



Current Status and Challenges in the Control of Foot-And-Mouth Disease in Vietnam: Epidemiological, Vaccination, and Molecular Perspectives (2021–2024)

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ARTICLE INFO	ABSTRACT
Published Online: 03 July 2025	Foot-and-mouth disease (FMD) continues to pose a substantial threat to livestock production in Vietnam, primarily due to the dominance of smallholder farming systems and inadequate biosecurity practices. This study provides a comprehensive assessment of the current status, epidemiological trends, and control measures for FMD in Vietnam, with particular emphasis on recent outbreaks, molecular identification of viral serotypes, and regional comparisons. Drawing on official data from national surveillance programs, peer-reviewed molecular studies, and international reports spanning 2007 to 2024, the research identifies serotype O (Southeast Asia topotype, Mya-98 lineage) as the most commonly detected strain in Vietnam. Phylogenetic analyses reveal a high degree of genetic similarity between Vietnamese isolates and strains circulating in neighboring countries such as China, South Korea, and Laos. Despite advancements in domestic vaccine development and production, Vietnam continues to face major challenges, including inconsistent disease surveillance, limited sample collection from historical hotspots, and inadequate implementation of nationwide vaccination strategies. Genetic divergence among circulating strains further underscores the need for continuous molecular monitoring and periodic vaccine updates. Compared to regional counterparts, Vietnam lags in terms of outbreak response capacity, laboratory infrastructure, and inter-agency coordination. To improve FMD control and progress toward eradication, it is essential to enhance local surveillance systems, strengthen regional collaboration, and adopt a more dynamic and data-driven vaccination policy.
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I. INTRODUCTION

Foot-and-mouth disease (FMD) is an acute and highly contagious viral infection affecting clovenhoofed animals, including buffaloes, cattle, goats, sheep, and pigs. The etiological agent, foot-and-mouth disease virus (FMDV), belongs to the genus *Aphthovirus* in the family *Picornaviridae* and is classified into seven immunologically distinct serotypes: A, O, C, SAT1, SAT2, SAT3, and Asia 1. Since 2004, however, no cases of serotype C have been reported to the World Organisation for Animal Health (WOAH) or the Food and Agriculture Organization (FAO), while the remaining serotypes continue to circulate in various regions globally [17].

FMD is characterized by its rapid transmission and high infectivity, with morbidity rates approaching 100% in

susceptible populations. The disease remains endemic in over 100 countries, particularly in Africa, the Middle East, and Asia [16]. It is estimated that approximately 77% of the global livestock population resides in areas where FMD is still present, including large parts of Asia, Africa, and the Middle East, as well as limited regions of South America [1, 17].

In Southeast and East Asia, FMD prevalence varies by country. High incidence rates have been reported in Cambodia, Thailand, Laos, China, and Vietnam. Although some countries remain FMD-free without implementing vaccination programs, they remain vulnerable to reintroduction due to transboundary livestock movement and regional disease dynamics [17].

Clinically, FMD manifests as fever, lameness, excessive salivation, and vesicular lesions on the tongue, hooves, and udders [2]. The virus is shed in high concentrations through vesicular fluid, epithelial tissue, aerosols, respiratory droplets, milk, urine, and semen of infected animals. Transmission occurs primarily through direct contact with infected secretions, as well as via indirect routes including contaminated environments, fomites, and mechanical vectors such as humans, vehicles, wildlife, and birds [3].

FMD results in substantial economic losses through reduced milk yield (up to 33%), decreased weight gain, calf mortality, abortions, and the loss of draft power [4]. Although mortality is generally low, the disease exerts a disproportionate economic burden due to the high number of animals affected. Losses arise from diminished productivity, altered herd dynamics, high costs of vaccination and disease control, and limitations on international trade. In endemic regions, the combined annual economic impact of production losses and vaccination efforts is estimated to range from USD 6.5 to 21 billion.

Given its potential for rapid spread and profound economic consequences, FMD is classified as a Category A disease by the World Organisation for Animal Health (WOAH), signifying a highly transmissible infection that mandates immediate notification. Countries affected by FMD face strict trade sanctions and are barred from exporting live animals and animal products.

In Vietnam, FMD has been endemic for over a century. The most severe recent outbreak occurred between 2006 and 2012, during which more than 200,000 livestock were infected, with an average of 32,000 cases per year. A notable resurgence in 2018–2019 primarily affected pigs that were not vaccinated, as they were excluded from the mandatory vaccination list under the National Program for FMD Prevention and Control (2016–2020). This policy gap led to significant financial losses for producers and undermined Vietnam’s ability to participate in international trade [<https://nongnghiep.vn/thanh-toan-benh-lo-mom-long-mong-bai-cuoi-da-giam-tren-90tai-viet-nam-d366928.html>], Source: Agriculture Newspaper, 2024].

To address persistent challenges, the Vietnamese government has taken strategic action. On

October 22, 2020, the Prime Minister issued Decision No. 1632/QĐ-TTg, formally approving the National Program for the Prevention and Control of Foot-and-Mouth Disease (2021–2025). This marked the first time an FMD control program received direct approval at the national executive level, underscoring the disease’s strategic significance. The program provides detailed guidance and a unified framework for ministries, local authorities, private stakeholders, and the general public to implement coordinated disease control efforts.

This study aims to compile and analyze the recent epidemiological status of FMD in Vietnam from 2021 to

2024, identify ongoing challenges, and propose new directions for disease prevention and control. The analysis is aligned with the objectives set forth in Decision No. 1632/QĐ-TTg and is intended to support national efforts toward the long-term eradication of FMD.

II. METHODOLOGY

1. Data Sources

Data were collected from a wide range of sources, including peer-reviewed international journal articles, research reports, scientific and technical bulletins, and official websites of relevant governmental and international agencies. The selected documents, published between 2006 and 2024, provided comprehensive information on the epidemiological status, outbreak characteristics, and economic impact of foot-and-mouth disease (FMD) in Vietnam. Additionally, molecular data from published studies were reviewed to evaluate the evolutionary dynamics and genetic variability of FMDV.

2. Data Collection, Synthesis, Analysis, and Visualization

2.1. Traditional Epidemiological Analysis

Reports on FMD outbreaks were compiled, focusing on infection rates, number of reported cases, and the spatiotemporal distribution of outbreaks across different provinces and time periods. These data were used to identify potential risk factors such as animal movement routes, farming practices, and regional biosecurity measures. Epidemic trends and transmission dynamics were visualized using outbreak progression maps and spatial analysis tools.

2.2. Molecular Epidemiological Assessment

Published molecular studies involving nucleotide sequencing of FMDV isolates were analyzed to identify prevalent viral serotypes and potential recombinant variants. Emphasis was placed on tracking mutational patterns, assessing possible vaccine escape mutations, and evaluating phylogenetic relationships between Vietnamese and regional virus strains. These analyses aimed to inform future projections of viral transmission and support improved vaccine development and selection.

III. SUMMARY OF RESEARCH RESULTS

3.1. Epidemiological Overview of FMD in Vietnam

Foot-and-mouth disease (FMD) was first recorded in Vietnam in 1898 in Nha Trang, Khanh Hoa Province (Dao Trong Dat, 2000). Initially concentrated in the southern provinces bordering Cambodia (1954–1975), the disease gradually became endemic nationwide, now present in all 63 provinces and municipalities.

