10% at the village level and 20% at the animal level was determined based on the observed annual incidence rate of FMD in this region. The annual incidence rate of FMD could be approximated by indicators such as the seroprevalence of antibodies to field virus strains in young animals, differentiating from vaccine-induced antibodies, maternal immunity or historical infection that occurred many years ago. In our previous study in Lao PDR, the seroprevalence in calves under 18 months old was estimated to be 20% in 2016 and 39% in 2020, supporting our design incidence rate at the animal level (Han et al., 2022). At the village level, the annual incidence was estimated to be 46% in the area severely affected by the outbreaks in Cambodia in 2009 (Vergne et al., 2012). These incidence rates likely fluctuate by locality and by year, influenced by the prevailing virus lineage and vaccination coverage in the region. Therefore, it is important to note that our results may not apply to scenarios that deviate from these assumed conditions.

Due to challenges in collecting data on existing immunity in the older animals, the models assumed all non-vaccinated animals were susceptible and would become clinically infected if exposed to the virus. However, given that the region is endemic, non-vaccinated animals may have naturally acquired immunity due to past infection, resulting in either resistance to infection or asymptomatic infection. Thus, our design incidence rate could be interpreted as the overall incidence in the susceptible population, excluding historically infected animals with acquired immunity.

A limitation of this study is that there was limited input from country experts, with a median of two responses per country. The questionnaire survey required deep knowledge of sampling protocols, field practices, farmer's behaviours, and laboratory operations; therefore, it is ideal to gather multiple opinions per country from government officials, field veterinarians, and laboratory personnel. The most influential parameters were derived from

China and Mongolia, where we could only obtain one response each. Refining these parameters could enhance the accuracy of our model estimates.

Conclusion

Based on the findings, we conclude that while passive surveillance is effective for detecting any dominant FMD serotypes circulating within SEACFMD, its sensitivity for detecting serotype Asia 1 is limited due to its near-zero incidence. The absence of FMDV serotype Asia 1 reports in recent years may provide some confidence in regional freedom from this serotype, only if the annual reintroduction risk from endemic areas in South Asia is maintained low. The assumptions regarding design incidence rates and the challenges in data collection and expert input emphasise the need for further research to refine parameters and better understand the dynamics of FMDV introduction risks. Overall, this study highlights the importance of enhancing surveillance efforts and establishing comprehensive data-sharing mechanisms among countries to effectively manage and mitigate the risks associated with FMD in the region.

Reference

Aslam, M., & Alkheraije, K. A. (2023). The prevalence of foot-and-mouth disease in Asia. *Frontiers in Veterinary Science*, *10*. https://doi.org/10.3389/fvets.2023.1201578

Blacksell, S. D., Siengsanan-Lamont, J., Kamolsiripichaiporn, S., Gleeson, L. J., & Windsor, P. A. (2019). A history of FMD research and control programmes in Southeast Asia: lessons from the past informing the future. *Epidemiology and Infection*, *147*, e171, Article e171. https://doi.org/10.1017/S0950268819000578

Blower, S. M., & Dowlatabadi, H. (1994). Sensitivity and Uncertainty Analysis of Complex Models of Disease Transmission: an HIV Model, as an Example. *International Statistical Review*, *62*, 229-243.

Bo, L. L., Lwin, K. S., Ungvanijban, S., Knowles, N. J., Wadsworth, J., King, D. P., Abila, R., & Qiu, Y. (2019). Foot-and-mouth disease outbreaks due to an exotic serotype Asia 1 virus in Myanmar in 2017. *Transboundary and Emerging Diseases*, *66*(2), 1067-1072. https://doi.org/https://doi.org/10.1111/tbed.13112

Brito, B. P., Rodriguez, L. L., Hammond, J. M., Pinto, J., & Perez, A. M. (2017). Review of the Global Distribution of Foot-and-Mouth Disease Virus from 2007 to 2014. *Transboundary and Emerging Diseases*, *64*(2), 316-332. https://doi.org/https://doi.org/10.1111/tbed.12373

Cannon, R. M. (2002). Demonstrating disease freedom—combining confidence levels. *Preventive Veterinary Medicine*, *52*(3), 227-249. https://doi.org/https://doi.org/10.1016/S0167-5877(01)00262-8

