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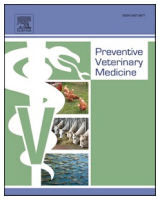

Probability of freedom from foot-and-mouth disease virus serotype Asia 1 in Southeast Asia, China and Mongolia

Masako Wada [a,*], Jun-Hee Han [a], Bolortuya Purevsuren [b], Karma Rinzin [b], Ashish Sutar [b], Ronello Abila [b], Supatsak Subharat [a]

[a] EpiCentre, School of Veterinary Science, Massey University, Palmerston North, New Zealand
[b] Sub-Regional Representation for South-East Asia, World Organisation for Animal Health, Bangkok, Thailand

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ABSTRACT

Foot-and-mouth disease virus (FMDV) serotype Asia 1 has not been reported in Southeast Asia, China and Mongolia between 2018 and 2024, despite the endemicity of FMD in this region and the continued circulation of serotype Asia 1 in South Asia. While vaccines against Asia 1 are still occasionally used in this region, it is unknown whether the absence of reports indicates true disease freedom or surveillance gaps. This study aimed to estimate the sensitivity of existing passive surveillance systems, and the probability of regional freedom from serotype Asia 1 across eight countries using the scenario tree approach. Two stochastic scenario tree models were developed to estimate surveillance sensitivity for FMD (any serotypes) and serotype Asia 1 specifically. Country-specific input parameters were derived from a questionnaire survey of in-country experts on FMD vaccination practices, smallholders' behaviour, sampling protocols and diagnostic laboratory capacity. Additionally, 2010 – 2022 data on FMD clinical samples submitted and confirmed Asia 1 cases were obtained from the World Reference Laboratory for FMD. Under a design annual incidence rate of 10 % at the village level and 20 % at the animal level, estimated surveillance sensitivity for FMD ranged from 100.0 % in Mongolia and 95.9 % in China to 1.7 % in Cambodia and < 0.1 % in Myanmar. Using the effective design incidence rate with a median of 0.02 – 0.07 % at the village level and 20 % at the animal level, the probability of detecting Asia 1 was estimated to be 0.0 – 6.7 % per country and 14.5 % for the region. The estimated probability of regional freedom from Asia 1 was 53.9 % after the first year without reporting. Over years of no reporting, this probability would increase, only if an annual risk of introduction remained below 6 %. The results were most sensitive to parameters related to sampling intensity and smallholders' behaviour, particularly in countries with high surveillance sensitivity, such as Mongolia and China. Our findings highlight the low sensitivity of passive surveillance in the region, suggesting that serotype Asia 1 may have remained undetected under the current surveillance efforts. Strengthening data collection and continued efforts in increasing surveillance intensity are essential to improving confidence in the regional freedom from serotype Asia 1.

1. Introduction

Foot-and-mouth disease (FMD) remains endemic in Southeast Asia (SEA), China and Mongolia, imposing significant socioeconomic burdens through reduced livestock productivity and restrictions on international trade. While vaccination has historically been key to eradicating FMD in other regions (Moura et al., 2024), its control in SEA is challenging, amid increasing demand for animal products, frequent unofficial livestock movements, and inadequate border control (Blacksell et al., 2019). A major obstacle is the short life of vaccine-induced immunity and poor cross immunity between or within serotypes (Kenubih, 2021; Robinson et al., 2016; Singh et al., 2019), complicating routine vaccination efforts in a landscape dominated by resource-poor smallholders. Additionally, limited diagnostic capacity

Abbreviations: FAO, Food and Agriculture Organization 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 campaign; WOAH, World Organisation for Animal Health; WRLFMD, World Reference Laboratory for Foot and Mouth Disease.

* Corresponding author.
E-mail address: m.wada@massey.ac.nz (M. Wada).

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and shortages of field veterinary professionals (Auplish et al., 2024; Subharat et al., 2023) would hinder comprehensive monitoring of circulating virus strains, making it difficult to deploy appropriate vaccines effectively.

Understanding which FMD virus (FMDV) serotypes are emerging, circulating or at risk of introduction is critical for informing surveillance strategies, selecting appropriate vaccines and efficiently allocating resources for FMD control. In SEA, China and Mongolia, FMDV serotypes O and A have consistently been reported (Brito et al., 2017). Serotype Asia 1 has only been detected sporadically, since major outbreaks in 2003 – 2007 (Brito et al., 2017; Tum et al., 2015; Valarcher et al., 2009). The Asia 1 strain detected in Myanmar in 2017 was suggested to be an imported strain, rather than one circulating in the region (Bo et al., 2019). No evidence indicates ongoing circulation of Asia 1, raising the question of whether this serotype has been eliminated from this region.

Demonstration of disease freedom typically requires intensive active surveillance and extensive testing, which is not feasible or economically reasonable in this region. Instead, this research aimed to address the knowledge gaps regarding the effectiveness of existing passive surveillance, which was the main mechanism of FMD detection in the region, considering routine vaccination practices and vaccine-induced immunity. The aim of this study was to estimate the sensitivity of existing passive surveillance systems and the probability of regional freedom from FMDV serotype Asia 1 in SEA, China and Mongolia by developing a stochastic scenario tree model.

2. Materials and methods

All analysis was conducted using R 4.3.2 (R Core Team 2023). The scenario tree models are available as an interactive Shiny application at https://shiny.massey.ac.nz/mwada/asia1/.