To date, three FMDV serotypes—O, A, and Asia 1—have been detected in Vietnam, with serotype O being the most prevalent. According to Associate Professor Nguyen Van Giap (Vietnam

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National University of Agriculture), serotype O remains the dominant strain in circulation (source: Agriculture Newspaper). Although mortality rates are low, FMD is designated by the World Organisation for Animal Health (WOAH) as a notifiable disease due to its severe trade implications. Active outbreaks result in export bans on live animals and related products, causing significant economic and social disruption.

From 2021 to 2024, data from the Ministry of Agriculture and Rural Development (MARD) recorded 211 FMD outbreaks in 211 communes, 134 districts, and 61 provinces. A total of 7,361 animals were infected, with 645 animals either culled or deceased. Affected species included 5,359 cattle, 1,515 buffaloes, 442 pigs, and 45 goats.

MARD attributed the persistent recurrence of FMD to multiple factors: re-emergence in historical hotspots, insufficient vaccination coverage, uncontrolled animal movement, delayed or underreported cases, and inconsistent local enforcement. Many outbreaks were only identified through clinical signs, without laboratory confirmation or official declaration, allowing further transmission.

Temporal Patterns of FMD Outbreaks (2021–2024)

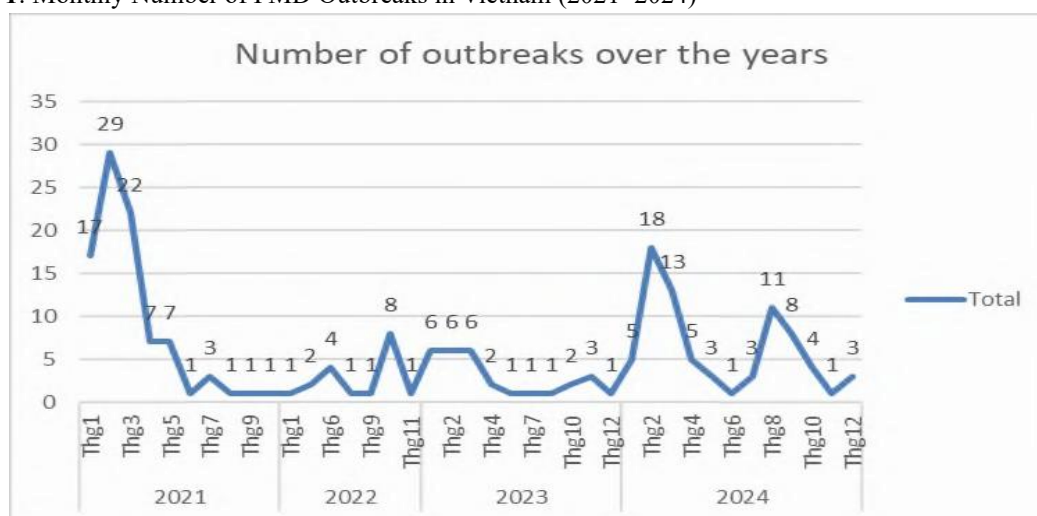
Analysis of monthly outbreak data shows no consistent seasonal trend. Key patterns include:

- **2021:** Peak in February (29 outbreaks), lowest in June (1 outbreak).
- **2022:** Modest increase in October (8 outbreaks), followed by a sharp decline.
- **2023:** Sporadic and low outbreak numbers, reflecting improved control.
- **2024:** A sudden resurgence in February (18 outbreaks), again with low incidence in June and November.

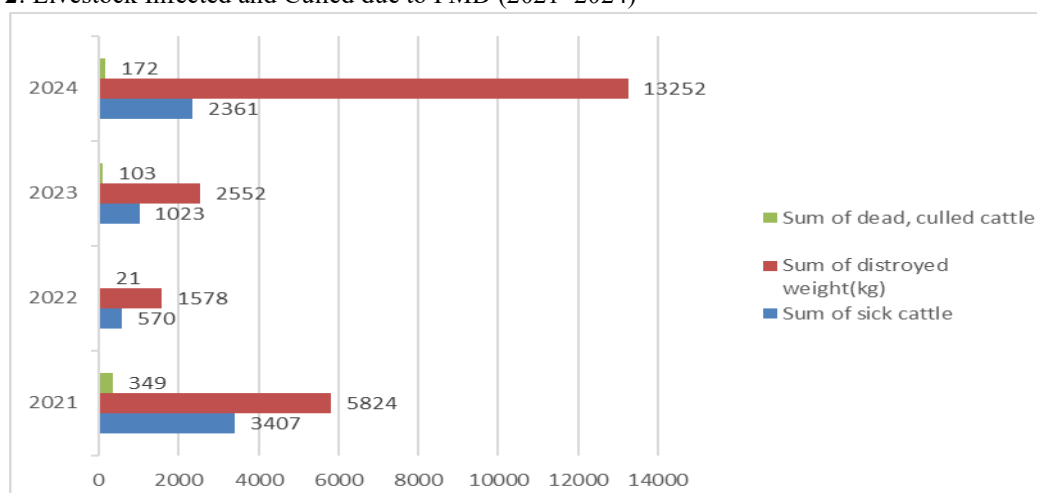
These irregular patterns suggest that temporary improvements may create a false sense of security, leading to decreased vigilance and renewed outbreaks. A critical concern is the presence of clinically recovered but asymptomatic carrier animals, particularly cattle and buffaloes. These carriers can shed the virus for months or even years, contributing to re-infection and the spread of FMDV through unregulated trade and slaughter activities.

Figures and Tables

- **Chart 1:** Monthly Number of FMD Outbreaks in Vietnam (2021–2024)



- **Chart 2:** Livestock Infected and Culled due to FMD (2021–2024)



Trends in Outbreak Magnitude

Table 1. The epidemic progression during 2021–2024 reveals complex and fluctuating dynamics:

Time of Outbreak Detection	Location	Scale of influence	Statistics	Locality detected epidemic, disease type
02/01/2021	18 provinces Key: Quang Ngai Ha Tinh, Kon Tum Son La, Bac Kan	sick 3407 cattle	349 cattle died and were destroyed Amount destroyed: 5824 kg	The outbreak started in Tien Giang, type O.
02/01/2022	8 provinces: Bac Kan, Dong Thap Gia Lai, Hanoi Ha Tinh, Son La Thai Nguyen	sick 570 cattle	21 cattle died and were destroyed Amount destroyed: 1578kg	The outbreak started in Ky Anh, Ha Tinh, type O.
04/01/2023	14 provinces: Ben Tre, Cao Bang, Dak Lak, Dong Thap Gia Lai, Hoa Binh Lang Son, Long An Ninh Binh, Phu Yen Quang Ngai, Son La Thai Nguyen	sick 1023 cattle	103 cattle died and were destroyed Amount destroyed: 2552 kg	The outbreak started in Ha Long, Cao Bang, Typ O
01/01/2024	22 provinces and cities	sick 2361 cattle	172 cattle died and were destroyed	The outbreak started in Lang Son, Hoa Binh, Typ O
			Amount destroyed: 13252 kg	

(Source: Report of the Department of Animal Health (Ministry of Agriculture and Rural Development, Vietnam 2024):

Epidemiological Considerations

The recurrence of outbreaks despite vaccination coverage rates exceeding 100% in designated zones (e.g., 101.68% in 2024) indicates persistent gaps in disease surveillance and enforcement. Notably, 2023 marked a temporary decline in cases, likely reflecting the impact of the National Program for FMD Prevention and Control (2021–2025). However, the resurgence in 2024 underscores the need for enhanced biosecurity, improved detection, and better inter-agency coordination.