Han, J. H., Subharat, S., Wada, M., Vink, D., Phiri, B. J., Sutar, A., Abila, R., Khounsy, S., & Heuer, C. (2022). Impact of risk-based partial vaccination on clinical incidence and seroprevalence of foot and mouth disease in Lao PDR. *Transbound Emerg Dis*, *69*(4), e309-e321. https://doi.org/10.1111/tbed.14299

King, D., Nardo, A. D., & Henstock, M. (2010-2022). *WOAH/FAO Foot-and-Mouth Disease Reference Laboratory Network Annual Report*. https://www.wrlfmd.org/ref-lab-reports#panel-2092

Martin, P. A., Cameron, A. R., & Greiner, M. (2007). Demonstrating freedom from disease using multiple complex data sources 1: a new methodology based on scenario trees. *Prev Vet Med*, *79*(2-4), 71-97. https://doi.org/10.1016/j.prevetmed.2006.09.008

Meletis, E., Conrady, B., Hopp, P., Lurier, T., Frössling, J., Rosendal, T., Faverjon, C., Carmo, L. P., Hodnik, J. J., Ózsvári, L., Kostoulas, P., van Schaik, G., Comin, A., Nielen, M., Knific, T., Schulz, J., Šerić-Haračić, S., Fourichon, C., Santman-Berends, I., & Madouasse, A. (2024). Review state-of-the-art of output-based methodological approaches for substantiating freedom from infection. *Front Vet Sci*, *11*, 1337661. https://doi.org/10.3389/fvets.2024.1337661

Moura, P., Kihm, U., Schudel, A., Bergmann, I., & Buholzer, P. (2024). Why Foot-and-Mouth Disease-Free with Vaccination Should Be Equivalent to Foot-and-Mouth Disease-Free without Vaccination. *Veterinary Sciences*, *11*(6), 281.

Paton, D. J., Di Nardo, A., Knowles, N. J., Wadsworth, J., Pituco, E. M., Cosivi, O., Rivera, A. M., Kassimi, L. B., Brocchi, E., de Clercq, K., Carrillo, C., Maree, F. F., Singh, R. K., Vosloo, W., Park, M.-K., Sumption, K. J., Ludi, A. B., & King, D. P. (2021). The history of foot-and-mouth disease virus serotype C: the first known extinct serotype? *Virus Evolution*, *7*(1). https://doi.org/10.1093/ve/veab009

Tum, S., Robertson, I. D., Edwards, J., Abila, R., & Morzaria, S. (2015). Seroprevalence of foot-and-mouth disease in the southern provinces of Cambodia. *Tropical Animal Health and Production*, *47*(3), 541-547. https://doi.org/10.1007/s11250-015-0760-4

Valarcher, J. F., Knowles, N. J., Zakharov, V., Scherbakov, A., Zhang, Z., Shang, Y. J., Liu, Z. X., Liu, X. T., Sanyal, A., Hemadri, D., Tosh, C., Rasool, T. J., Pattnaik, B., Schumann, K. R., Beckham, T. R., Linchongsubongkoch, W., Ferris, N. P., Roeder, P. L., & Paton, D. J. (2009). Multiple origins of foot-and-mouth disease virus serotype Asia 1 outbreaks, 2003-2007. *Emerg Infect Dis*, *15*(7), 1046-1051. https://doi.org/10.3201/eid1507.081621

Vergne, T., Grosbois, V., Durand, B., Goutard, F., Bellet, C., Holl, D., Roger, F., & Dufour, B. (2012). A capture-recapture analysis in a challenging environment: assessing the epidemiological situation of foot-and-mouth disease in Cambodia. *Prev Vet Med*, *105*(3), 235-243. https://doi.org/10.1016/j.prevetmed.2011.12.008

Appendix 1 – Questionnaire survey

Thank you for participating in this questionnaire!

This questionnaire aims to gather information on the Foot and Mouth Disease (FMD) surveillance systems in SEACFMD member countries. The data collected will be used to evaluate the effectiveness of current surveillance systems in detecting FMD in this region, with particular interest in FMD virus serotype Asia1. The data obtained here may help us to choose suitable FMD vaccines, allocate resources more efficiently and optimize FMD control efforts in this region.