2.1. Target countries

The scenario tree models targeted eight member countries of the SEA, China and Mongolia Foot and Mouth Disease campaign (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 excluded from the scenario tree model because it was free from FMD until 2022. However, Indonesia was invited to participate in the questionnaire survey.

2.2. WRLFMD data

We obtained the WOAH/FAO FMD Reference Laboratories (WRLFMD) Network Annual Reports for each year 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, as well as the number of samples positive for FMDV serotype Asia 1 were manually extracted from the reports by the authors. The period of retrospective data analysis was restricted to 1 January 2010–31 December 2022.

2.3. Questionnaire survey

A questionnaire was developed to gather information on FMD surveillance systems, sampling protocols, diagnostic capacities and vaccination practices in the country, with a focus on passive surveillance (see Supplementary Material 1). As exact information or data were likely absent, the questionnaire employed Likert methods, where participants indicated possible ranges (e.g., <10 %, 10–40 %, 40–60 %, 60–90 %, >90 %) based on their knowledge instead of providing specific estimates. Responses were made for the most common livestock species susceptible to FMD in the country, as specified by the respondents. Livestock species not selected by the respondents, as well as wildlife species, were not included in the survey.

The survey was delivered to local experts in June 2024 via Qualtrics, a cloud-based platform for administering online surveys. A total of 35 personnel were identified as local experts by the coordinators from WOAH Sub-Regional Representation for Southeast Asia through their existing professional networks, including National Coordinators, EpiNet focal points, LabNetwork focal points, and Upper Mekong Working Group Member. The survey link was circulated via email by a WOAH coordinator, and respondents were encouraged to share it with relevant colleagues. As part of the validation process, digital identifiers associated with each response were reviewed to identify potential duplicates.

Responses were summarised at the country level, averaging the middle point, minimum and maximum values across participants, so that the range was the widest possible based on responses. The survey summary results were shared with the initially targeted local experts for their review, and once agreement was reached, we treated the results as a collective response.

2.4. Asia 1 positivity

We applied the WRLFMD data to estimate the posterior distribution of the proportion of serotype Asia 1 positive samples among all the FMD clinical samples tested by the WRLFMD (herein referred to as Asia 1 positivity, or *p.Asia1*), 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:

$$k_{i,t} \sim Binomial(n_{i,t}, \rho_{i,t}) \quad (1)$$

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:

$$\pi(\rho_{i,t}) \sim Beta(1+A, \quad 1+B) \quad (2)$$

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

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

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

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

2.5. 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 each of the target countries and all countries combined (i.e. region). This scenario tree approach 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; 'FMD model'), and the other specifically for serotype Asia 1 ('Asia 1 model'). These models incorporated passive surveillance components for each of the eight countries, accounting for differences in vaccination practice and surveillance intensity by country (Fig. 1). While the two models followed a similar structure, the Asia 1 model incorporated two additional parameters to adjust the incidence and susceptibility, i.e., Asia 1 positivity (*p.Asia1*) and probability of using trivalent vaccines (*p.triv*) (Table 1). Parameters were estimated for each country based on the 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 countries.

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 ($DIR_{village}$) and 20 % at the animal level (DIR_{animal}) to reflect the level of FMD circulation among the livestock populations in the target countries. These incidence rates aligned with field observations in the region, while maintaining a conservative approach. For the Asia 1 model, the design incidence rates were adjusted by Asia 1 positivity (*p.Asia1*) to reflect the likely incidence of Asia 1 circulating in this region, if present. This means that the effective design incidence rates for Asia 1 at the village level ($DIR_{village}$*), or the proportion of villages assumed to be infected with Asia 1, was calculated as $DIR_{village}$ x *p.Asia1*. Since this adjustment substantially lowered the effective design incidence rates for Asia 1, $DIR_{village}$*, to below 1 %, we used the Asia 1 model to estimate the probability of freedom from disease – that is, the probability that Asia 1 was not present at or above the adjusted design incidence rate, given all negative reports. In contrast, the generic FMD model was used only to assess the surveillance sensitivity, not to estimate the probability of disease freedom.

2.6. Model 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. We chose 100 iterations as it was sufficient to produce stable outcome estimates, while maintaining a reasonable computational time.

2.7. FMD model

For the design incidence rate of 10 % at the village level ($DIR_{village}$) and 20 % at the animal level (DIR_{animal}), 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:

$$SeP_{vi} = 1 - (1 - DIR_{animal} \times (1 - p.vac_i) \times p.clin \times p.\mathrm{det}_i \times p.rep_i \times p.vet_i \times p.smp_i \times p.test_i \times SeT)^{n.smp_i}$$

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

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

2.8. Asia 1 model

Unlike the generic FMD model, the effective design incidence rates for Asia 1 ($DIR_{village}$*) were calculated as:

$$DIR_{village}{}^* = DIR_{village} \times p.Asia1_i$$

Therefore, $DIR_{village}$* was dependent on Asia 1 positivity (*p.Asia1*), which varied by year and country. The population sensitivity of passive surveillance for serotype Asia 1 (the probability of detecting Asia 1 by passive surveillance at the adjusted design incidence rate) for a village (SeP_{vi}*), country i (SeP_i*) and the whole region (*SeP*r*) were estimated as:

$$SeP_{vi}{}^* = 1 - (1 - DIR_{animal} \times (1 - p.vac_i \times p.triv_i) \times p.clin \times p.\mathrm{det}_i \times p.rep_i \times p.vet_i \times p.smp_i \times p.test_i \times SeT)^{n.smp_i}$$

$$SeP_i{}^* = 1 - (1 - DIR_{village} \times p.Asia1_i \times SeP_{vi}{}^*)^{n.vil_i}$$

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

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 the absence of reports of Asia 1 for multiple years, the accumulated probability of regional freedom from Asia 1 after t years (PF_t) was estimated as:

[1] For example, if there were 100 animals per village and a total of 1000 villages in the region, each year 100 villages (1000 villages x 10 %) and 2000 animals (100 animals/village x 20 % x 100 villages) would be infected. Of these infected animals, *p.Asia1* (approximately 0.04), or 80 animals (2000 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.