3.2. Pathology of Foot-and-Mouth Disease (FMD)

The incubation period of Foot-and-Mouth Disease Virus (FMDV) typically ranges from 1 to 12 days [1], [2], after which clinical manifestations appear in infected animals. Affected livestock exhibit high fever (40–41°C) accompanied by the development of vesicles in thin-skinned regions such

as the tongue, oral mucosa, dental pad, lips, gums, snout, interdigital spaces, and, in lactating females, the udder. In acute cases, symptoms include excessive salivation, reluctance or inability to stand, and prolonged recumbency. Vesicles may rupture and coalesce into erosive lesions, which generally resolve within approximately 11 days. Secondary bacterial infections are common, particularly mastitis in dairy cattle, due to vesicular lesions on the udder, leading to reduced milk production and overall debilitation. In young calves, FMDV may cause sudden death without preceding clinical signs, often associated with viral myocardial degeneration—a condition referred to as “tiger heart” lesions [3], [17]. Following recovery, ruminants may become asymptomatic carriers, capable of harboring and shedding the virus for extended periods. These carrier animals represent a significant reservoir and epidemiological risk for disease

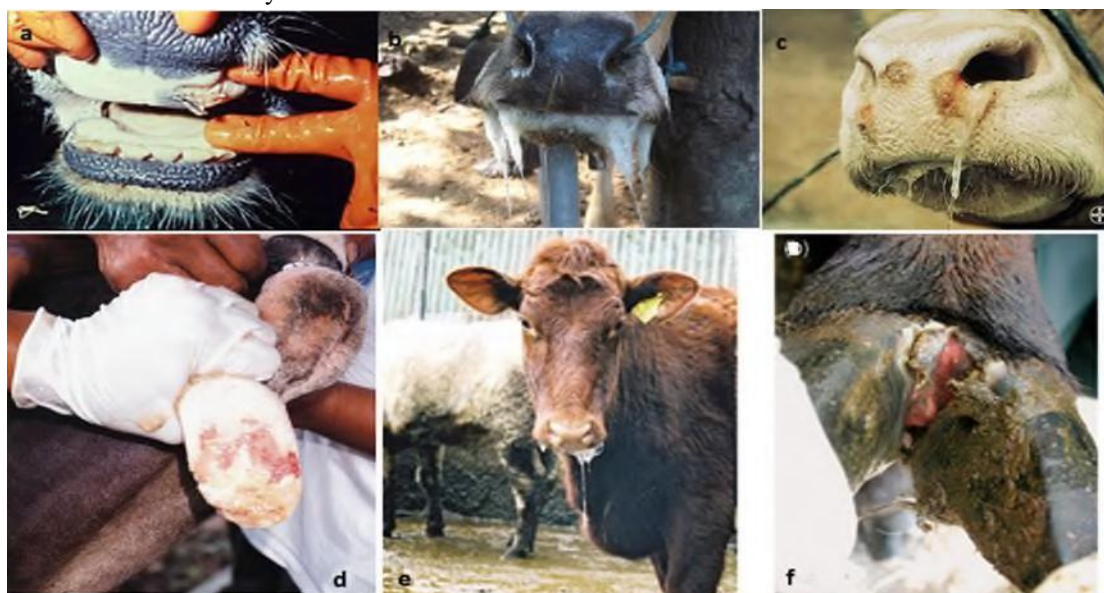
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recurrence. Conversely, domestic pigs do not become long-term carriers; however, transient persistence of FMDV RNA

and proteins in lymphoid tissues is frequently observed post-infection, both in clinical and subclinical cases [4].

Figure 1. Clinical signs of FMD in cattle and buffaloes

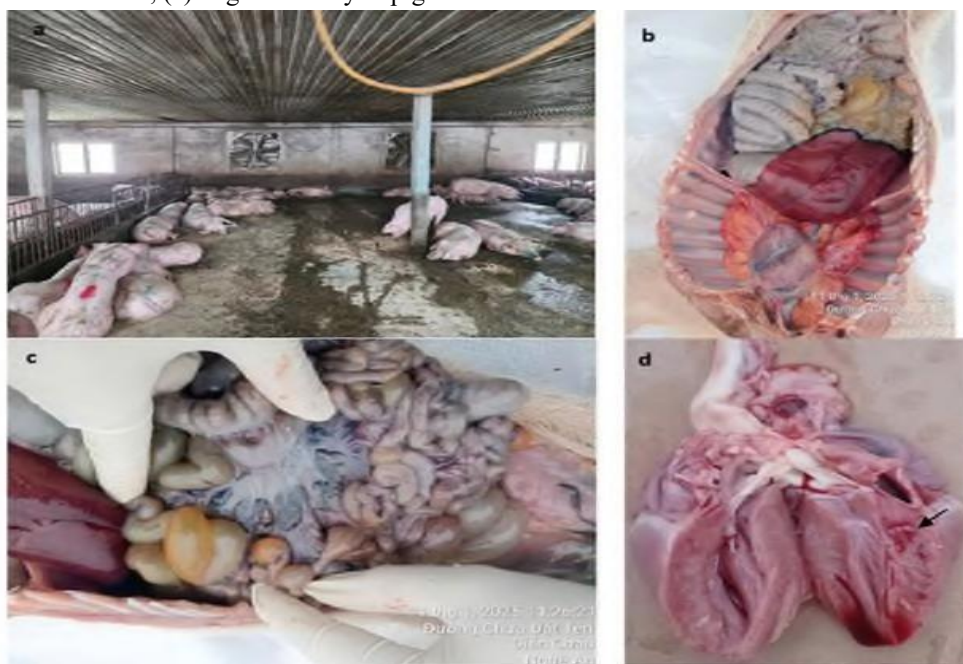
- (a) Ruptured vesicles on the gingiva;
- (b) Profuse salivation;
- (c) Nasal discharge;
- (d) Vesicular erosion on the tongue;
- (f) Interdigital inflammation secondary to bacterial infection.



Source: Wikipedia – Foot-and-mouth disease; North Dakota Department of Agriculture.

Figure 2. Clinical signs of FMD in pigs

- (a) Fever and lethargy;
- (b) Damaged hooves;
- (c) Vesicular lesions on the snout; (e) High mortality in pig herds.



Source: Photographic documentation from a pig farm in Ninh Binh Province, Vietnam.

Figure 3. Pathological lesions associated with FMD in pigs

- (a) Fever, lethargy, and piglet mortality;
- (b) Flaccid myocardium with localized hemorrhages;
- (c) Hemorrhagic mesenteric lymph nodes;
- (d) Myocardial necrosis in a 3-week-old piglet (arrow) that died on February 11, 2025.



Source: Photographic documentation from a pig farm in Dien Chau District, Nghe An Province, Vietnam.

These observations are consistent with previous literature [1–3], which emphasizes that while FMD rarely causes mortality in adult animals, it remains a major cause of death in young livestock due to viral myocarditis.

3.3. Disease Progression and Epidemiological Data

The progression of the Foot-and-Mouth Disease (FMD) epidemic in Vietnam between 2021 and 2024 exhibited a highly complex and heterogeneous pattern, lacking any consistent seasonal or geographic trends. Outbreaks were recorded across a wide range of provinces and municipalities, with a noticeable concentration in high-risk and border regions characterized by rugged terrain, porous borders, and diverse livestock production systems.