All responses will be treated confidentially, and any personal information will be anonymized for analysis.

Q1 Your gender

☐ Male
☐ Female
☐ Other

Q2 Your age range

☐ 30 or less
☐ 31-40
☐ 41-50
☐ 51-60
☐ 61+

Q3 Your educational background

☐ Veterinarian
☐ Para-veterinarian
☐ Other (please specify)

Q4 Your affiliation

☐ International organization
☐ Central government
☐ Regional/provincial/district authority
☐ Diagnostic laboratory
☐ Private veterinary practice
☐ Other

Q5 Country

Please specify the country you are answering for.

☐ Brunei
☐ Cambodia
☐ China
☐ Indonesia
☐ Lao PDR
☐ Malaysia
☐ Mongolia
☐ Myanmar
☐ Philippines
☐ Singapore
☐ Thailand
☐ Vietnam

Q6 **Animal species**
What are the most common livestock species in your country that are susceptible to FMD?

☐ Cattle
☐ Buffalo
☐ Pig
☐ Goat
☐ Sheep

Q8 **Vaccination practice**
For the most common livestock species in your country, what proportion are routinely vaccinated against FMD?

☐ <10%
☐ 10-40%
☐ 40-60%
☐ 60-90%
☐ >90%

Q9 **FMD Asia1 vaccines**

<u>Among the vaccinated animals</u>, what proportion are vaccinated against FMD virus serotype Asia1, by, for example, trivalent vaccines?

- ☐ <10%
- ☐ 10-40%
- ☐ 40-60%
- ☐ 60-90%
- ☐ >90%

Q10 **Detection**

What is the likelihood of a typical livestock owner in your country to <u>detect</u> clinical signs of FMD?

- ☐ <10%
- ☐ 10-40%
- ☐ 40-60%
- ☐ 60-90%
- ☐ >90%

Q11 **Reporting**

What is the likelihood of a typical livestock owner in your country, suspecting FMD, to <u>report</u> it to the authority (e.g. village head or district officer)?

- ☐ <10%
- ☐ 10-40%
- ☐ 40-60%
- ☐ 60-90%
- ☐ >90%

Q12 **Vet visit**

If an FMD outbreak is suspected, what is the likelihood of a veterinarian (including para-veterinarian) to visit the village?

- ☐ <10%
- ☐ 10-40%
- ☐ 40-60%
- ☐ 60-90%
- ☐ >90%

Q13 **Sampling**

If an FMD outbreak is suspected and a vet visits the village, what is the likelihood of them collecting samples for laboratory diagnostic testing?

☐ <10%
☐ 10-40%
☐ 40-60%
☐ 60-90%
☐ >90%

Q14 **Number of samples per village**

If samples are collected from an FMD outbreak village, how many animals are typically sampled per village? Please select.

☐ 1
☐ 2
☐ 3
☐ 4
☐ 5
☐ 6
☐ 7
☐ 8
☐ 9
☐ 10
☐ 11-50
☐ 51-100
☐ 101-500
☐ >500

Q15 **Laboratory testing**

If the laboratory receives samples of FMD suspect cases, what is the likelihood of them tested for FMD?

☐ <10%
☐ 10-40%
☐ 40-60%
☐ 60-90%
☐ >90%

Q16 **Serotyping**

If the laboratory receives samples of FMD suspect cases, what is the likelihood of them typed for serotypes?

☐ <10%
☐ 10-40%
☐ 40-60%
☐ 60-90%
☐ >90%

Q17 **Number of villages**

In the last 3 years, approximately how many villages in your country sent samples for FMD testing?

2021

- ☐ 0-10
- ☐ 11-50
- ☐ 51-100
- ☐ 101-500
- ☐ >500

2022

- ☐ 0-10
- ☐ 11-50
- ☐ 51-100
- ☐ 101-500
- ☐ >500

2023

- ☐ 0-10
- ☐ 11-50
- ☐ 51-100
- ☐ 101-500
- ☐ >500

Q18 **Active surveillance**

Is there any ongoing active surveillance schemes in place in your country? Select all that applies:

- ☐ Slaughterhouse surveillance
- ☐ Outbreak surveillance
- ☐ Zone surveillance
- ☐ Other (specify)
- ☐ I don't know

Q19 **Diagnostic laboratories**

Please list the laboratories in your country that are involved in FMD testing.