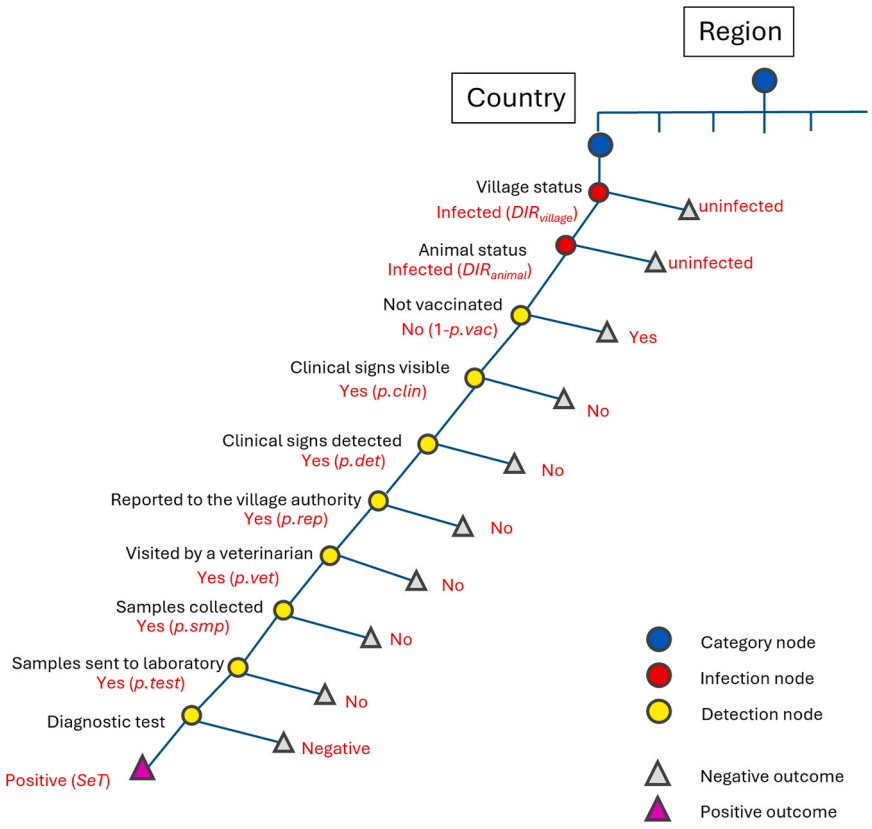

Fig. 1. Scenario tree for detecting foot-and-mouth disease (FMD) by passive surveillance in the region encompassing Southeast Asia, China and Mongolia. Only one county's branch is shown, and all other country branches are identical.

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
$DIR_{village}$	Design annual incidence rate of FMD (any serotypes) at the village level (% villages per year)
DIR_{animal}	Design annual incidence rate of FMD (any serotypes) at the animal level within an infected village (% animals 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 the 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*)

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

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 outside the study region where Asia 1 is known to be circulating, such as South Asia, or from other animal species not included in the survey, each year. There is no data to estimate this, hence *p.intro* of 0 %, 2 %, 4 %, 6 %, 8 % and 10 % were applied.

2.9. Sensitivity analysis

To assess the robustness of the conclusions, given the parameter uncertainty, a sensitivity analysis was performed using Latin Hypercube Sampling and Partial Rank Correlation Coefficient (LHS/PRCC) methods (Blower and Dowlatabadi, 1994). In this analysis, parameter values were simultaneously varied within the assigned distributions across 100 bootstrap iterations, 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.

Table 2
The number of clinical samples submitted to the World Reference Laboratory for foot-and-mouth disease (WRLFMD) between 2010 and 2022 for target countries in the Southeast Asia, China and Mongolia FMD program (SEACFMD).