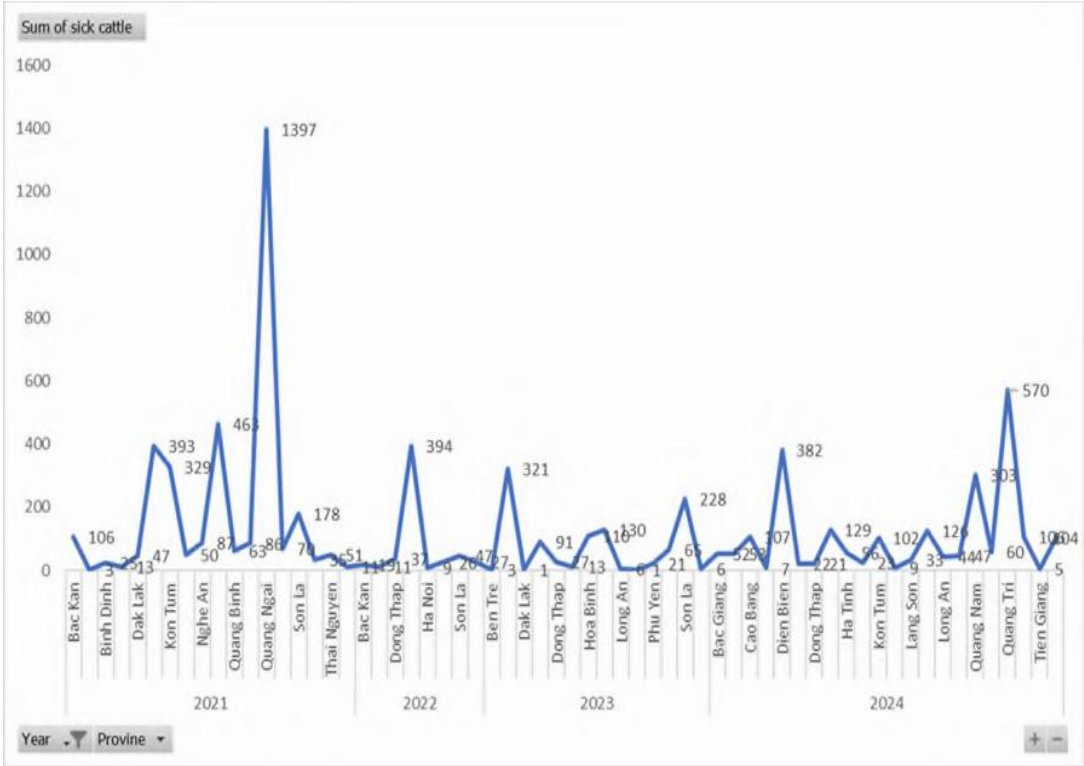
In 2021, the highest numbers of infected, deceased, and culled animals were reported, marking the peak of the epidemic during the study period. Quang Ngai Province recorded the most severe outbreak, with a total of 1,397 affected animals—surpassing all other provinces. Several

localities experienced repeated outbreaks over consecutive years, including Bac Kan (2021, 2022), Dong Thap (2022–2024), and Son La (2021–2023) (Figure 4).

Notable epidemic peaks were observed in February 2021, August 2022, and March 2024, coinciding partially with the dry season in many regions. These findings are consistent with the observations of Hu Suk Lee et al. (2020), who noted that FMD is endemic in Vietnam, with increased outbreak activity typically occurring during the dry season (November–March), particularly outside the Central Highlands.

The current study contributes to the growing body of knowledge on FMD epidemiology in Southeast Asia and provides critical insights for policymakers. Specifically, identifying temporal and geographic outbreak hotspots can facilitate the design of more effective surveillance systems and targeted vaccination campaigns under the National Program for the Prevention and Control of FMD (2021–2025).

Figure 4. Total number of animals affected by FMD in Vietnamese provinces, 2021–2024



This figure provides a comparative overview of provinces reporting the highest cumulative numbers of sick, dead, and culled animals. Quang Ngai exhibited the most severe outbreak, while Bac Kan, Dong Thap, and Son La

experienced recurrent annual epidemics. The data highlight regional disparities in outbreak severity and underline the need for geographically targeted control measures.

Figure 5. Temporal dynamics of FMD outbreaks in Vietnam, 2021–2024

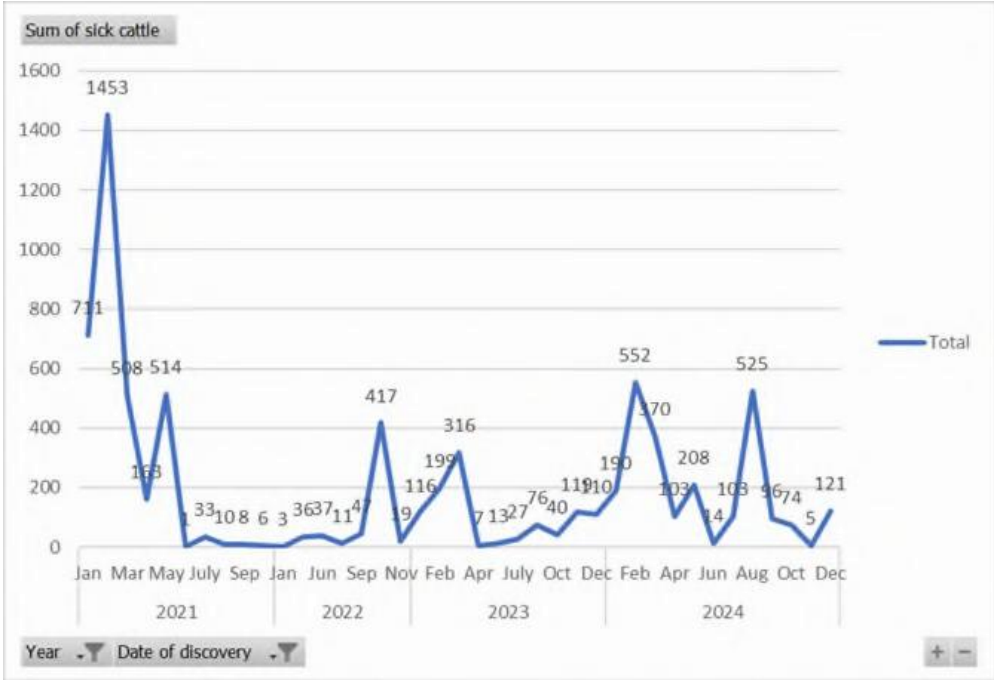
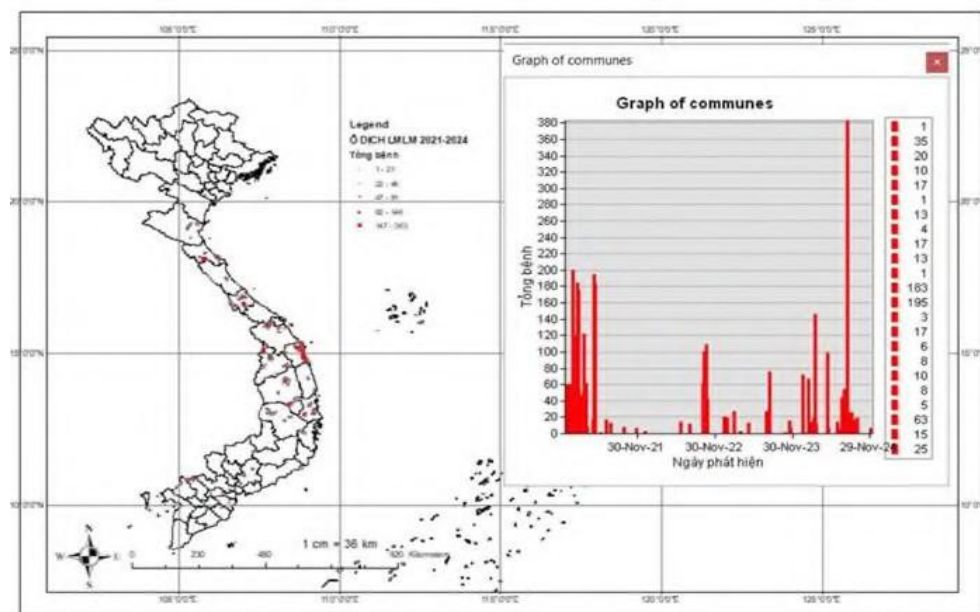