Q20 **Diagnostic capacity**

Within your country,

Can any laboratory detect FMD?

- ☐ Yes
- ☐ No

Can any laboratory perform FMD serotyping (O, A, Asia1, etc)?

- ☐ Yes
- ☐ No

Can any laboratory perform FMD strain typing (sequencing)?

- ☐ Yes
- ☐ No

Q21 Costs

Who typically covers the costs associated with FMD testing in your country?

- ☐ Livestock owner
- ☐ Government
- ☐ Both
- ☐ Other (please specify)

Q22 Contact details

If you are willing to be contacted for further information or clarification, please provide your contact details.

Email

Phone

Appendix 2 – Questionnaire survey responses

FMD surveillance response summary

Date: 16 September 2024

Number of respondents: 20

Respondent profile

Gender: Female (12) Male (8)

Age: 30 or less (3) 31-40 (2) 41-50 (11) 51-60 (4)

Education: Veterinarian (20)

Affiliation: Central government (12) Diagnostic laboratory (6) International organization (1) Regional/provincial/district authority (1)

Median (mean) response duration: 9 (18) minutes

Country:

Thailand	Cambodia	Indonesia	Lao PDR	Malaysia	Vietnam	China	Mongolia	Myanmar
7	2	2	2	2	2	1	1	1

Animal species:

what are the most common livestock species in your country that are susceptible to FMD?

	Cambodia	China	Indonesia	Lao PDR	Malaysia	Mongolia	Myanmar	Thailand	Vietnam
Buffalo	0	0	0	0	0	0	0	1	0
Cattle	2	1	2	2	2	1	1	6	2

Vaccination practice:

For the most common livestock species in your country, what proportion are routinely vaccinated against FMD?

<10%	10-40%	40-60%	60-90%	>90%
3	3	5	9	0

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	2	0	0	0	0
China	0	0	0	1	0
Indonesia	0	0	1	1	0
Lao PDR	0	1	1	0	0
Malaysia	0	1	1	0	0
Mongolia	0	1	0	0	0
Myanmar	0	0	0	1	0
Thailand	1	0	1	5	0
Vietnam	0	0	1	1	0

FMD Asia1 Vaccines:

Among the vaccinated animals, what proportion are vaccinated against FMD virus serotype Asia 1, by, for example, trivalent vaccines?

<10%	10-40%	40-60%	60-90%	>90%
8	6	4	1	1

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	2	0	0	0	0
China	1	0	0	0	0
Indonesia	2	0	0	0	0
Lao PDR	0	2	0	0	0
Malaysia	0	0	1	0	1
Mongolia	1	0	0	0	0
Myanmar	0	0	1	0	0
Thailand	0	4	2	1	0
Vietnam	2	0	0	0	0

Detection

What is the likelihood of a typical livestock owner in your country to detect clinical signs of FMD?

<10%	10-40%	40-60%	60-90%	>90%
1	3	7	8	1

	<10%	10-40%	40-60%	60-90%	>90%

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	1	1	0	0
China	1	0	0	0	0
Indonesia	0	0	2	0	0
Lao PDR	0	1	0	1	0
Malaysia	0	0	1	1	0
Mongolia	0	0	0	1	0
Myanmar	0	0	1	0	0
Thailand	0	1	1	4	1
Vietnam	0	0	1	1	0

Reporting

What is the likelihood of a typical livestock owner in your country, suspecting FMD, to report it to the authority (e.g. village head or district officer)?

<10%	10-40%	40-60%	60-90%	>90%
2	4	9	5	0

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	1	1	0	0
China	0	0	0	1	0
Indonesia	0	0	2	0	0
Lao PDR	2	0	0	0	0
Malaysia	0	0	2	0	0
Mongolia	0	0	1	0	0
Myanmar	0	1	0	0	0
Thailand	0	1	3	3	0
Vietnam	0	1	0	1	0

Vet visit:

If an FMD outbreak is suspected, what is the likelihood of a veterinarian (including para-veterinarian) to visit the village?