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

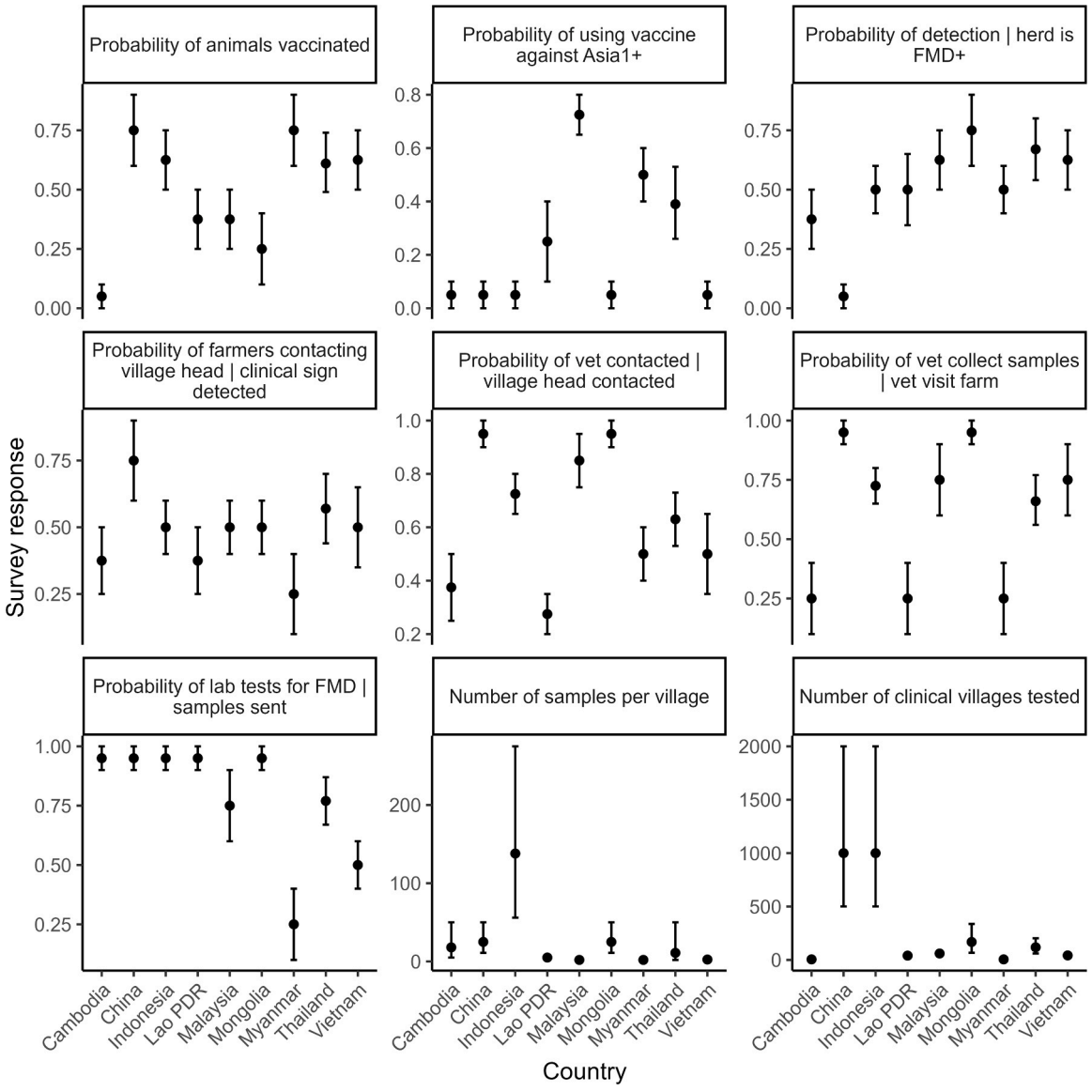

Fig. 2. Summary results of the questionnaire survey regarding vaccination practice and passive surveillance for foot-and-mouth disease (FMD) by country in Southeast Asia, China and Mongolia. The error bars represent the mean minimum and maximum values, and the points represent the mean.

3. Results

3.1. Retrospective analysis

The number of clinical FMD samples submitted to WRLFMD between 2010 and 2022 by year and country is shown in Table 2. In total, 4602 samples were submitted from the region during the 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). Among the 4602 samples, 4 (0.087 %) tested positive for serotype Asia 1: 2 in Cambodia in 2015 and 2 in Myanmar in 2017.