Figure 6. Spatiotemporal spread of FMD outbreaks in Vietnam (Feb 2021–Dec 2024)



Panel A maps the spatial distribution of outbreaks, revealing provinces with high recurrence rates and those situated along international borders. Panel B presents a timeline of outbreak emergence, allowing for assessment of epidemic velocity and the potential influence of intervention measures implemented under the national control strategy. These data offer an important basis for evaluating outbreak trajectories and refining future control programs.

Despite modest progress observed in 2022 and 2023, the resurgence of outbreaks in 2024 underscores persistent weaknesses in Vietnam’s FMD surveillance and control infrastructure. These include uneven vaccination coverage, limited public awareness, delayed reporting, and insufficient regulation of animal movement—particularly across provincial and international borders.

To achieve the long-term goal of FMD containment and eradication, it is essential that authorities in affected localities intensify public communication, expand vaccination efforts, and implement stricter controls on livestock transportation. These actions are critical to minimizing the economic losses associated with trade restrictions and preventing future disease resurgence.

3.4. Specific Data by Year

The Foot-and-Mouth Disease (FMD) epidemic in Vietnam from 2021 to 2024 exhibited considerable interannual

variation in outbreak frequency, geographic distribution, and species affected (Figure 7, Table 3).

In **2021**, FMD was first detected in pig herds in Cai Be District, Tien Giang Province, with 35 pigs culled, corresponding to a total culling weight of 3,917 kg. The disease quickly spread nationwide, resulting in **3,407 infected animals** and **349 deaths or cullings**, including:

- 2,804 cattle (72.8%)
- 376 buffaloes (20.6%)
- 182 pigs (6.0%)
- 45 goats (0.6%)

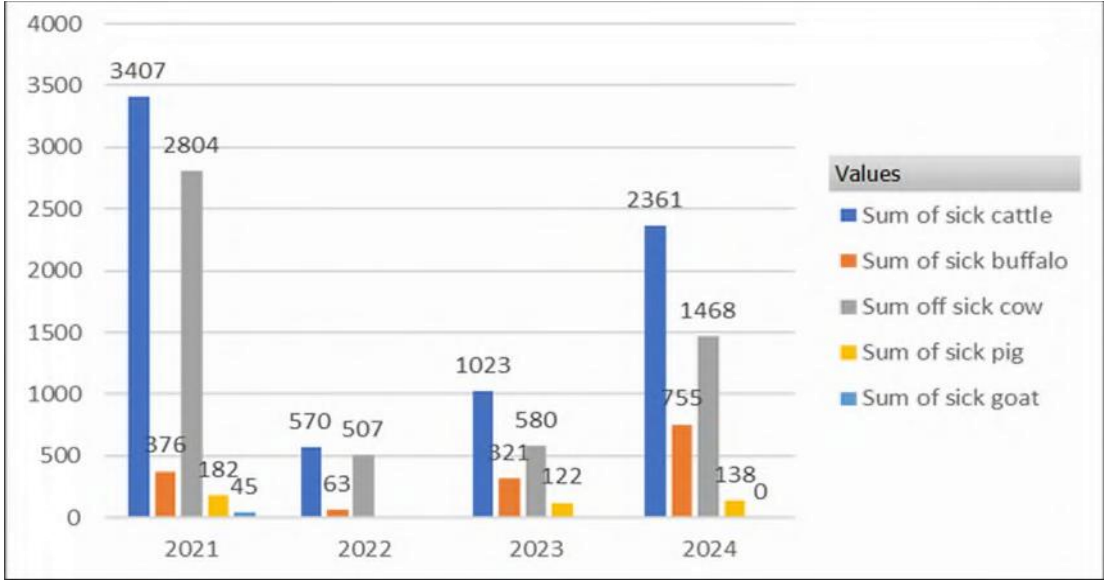
In **2022** and **2023**, there was a marked decline in both the number of outbreaks and affected animals, suggesting temporary improvements in disease control, possibly attributable to intensified vaccination and biosecurity measures.

However, a resurgence occurred in **2024**, with **75 outbreaks** reported across **22 provinces**, leading to **2,361 infected animals** and **172 animals culled or deceased**, comprising:

- 1,468 cattle
- 755 buffaloes
- 138 pigs

These figures reflect fluctuating epidemic intensity and underscore the persistent risk of FMD reemergence, particularly in provinces with a history of recurrent outbreaks.

Figure 7. Total number of livestock affected by FMD in Vietnam (2021–2024)



This figure illustrates annual FMD statistics by species (cattle, buffaloes, pigs, and goats). A sharp peak in 2021 was followed by a decline in 2022–2023, with a notable

resurgence in 2024. Cattle consistently represented the majority of affected livestock across all years

Table 3. Summary of Major Developments in the FMD Situation in Vietnam (2021–2024)

Year	Disease Progression	Number of Infected Animals	Number of Culled Animals	Culling Weight (kg)	Affected Areas	Total Vaccination	Response Measures
2021	Outbreaks increased significantly, spreading across multiple provinces, especially in mountainous areas and North Central regions.	3407	349	5824	18 provines & cities, 89 outbreak	Không rõ	Implemented measures under the “National Program for FMD Prevention and Control 2021-2025”
2022	Compared to 2021, the number of outbreaks, infected cases, and affected provinces decreased significantly.	570	21	1578	8 provines & cities, 18 outbreak	Không rõ	Implemented measures under the “National Program for FMD Prevention and Control 2021-2025
2023	The number of outbreaks and cullings decreased sharply compared to 2021.	1023	103	2552	13 provines, 29 outbreak	785	Monitored the disease in key areas, implemented biosecure livestock practices, and conducted vaccination campaigns.

2024	The disease resurged, with 75 outbreaks and signs of further spread.	2361	172	13252	22 provinces & cities, 75 outbreak	183	Monitored the disease in key areas and conducted targeted vaccination campaigns, achieving a 101,68% coverage rate.
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Several factors have contributed to the recurring nature of FMD outbreaks in Vietnam. Notably, livestock that appear clinically recovered may continue to shed the virus into the environment for extended periods. This persistent viral shedding, combined with variable climatic conditions and increased animal trade and transportation, substantially raises the risk of re-emergence— particularly in unvaccinated or partially vaccinated herds.