<10%	10-40%	40-60%	60-90%	>90%
1	3	7	3	6

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	1	1	0	0

China	0	0	0	0	1
Indonesia	0	0	1	0	1
Lao PDR	1	0	1	0	0
Malaysia	0	0	0	1	1
Mongolia	0	0	0	0	1
Myanmar	0	0	1	0	0
Thailand	0	1	3	1	2
Vietnam	0	1	0	1	0

Sampling:

If an FMD outbreak is suspected and a vet visits the village, what is the likelihood of them collecting samples for laboratory diagnostic testing?

<10%	10-40%	40-60%	60-90%	>90%
2	4	3	6	5

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	2	0	0	0
China	0	0	0	0	1
Indonesia	0	0	1	0	1
Lao PDR	2	0	0	0	0
Malaysia	0	0	0	2	0
Mongolia	0	0	0	0	1
Myanmar	0	1	0	0	0
Thailand	0	1	2	2	2
Vietnam	0	0	0	2	0

Number of samples per village:

If samples are collected from an FMD outbreak village, how many animals are typically sampled per village? Please select.

1	2	3	4	5	6	7	8	9	10	11-50	51-100	101-500	>501
0	6	3	0	3	1	0	0	0	0	6	0	1	0

	1	2	3	4	5	6	7	8	9	10	11-50	51-100	101-500	>501
Cambodia	0	0	0	0	1	0	0	0	0	0	1	0	0	0
China	0	0	0	0	0	0	0	0	0	0	1	0	0	0

```
Indonesia 0 0 0 0 0 0 0 0 0    1      0      1    0
Lao PDR   0 0 1 0 0 1 0 0 0    0      0      0    0
Malaysia  0 2 0 0 0 0 0 0 0    0      0      0    0
Mongolia  0 0 0 0 0 0 0 0 0    1      0      0    0
Myanmar   0 1 0 0 0 0 0 0 0    0      0      0    0
Thailand  0 2 1 0 2 0 0 0 0    2      0      0    0
Vietnam   0 1 1 0 0 0 0 0 0    0      0      0    0
```

Laboratory testing:

If the laboratory receives samples of FMD suspect cases, what is the likelihood of them tested for FMD?

<10%	10-40%	40-60%	60-90%	>90%
0	2	1	3	9

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	0	0	0	1
China	0	0	0	0	1
Indonesia	0	0	0	0	1
Lao PDR	0	0	0	0	2
Malaysia	0	0	0	1	0
Mongolia	0	0	0	0	1
Myanmar	0	1	0	0	0
Thailand	0	1	0	2	3
Vietnam	0	0	1	0	0

Serotyping:

If the laboratory receives samples of FMD suspect cases, what is the likelihood of them typed for serotypes?

<10%	10-40%	40-60%	60-90%	>90%
0	2	0	5	8

	<10%	10-40%	40-60%	60-90%	>90%
Cambodia	0	0	0	1	0
China	0	0	0	0	1
Indonesia	0	0	0	0	1
Lao PDR	0	0	0	0	2
Malaysia	0	0	0	1	0
Mongolia	0	0	0	0	1
Myanmar	0	1	0	0	0
Thailand	0	1	0	2	3
Vietnam	0	0	0	1	0

Number of villages:

In the last 3 years, approximately how many villages in your country sent samples for FMD testing?

2021

0-10	11-50	51-100	101-500	>500	NA
5	2	5	2	1	5

	0-10	11-50	51-100	101-500	>500	NA
Cambodia	1	0	0	0	0	1
China	0	0	0	0	1	0
Indonesia	1	0	0	0	0	1
Lao PDR	1	0	1	0	0	0
Malaysia	0	0	1	0	0	1
Mongolia	0	0	0	1	0	0
Myanmar	1	0	0	0	0	0
Thailand	1	2	2	1	0	1
Vietnam	0	0	1	0	0	1

2022

0-10	11-50	51-100	101-500	>500	NA
3	4	4	1	3	5

	0-10	11-50	51-100	101-500	>500	NA
Cambodia	1	0	0	0	0	1
China	0	0	0	0	1	0
Indonesia	0	0	0	0	1	1
Lao PDR	1	0	1	0	0	0
Malaysia	0	0	1	0	0	1
Mongolia	0	0	0	1	0	0
Myanmar	1	0	0	0	0	0
Thailand	0	3	2	0	1	1
Vietnam	0	1	0	0	0	1