The estimated Asia 1 positivity among the clinical FMD samples for

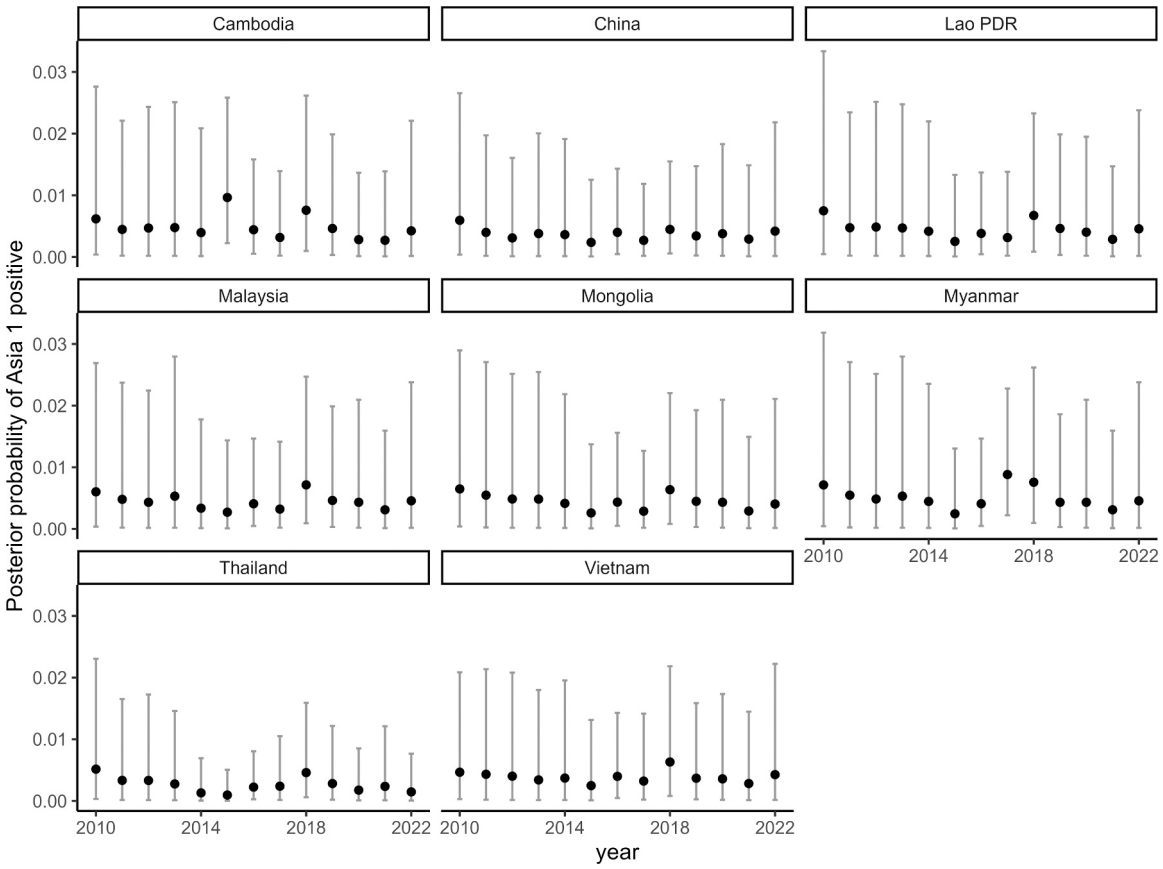

Fig. 3. Posterior positivity of foot-and-mouth disease (FMD) virus serotype Asia 1 among all clinical FMD samples sent to WRLFMD between 2010 and 2022 by countries in Southeast Asia, China and Mongolia. The error bars represent the 5th and 95th percentiles, and the points represent the median.

each country from 2010 to 2022 is shown in Fig. 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.

Responses were obtained from 20 individuals across nine countries (median: 2 per country), relative to the original 35 targeted individuals (approximate response rate: 57 %, including Indonesia). The number of responses per country was: Thailand 7, Cambodia 2, Indonesia 2, Lao PDR 2, Malaysia 2, Vietnam 2, China 1, Mongolia 1, Myanmar 1. All respondents had veterinary background, 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.

The summary results of the questionnaire survey are shown in Fig. 2. The detailed results of the questionnaire survey are provided in Supplementary Material 2. For all countries, cattle was selected as the primary livestock species susceptible to FMD; hence the scenario tree reflects passive surveillance for cattle for all countries.

3.2. Scenario tree model

The parameters estimated for use in the scenario tree models are summarised in Table 3. The estimated population sensitivity of passive surveillance for FMD detection, assuming a design annual incidence of 10 % at the village level ($DIR_{village}$) and 20 % at the animal level (DIR_{animal}), varied significantly across countries (Table 4). Mongolia had the highest population sensitivity with a median of 100.0 % (5th and 95th percentiles: 99.7 %, 100.0 %), followed by China (median: 95.9 %; 5th and 95th percentiles: 64.6 %, 100.0 %), Thailand (median: 71.5 %; 5th and 95th percentiles: 32.2 %, 94.9 %) and Malaysia (median: 16.3 %; 5th and 95th percentiles: 10.6 %, 22.6 %), while the remaining countries had extremely low median population sensitivities of below 4 %.

For Asia 1, the effective design annual incidence rates at the village level ($DIR_{village}$*), reflecting the estimated distribution of *p.Asia 1*, had a median of 0.02 % for Thailand, 0.06 % for Cambodia, China, Malaysia, Mongolia, Myanmar, and Vietnam and 0.07 % for Lao PDR. The probability of detecting serotype Asia 1 by passive surveillance was estimated to be below 7 %, with the highest in Mongolia (median: 6.7 %; 5th and 95th percentile: 1.4 %, 17.8 %), followed by China (median: 6.1 %; 5th and 95th percentile: 1.3 %, 19.1 %). When all the countries were combined, the population sensitivity for detecting Asia 1 for the whole region was a median of 14.5 % (5th and 95th percentile: 6.1 %, 28.4 %).

The estimated regional probability of freedom from Asia 1 after the first year of absence of reporting was a median of 53.9 % (5th and 95th percentiles: 51.6 %, 58.3 %). The estimated accumulated confidence in regional Asia 1 freedom increased over time, if the annual risk of introduction was below 6 % (Fig. 4). After seven years without Asia 1 detection, the median confidence of regional freedom from Asia 1 was 75 %, if the annual risk of introduction were 0 %. This cumulative confidence of regional freedom became lower with a higher annual risk of introduction, with a 47 % confidence after 7 years when an annual risk of introduction was set at 10 %.

Fig. 5 shows the estimated PRCC values, illustrating the magnitude of influence that parameter uncertainty has on the model outcome, the regional surveillance sensitivity for Asia 1 (SeP_r*). The key parameters identified as important, were those from countries with higher surveillance sensitivity, notably Mongolia and China. Particularly, the

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

Parameter	
$DIR_{village}$	0.1
DIR_{animal}	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

probability of farmers' detection for China (PRCC=0.72), the number of villages tested per year for Mongolia (0.62) and China (0.59) and the number of animals sampled per village for China (0.58) had higher PRCC values, indicating a strong correlation with the model outcomes.

In contrast, parameters from the remaining countries with lower surveillance sensitivity showed PRCC values close to 0, indicating that their uncertainty was relatively less important in the overall model conclusions.

4. Discussion

This study developed scenario tree models to estimate the sensitivity of passive surveillance, the primary method for detecting FMD in this region. To the best of authors' knowledge, this is the first study to assess whether the absence of FMDV serotype Asia 1 reports within SEACFMD indicates regional freedom from Asia 1, or if its presence has been missed by the current surveillance scheme.