Molecular epidemiological studies have further revealed a genetic divergence between circulating field strains and the strains used in commercially available vaccines. Specifically, amino acid variations in the VP1 protein have been documented, indicating antigenic mismatches that may reduce vaccine efficacy (Van Diep N. et al., 2020) [5]. This is consistent with the occurrence of FMD outbreaks even among vaccinated livestock populations.

Recent outbreaks have been predominantly caused by serotype O, which remains the most prevalent FMDV serotype in Vietnam. Genetic analysis of field strains has consistently identified the O/Mya-98 lineage of the O/Southeast Asia genotype as the causative variant. Nucleotide identity among these strains ranged from 99.06% to 100%, with amino acid similarity from 97.65% to 100%, indicating that these are locally re-emerging strains rather than new introductions (Nguyen Van Diep et al., 2020) [5]. These findings underscore the critical importance of continuous molecular surveillance and regular updating of vaccine strains to better match circulating field viruses. Improved antigenic compatibility is essential for enhancing vaccine effectiveness and reducing the risk of future outbreaks.

3.5. Molecular Characteristics of Circulating FMDV in Vietnam

Molecular epidemiology and genome sequencing have become essential tools in understanding the evolution and transmission of FMDV. These approaches help identify antigenic variations among strains and support the design of effective vaccines. The World Organisation for Animal Health (WOAH) maintains a global network of reference laboratories that regularly monitor FMDV evolution and provide guidance for vaccine updates.

In Vietnam, numerous studies have focused on the VP1 coding region of FMDV, a critical determinant of host immune recognition and viral serotype specificity. VP1-based phylogenetic analyses have revealed the diversity, evolutionary relationships, and origins of FMD outbreaks. These data are crucial for evaluating the compatibility between field strains and vaccine strains.

The first comprehensive analysis of serotype A FMDV in Vietnam was conducted by Le et al. (2010) [7], who sequenced six isolates from the 2009 outbreaks. All belonged to genotype IX and exhibited 98.1–100% amino acid similarity in VP1, showing close genetic relationships with strains from Laos, Thailand, and Malaysia. These isolates shared a unique deletion at position 140 in VP1, absent in older and global strains.

In the same year, Le et al. (2010) [6] also reported on the complete genome sequences of four serotype O and two Asia 1 isolates. The serotype O viruses belonged to the SEA/Mya-98 lineage and displayed high genetic similarity with other Southeast Asian strains. This marked a shift from earlier lineages such as Cam-94, ME-SA, and Cathay. Asia 1 strains were classified into genogroups IV and V.

More recent studies by Van Diep et al. (2020) [5] and others confirmed that recurrent serotype O outbreaks in Vietnam from 2021 to 2024 were caused by viruses within the O/SEA/Mya-98 lineage, showing 99.06–100% nucleotide and 97.65–100% amino acid identity—evidence of local re-emergence. These field strains exhibited antigenic divergence from vaccine strains, highlighting the need for local surveillance and vaccine updates.

Serotype O remains the most prevalent in Vietnam, followed by serotype A. During the 2021– 2024 period, both SEA and ME-SA genotypes of serotype O were detected, while serotype A viruses consistently belonged to genotype IX. Phylogenetic data revealed strong genetic links between Vietnamese strains and isolates from neighboring countries, reflecting transboundary spread.

FMDV is a single-stranded RNA virus with four structural proteins (VP1–VP4) and several nonstructural proteins. Among these, VP1 is the most variable and immunodominant, making it a primary target for genotyping and vaccine design (Samuel & Knowles, 2001; Knowles et al., 2005). Extensive VP1 analyses conducted between 2006

and 2014, particularly in northern and central Vietnam, emphasized the vulnerability of border provinces with active livestock trade, such as those adjacent to China, Laos, Cambodia, and Thailand [9, 14, 16]. Recent findings continue to confirm the predominance of serotype O in Vietnam (Nguyen et al., 2023) [8].

Figure 8. Phylogenetic trees of FMDV based on the nucleotide sequences of the VP1 gene. The phylogenetic trees were constructed using the Neighbor-Joining method in MEGA X software (<https://www.megasoftware.net/>), based on nucleotide sequences of the VP1 coding gene. Bootstrap values greater than 70% (based on 1000 replicates) are shown

at the nodes to indicate the robustness of the branches. Field strains of FMDV collected and analyzed in this study are marked with black circles, whereas the vaccine strains used for comparative purposes are marked with black triangles. This analysis reveals the genetic relationships between circulating strains and vaccine strains, allowing for the assessment of genetic drift and the suitability of current vaccines for effective immunization.

(Source: Ngoc Hai Nguyen et al., 2023. *Phylogenetic and genotypic characteristics of the foot-and-mouth disease virus from outbreaks in southern Vietnam, 2019*, *Virology* 582: 43–47. <https://doi.org/10.1016/j.virol.2023.03.010>)