2023

0-10	11-50	51-100	101-500	>500	NA
4	4	5	0	2	5

	0-10	11-50	51-100	101-500	>500	NA
Cambodia	1	0	0	0	0	1
China	0	0	0	0	1	0
Indonesia	0	0	0	0	1	1
Lao PDR	1	0	1	0	0	0
Malaysia	0	1	0	0	0	1
Mongolia	1	0	0	0	0	0
Myanmar	1	0	0	0	0	0
Thailand	0	2	4	0	0	1
Vietnam	0	1	0	0	0	1

Active surveillance:

Is there any ongoing active surveillance schemes in place in your country? Select all that applies

Outbreak surveillance

	FALSE	TRUE
Cambodia	0	1
China	0	1
Indonesia	0	1

Lao PDR	0	2
Malaysia	0	1
Mongolia	0	1
Myanmar	0	1
Thailand	1	5
Vietnam	0	1

Zone surveillance

	FALSE	TRUE
Cambodia	1	0
China	0	1
Indonesia	0	1
Lao PDR	0	2
Malaysia	0	1
Mongolia	0	1
Myanmar	0	1
Thailand	2	4
Vietnam	0	1

Slaughterhouse surveillance

	FALSE	TRUE
Cambodia	0	1
China	0	1
Indonesia	1	0
Lao PDR	1	1
Malaysia	1	0
Mongolia	1	0
Myanmar	1	0
Thailand	5	1
Vietnam	1	0

Diagnostic laboratories:

Please list the laboratories in your country that are involved in FMD testing.

- Cambodia: Only at NAHPRI

- Indonesia: 9 disease investigation centres, 1 national vet drug assay lab, production for biological product lab
- Lao PDR: ELISA PCR(probang sample)

- Lao PDR: National Animal Health Laboratory

- Malaysia: 1. National FMD Laboratory, Eastern Zone Veterinary Laboratory (Kelantan) – do all the testing about FMD virus (serology, antigen detection etc) 2. Regional laboratory in states and Veterinary Research Institute for NSP FMDV ELISA.

- Mongolia: State central veterinary laboratory veterinary laboratory of Ulaanbaatar city veterinary laboratory of 21 provinces

- Thailand: RRL, Pakchong

- Thailand: National Institute of Animal Health, Veterinary research and diagnostic centers, University laboratories, private laboratories

- Thailand: RRL NIAH and VRDC regional center

- Thailand: 7 regional laboratories and 1 central laboratory with 1 FMD reference laboratory

- Thailand: Regional Reference Laboratory for Foot and Mouth Disease in South East Asia (RRL) National Institute of Animal Health (NIAH) Veterinary Research and Development Center (VRDC)

- Vietnam: NCVD and 7 RAHOs

Diagnostic capacity

Within your country, – Can any laboratory detect FMD?

	No	Yes	
Cambodia	1	0	1
China	0	0	1
Indonesia	1	0	1
Lao PDR	0	0	2
Malaysia	1	0	1
Mongolia	0	0	1
Myanmar	0	0	1
Thailand	1	1	5
Vietnam	1	0	1

Within your country, – Can any laboratory perform FMD serotyping (O, A, Asia1, etc)?

	No	Yes	
Cambodia	1	1	0
China	0	1	0
Indonesia	1	0	1
Lao PDR	0	0	2
Malaysia	1	0	1
Mongolia	0	1	0
Myanmar	0	0	1
Thailand	1	1	5
Vietnam	1	0	1

within your country, – Can any laboratory perform FMD strain typing (sequencing)?

```
           No Yes
Cambodia  1  1   0
China     0  1   0
Indonesia 1  0   1
Lao PDR   0  2   0
Malaysia  1  0   1
Mongolia  0  1   0
Myanmar   0  1   0
Thailand  1  2   4
Vietnam   1  1   0
```

Costs:

Who typically covers the costs associated with FMD testing in your country? – Selected Choice

```
           Both Government
Cambodia  1   0          1
China     0   0          1
Indonesia 1   1          0
Lao PDR   0   1          1
Malaysia  1   0          1
Mongolia  0   0          1
Myanmar   0   0          1
Thailand  1   1          5
Vietnam   1   1          0
```