Based on our scenario tree models, Mongolia and China demonstrated the highest surveillance sensitivity of approximately 100 % for FMD of any serotypes. This indicates that if FMD, of any serotypes, were circulating at or above 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 influenced by key input parameter values, such as a high number of animals tested (11–50 animals/village) and a high probability of farmers detecting clinical signs (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 surveillance sensitivity of 71 % for FMD, followed by Malaysia at 16 %. In contrast, Cambodia, Lao PDR, Myanmar and Vietnam had low surveillance sensitivities of below 4 % for FMD, suggesting that FMD in these countries would likely go unreported at or above the assumed incidence rates of 10 % at the village level and 20 % at the animal level. 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 surveillance sensitivity was notably lower than that of all FMDV serotypes combined, due to the lower design incidence rates to reflect its retrospectively low occurrence in this region. The surveillance sensitivity for Asia 1 dropped to 7 % for Mongolia and 6 % 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 15 % under the adjusted design incidence rates. 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 % (54 %). Confidence in regional freedom from Asia 1 would increase with consecutive years of no reports, only if the annual risk of introduction from other regions or from other animal populations remained below 6 %.

While the potential extinction of serotype C is currently under assessment (Paton et al., 2021), the key differences between serotypes Asia 1 and C are: (1) serotype C has not been reported globally since 2004 while Asia 1 has been evidently circulating in other parts of the world including South Asia (King et al., 2010–2022), (2) the use of vaccines against serotype C has been discontinued by many countries while trivalent vaccines against serotypes O, A and Asia 1 are still in use.

Although we considered an annual risk of introduction from 0 % to 10 % from neighbouring regions or from other animal populations, these

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 after the first year, for each country and all countries combined (region). Median and 5th and 95th percentile range are presented. The design annual incidence rate for FMD was 10 % at the village and 20 % at the animal level. The effective design incidence rate for Asia 1 was a median of 0.02 – 0.07 % at the village level and 20 % at the animal level.

	SeP (FMD)			SeP (Asia 1)			PF (Asia 1)		
	Median	5 %	95 %	Median	5 %	95 %	Median	5 %	95 %
Mongolia	100.00	99.69	100.00	6.69	1.43	17.78	51.73	50.36	54.88
China	95.88	64.62	99.97	6.14	1.31	19.14	51.58	50.33	55.29
Thailand	71.49	32.19	94.90	0.43	0.07	1.62	50.11	50.02	50.41
Malaysia	16.26	10.64	22.59	0.13	0.03	0.33	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	50.00	50.00	50.04
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	14.50	6.09	28.40	53.91	51.57	58.28

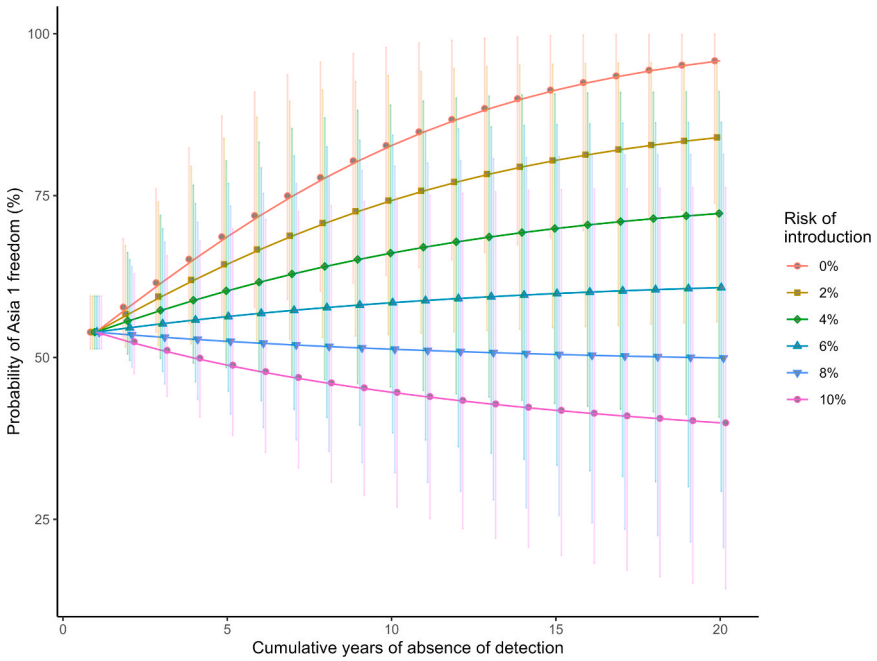

Fig. 4. Probability of regional freedom from foot-and-mouth disease (FMD) serotype Asia 1 at the assumed design incidence, given negative surveillance findings over 20 year period, with varying risk of introduction (0 %, 5 % and 10 %). The error bars represent the 5th and 95th percentiles, and the points represent the median.

assumptions are not supported by empirical data due to the absence of data. Myanmar and China share a border with India and Bangladesh, where Asia 1 is historically endemic (Aslam and 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 introduction 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 across different regions.

Standard scenario tree models have a design prevalence as a threshold, below which a population is considered free of disease. In our study, FMD was known to be endemic in the region, while the specific status of Asia 1 was unknown. Rather than directly setting the design incidence rates specifically for Asia 1, we adjusted the design incidence rates for FMD based on Asia 1 positivity. With this approach, the Asia 1 model's threshold reflected the level of Asia 1 presence expected from the past Asia 1 positivity in this region. 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 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 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.