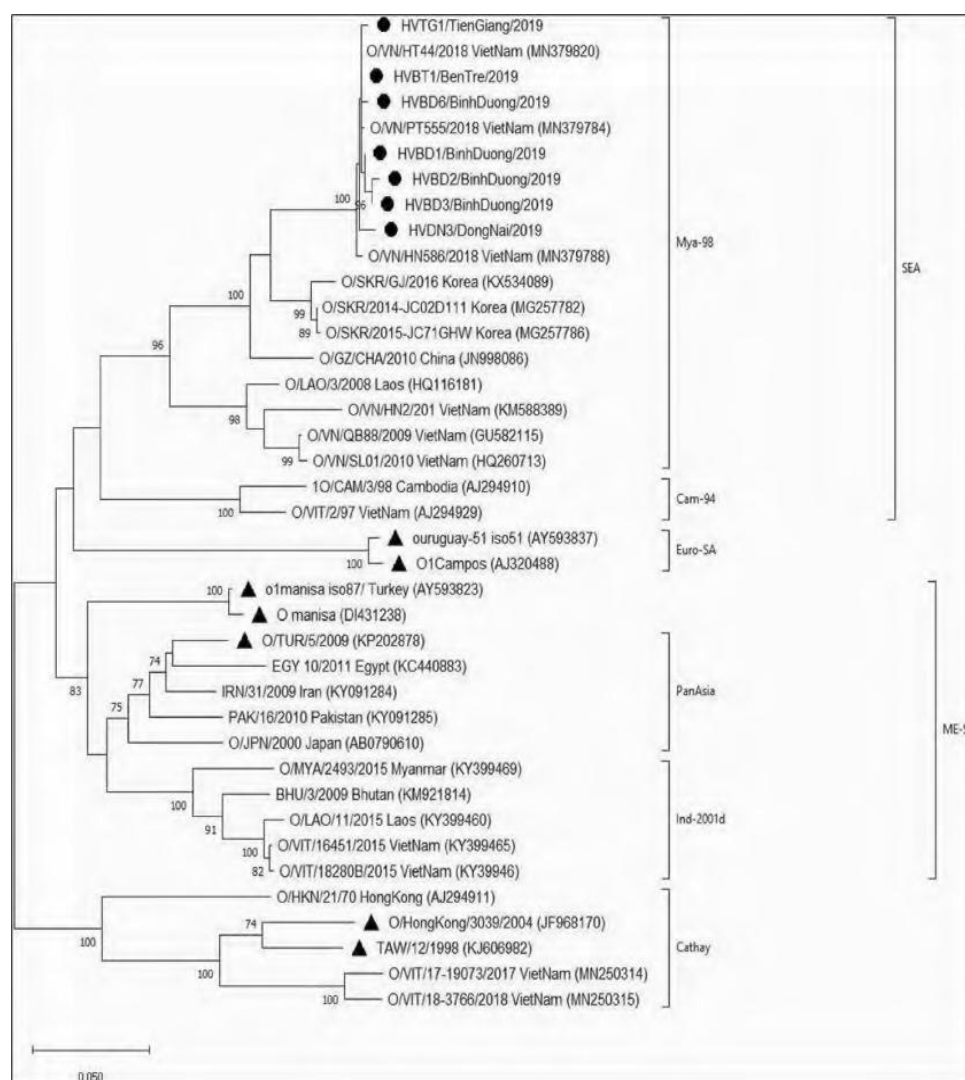


Figure 8. Phylogenetic tree based on VP1 nucleotide sequences (Nguyen et al., 2023): The phylogenetic tree was generated using the Neighbor-Joining method with 1,000 bootstrap replicates in MEGA X. Black circles represent field strains from this study, while black triangles denote reference vaccine strains. The analysis highlights genetic divergence between circulating field strains and vaccine strains, supporting evidence of antigenic drift and reduced vaccine-match efficacy.

In a study investigating the species emergence and genotypic characteristics of the virus responsible for FMD outbreaks in southern Vietnam in 2019, seven samples were collected from pigs exhibiting typical clinical signs of FMD. All samples tested positive for FMDV, and the VP1 coding gene was successfully amplified and sequenced. Phylogenetic analysis revealed that all seven field isolates belonged to serotype O, toptotype SEA/Mya-98. These strains exhibited high genetic similarity to FMDV strains previously isolated in Vietnam

(2018), South Korea, and China. However, they showed low sequence homology with the vaccine strains in use at the time. Notably, 21 amino acid substitutions were identified in the VP1 protein of the field strains, several of which were located at key antigenic sites involved in the virus neutralization process (notably in the H9 region). These findings suggest the continued occurrence of FMD outbreaks in pig farms in Vietnam may be partially attributed to antigenic mismatches between circulating field strains and the vaccine strains, underscoring the need for ongoing surveillance and vaccine strain updates. The authors further observed that FMDV infections remain widespread in pig farming operations, highlighting a persistent challenge for disease control efforts in the region. (Ngoc Hai Nguyen et al., 2023).

Figure 9. Amino acid sequences of antigenic regions in VP1 of FMDV.

This figure presents an alignment of amino acid sequences of the VP1 capsid protein from seven field strains of FMDV and

seven reference vaccine strains. Dots represent conserved amino acid positions, while letters indicate observed amino acid substitutions. The green-shaded boxes mark the positions of neutralizing epitopes, which are critical for antibody recognition and immune protection. The orange-shaded boxes highlight the positions of T-cell epitopes involved in cellular immune responses. The differences in these regions—particularly within the neutralizing epitope domains—provide molecular evidence of antigenic drift between the field strains and the vaccine strains. These differences likely contribute to reduced vaccine efficacy and underline the importance of continual molecular surveillance for optimizing vaccine matching and improving FMD control strategies.

(Source: Ngoc Hai Nguyen, Trung Quan Nguyen, Danh Cong Lai, My Duyen Nguyen Thi A, Minh Nam Nguyen. *Virology*, 582 (2023), 43–47.

<https://doi.org/10.1016/j.virol.2023.03.010>)

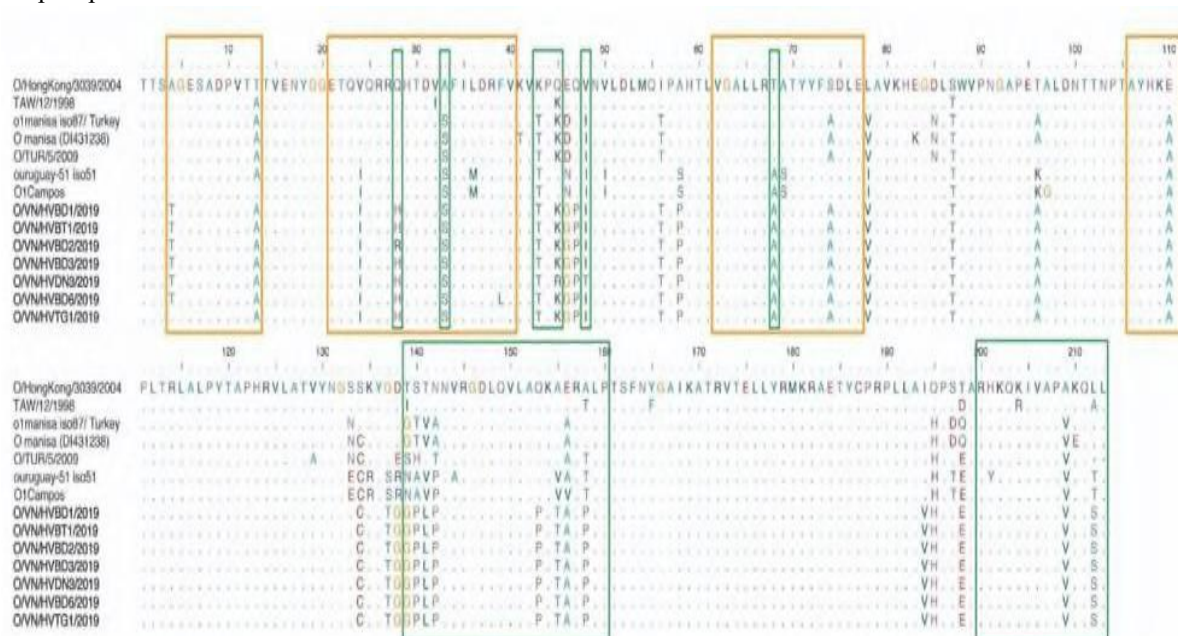
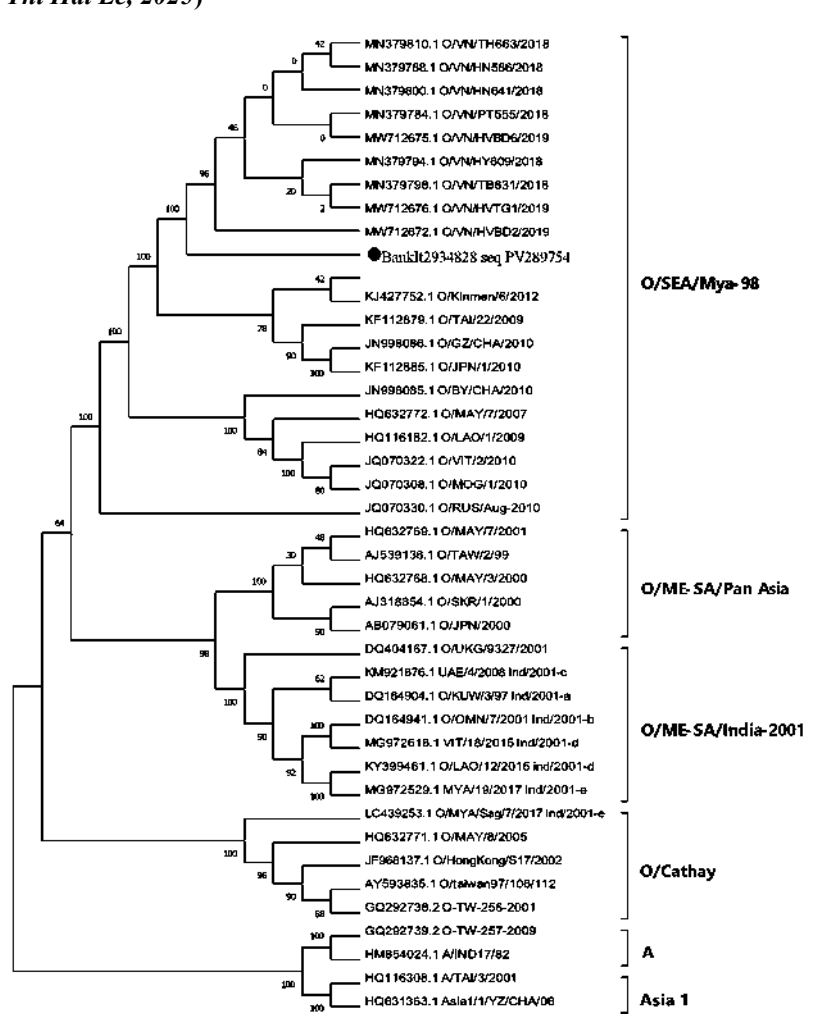