Our models were limited to passive surveillance in the cattle populations, which were considered the most dominant livestock species across all nine countries by the experts. Although other livestock species and wildlife were not included in the model, we assumed that cattle would play a major role in passive surveillance. The addition of other streams of surveillance, such as passive surveillance in other livestock species (e.g. pigs), or active surveillance, may increase overall surveillance sensitivity. 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.

Due to limited data, we could not fully capture the heterogeneity of risk of FMDV serotype Asia 1 introduction across countries. For simplicity, we assumed that all target countries were equally exposed to the risk of Asia 1. In reality, countries such as Myanmar and China, which border Bangladesh or India where Asia 1 is known to be circulating, are likely to face a higher risk of Asia 1 introduction than other countries. Consequentially, negative surveillance results for Asia 1 in Myanmar and China could have been weighed more heavily, given their presumed higher risk. However, to maintain transparency and consistency, we developed a simplified model without differentiating risk by country. A limitation of this study is the potential bias inherent in the data collected from the questionnaire survey and the WRLFMD. Although the survey results were reviewed by the targeted experts and treated as a collective response, the initial input was limited (a median of two responses per country), which may have introduced selection, attribution, confirmation or reporting bias, or errors. 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. The WRLFMD laboratory data may be subject to submission bias. However, while clinical manifestations may vary by FMD virus strain, there is limited evidence that serotype Asia 1 consistently causes milder or more severe clinical signs compared to

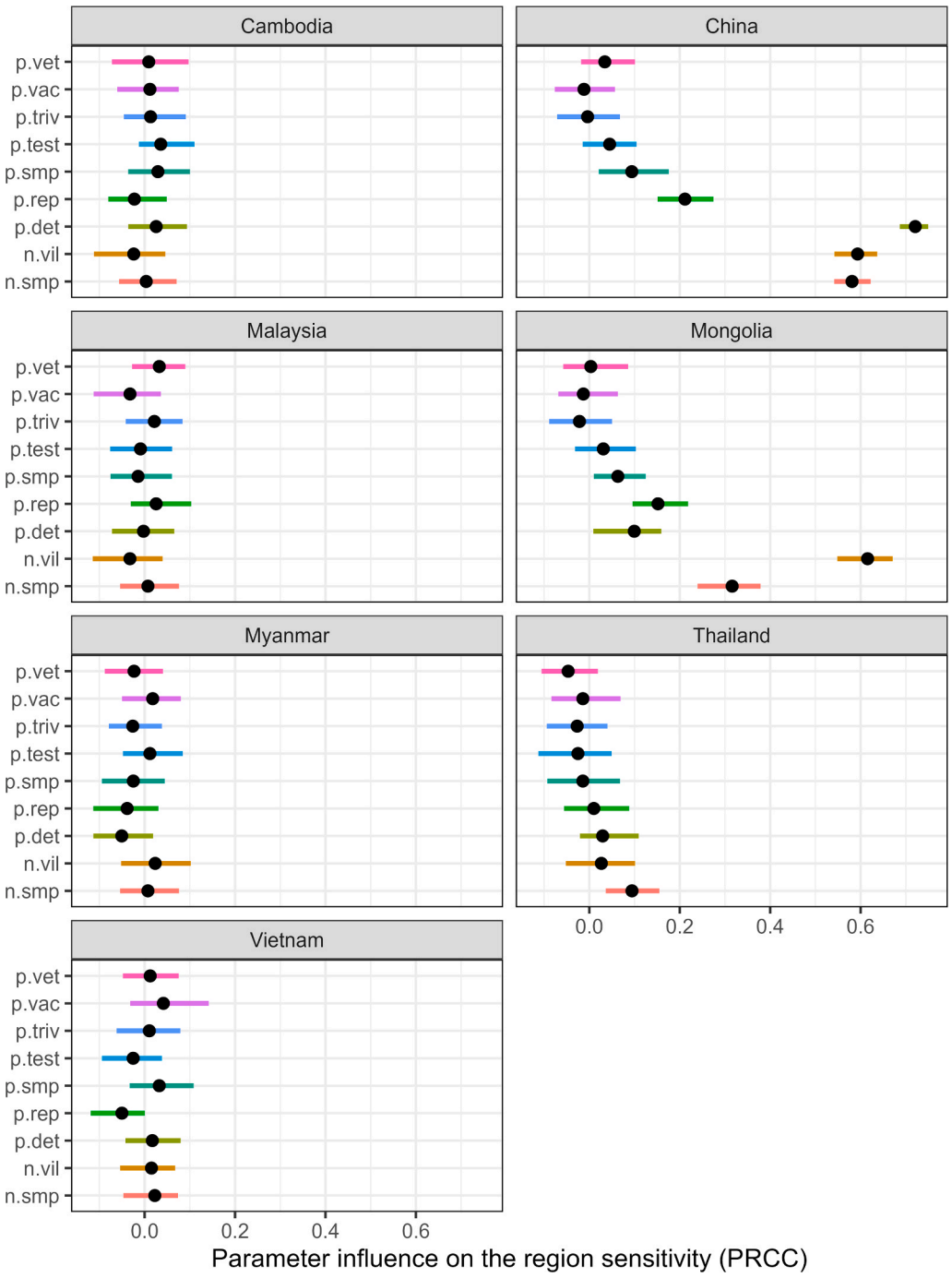

Fig. 5. Estimated partial rank correlation coefficient (PRCC) for parameters for the scenario tree model for Asia 1 on the regional surveillance sensitivity. The error bars represent 95 % confidence intervals, and the points represent the mean.

other serotypes. In South Asia, Asia 1 has been regularly detected in clinical FMD cases, aligning with the known circulation patterns of serotypes in the region (Ali et al., 2022; Islam et al., 2017). Therefore, we considered that it was unlikely that the WRLFMD data systematically underrepresent (or overrepresent) serotype Asia 1, and that any detection bias related to Asia 1, after adjusting for vaccination coverage, was likely minimal.

5. Conclusion

Based on the findings, we conclude that while passive surveillance is effective for detecting dominant FMD serotypes circulating within SEACFMD at the design annual incidence rate of 10 % at the village level and 20 % at the animal level, its sensitivity for Asia 1 is limited, because of the low expected incidence rates if it were present. The absence of FMDV serotype Asia 1 reports in recent years would not be sufficient to provide confidence in regional freedom from this serotype, when the introduction risk from South Asia is uncertain. To estimate the probability of Asia 1 freedom with a higher accuracy, further research is needed to refine key model 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.

CRediT authorship contribution statement

Ronello Abila: Writing – review & editing, Conceptualization. **Supatsak Subharat:** Writing – review & editing, Resources, Project administration, Investigation, Funding acquisition, Data curation, Conceptualization. **Ashish Sutar:** Writing – review & editing, Conceptualization. **Bolortuya Purevsuren:** Writing – review & editing, Resources, Project administration, Funding acquisition, Conceptualization. **Karma Rinzin:** Writing – review & editing, Conceptualization. **Masako Wada:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Jun-Hee Han:** Writing – review & editing, Validation, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Sub-Regional Representation for South-East Asia, World Organisation for Animal Health reports financial support was provided by Ministry of Agriculture and Rural Affairs of the People's Republic of China. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2025.106663.

References

Ali, I., Rehman, A., Mushtaq, M.H., Ijaz, M., Khaliq, M.S., Khan, M.S.U., Khalid, S., Masud, A., Abbas, A., Parveen, S., Saman, A., Sauter-Louis, C., Conraths, F.J., 2022. Outbreak investigation and identification of risk factors associated with the occurrence of foot and mouth disease in punjab, Pakistan. Prev. Vet. Med. 202, 105613. https://doi.org/10.1016/j.prevetmed.2022.105613.

Aslam, M., Alkheraije, K.A., 2023. The prevalence of foot-and-mouth disease in Asia. Front. Vet. Sci. 10. https://doi.org/10.3389/fvets.2023.1201578.

Auplish, A., Vu, T.T.T., Pham Duc, P., Green, A., Tiwari, H., Housen, T., Stevenson, M.A., Dhand, N., 2024. Capacity and needs assessment of veterinary services in Vietnam in biosecurity, biosafety and one health. PLoS One 19 (1), e0295898. https://doi.org/10.1371/journal.pone.0295898.

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. Article e171 Epidemiol. Infect. 147, 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. Int. Stat. Rev. 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. Transbound. Emerg. Dis. 66 (2), 1067–1072. 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. Transbound. Emerg. Dis. 64 (2), 316–332. https://doi.org/10.1111/tbed.12373.

Cannon, R.M., 2002. Demonstrating disease freedom—combining confidence levels. Prev. Vet. Med. 52 (3), 227–249. 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.

Islam, M.S., Habib, M.A., Islam, M.R., Mahmud, M.S., Saha, P.C., Ruba, T., Das, P.M., Khan, M.A.H., 2017. Clinicopathological investigation of foot and mouth disease and serotype identification of the viruses in cattle of Bangladesh. Immunology Infectious Diseases(CEASE PUBLICATION) 5 (2), 16–23. https://doi.org/10.13189/iid.2017.050202.

Kenubih, A., 2021. Foot and mouth disease vaccine development and challenges in inducing Long-Lasting immunity: trends and current perspectives. Vet. Med (Auckl.) 12, 205–215. https://doi.org/10.2147/vmrr.S319761.

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. Vet. Sci. 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 Evol. 7 (1). https://doi.org/10.1093/ve/veab009.

Robinson, L., Knight-Jones, T.J., Charleston, B., Rodriguez, L.L., Gay, C.G., Sumption, K. J., Vosloo, W., 2016. Global foot-and-mouth disease research update and gap analysis: 7 - pathogenesis and molecular biology. Transbound. Emerg. Dis. 63 (1), 63–71. https://doi.org/10.1111/tbed.12520.

Singh, R.K., Sharma, G.K., Mahajan, S., Dhama, K., Basagoudanavar, S.H., Hosamani, M., Sreenivasa, B.P., Chaicumpa, W., Gupta, V.K., Sanyal, A., 2019. Foot-and-Mouth disease virus: immunobiology, advances in vaccines and vaccination strategies addressing vaccine failures-an Indian perspective. Vaccines (Basel) 7 (3). https://doi.org/10.3390/vaccines7030090.

Subharat, S., Meunsene, D., Putthana, V., Tiwari, H., Firestone, S.M., 2023. Field epidemiology capacity of The National veterinary services of Lao PDR: an online survey. Front. Vet. Sci. 10. https://doi.org/10.3389/fvets.2023.1096554.

Tum, S., Robertson, I.D., Edwards, J., Abila, R., Morzaria, S., 2015. Seroprevalence of foot-and-mouth disease in the Southern provinces of Cambodia. Trop. Anim. Health Prod. 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.