Figure 9. VP1 amino acid sequence alignment of field vs. vaccine strains (Nguyen et al., 2023): This alignment compares VP1 amino acid sequences of seven field strains with seven vaccine strains. Conserved residues are marked with dots, while substitutions are shown by letters. Green

boxes denote neutralizing epitopes; orange boxes indicate T-cell epitopes. Observed differences in key neutralizing regions (e.g., G-H loop and H9 region) indicate antigenic drift, suggesting a mismatch between vaccine and field strains

Figure 10. VP1-based phylogenetic tree of 2025 FMDV strain -25020307 (*The red circles indicate the FMDV field strains in this study obtained by Vo Thi Hai Le, 2025*)



This tree, constructed using MEGA X with 1,000 bootstrap replicates, illustrates the phylogenetic position of strain -25020307 collected from pigs in Nghe An, February 2025. It clusters within the O/SEA/Mya-98 lineage, consistent with strains from Laos, Thailand, and previous Vietnamese outbreaks. These findings underscore persistent local circulation and evolution of the O/SEA/Mya98 topotype. The phylogenetic tree was constructed using the Neighbor-Joining method with 1,000 bootstrap replicates in MEGA X software (<https://www.megasoftware.net/>). The tree is based on the nucleotide sequences of the VP1 gene, which encodes a key structural capsid protein involved in viral entry and immune recognition. Numbers along the branches represent bootstrap values greater than 70%, indicating high confidence in the branching pattern. The red circles highlight the FMDV field strains obtained in this study, including strain -25020307, isolated from pigs during the FMD outbreak in Nghe An province in February 2025. This strain clusters closely with other strains belonging to the O/SEA/Mya-98 lineage, which has been identified as the predominant topotype circulating in Vietnam and neighboring Southeast Asian countries over the past decade.

The phylogenetic position of strain -25020307 further supports findings by Tran Duy Khang et al. (2024), who reported similar lineage characteristics among FMDV strains isolated from cattle in Tra Vinh province. The close genetic relationship between the studied strains and historical field isolates from Laos, Thailand, and Vietnam suggests the continued circulation and local adaptation of the O/SEA/Mya98 topotype within the region. These findings have important implications for the selection and update of vaccine strains, given the potential for antigenic mismatch due to accumulated mutations in key antigenic regions of the VP1 protein. From the synthesis of recent studies analyzing the VP1 gene and assessing nucleotide and amino acid similarity among FMDV strains detected in outbreaks across Vietnam, it is evident that mutations in the VP1 protein contribute significantly to the virus's ability to evade the host immune response. These amino acid substitutions alter key antigenic sites, leading to reduced recognition by the immune system, even in vaccinated animals. The genetic divergence between field strains and vaccine strains—particularly in regions responsible for neutralizing antibody responses—has

resulted in a lack of cross-protection. This highlights the urgent need to develop updated vaccine strains that are genetically and antigenically matched to currently circulating FMDV field strains in Vietnam.

3.6. Control Measures and Prevention

3.6.1. Current FMD Prevention Measures Implemented in Vietnam

The Vietnamese government has enacted the **National Program for the Prevention and Control of Foot-and-Mouth Disease (FMD) for 2021–2025**, as stipulated in Decision No. 1632/QĐ-TTg. According to Mr. Pham Van Dong, Director of the Department of Animal Health under the Ministry of Agriculture and Rural Development, this program aligns with recommendations from the World Organisation for Animal Health (WOAH, formerly OIE), particularly following the outcomes of the 25th virtual meeting of the OIE Regional Subcommittee on FMD Prevention in Southeast Asia, China, and Mongolia held on December 25, 2020.

The program underscores Vietnam’s long-term commitment to establishing FMD-free zones at the district and inter-district levels across various provinces and municipalities. The key objectives and strategic measures include:

- **a.** Reducing the number of FMD outbreaks and minimizing the number of infected animals across the country.
- **b.** Preventing transboundary introduction of FMDV through stricter animal quarantine procedures and compliance with veterinary regulations on the importation of animals and animal products.
- **c.** Enhancing monitoring, early detection, and strict management of illegal transport and trade of livestock and animal products across borders.
- **d.** Strengthening control of slaughtering activities and enforcing veterinary hygiene in accordance with Ministry of Agriculture and Rural Development guidelines.
- **e.** Implementing immediate isolation of animals displaying clinical signs or confirmed to be infected.
- **f.** Prohibiting the purchase, transport, slaughter, or consumption of infected or suspected animals, and ensuring proper disposal of carcasses to prevent environmental contamination.
- **g.** Expanding public awareness and education efforts, using multiple communication platforms to disseminate information on FMD risks, prevention strategies, and legal requirements.
- **h.** Conducting routine and systematic vaccination campaigns, particularly targeting buffaloes, cattle, sows, and breeding boars, with a national goal of achieving at least 80% vaccination coverage twice annually.
- **i.** Establishing and maintaining a minimum of 1,000 FMD-free livestock production facilities and supply chains, to be officially recognized by the WOAH.

- **j.** Implementing localized response measures, as seen in Ha Tinh province where recent FMD outbreaks in Ky Anh district prompted urgent integrated interventions, including intensified surveillance and expedited completion of the second vaccination round in 2024 as directed by the Provincial People’s Committee.

3.6.2. Status of FMD Vaccine Research and Development in Vietnam

Vietnam has made notable advancements in the research and development of domestic vaccines for the prevention of foot-and-mouth disease. Vietnamese veterinary authorities have successfully isolated field strains of FMDV and transferred these to domestic enterprises, thereby facilitating the development of vaccines targeting serotypes O and A [19].

In 2017, the Ministry of Agriculture and Rural Development officially transferred the seed virus strain RAHO6/FMD/O-135 (PanAsia lineage) to domestic vaccine manufacturers. As a result, the RTD Company developed the **AVAC-V6 FMD Emulsion vaccine**, which met national safety and efficacy standards and demonstrated protective immunity in vaccinated buffaloes and cattle [20], [21].

Vietnam has adopted a dual approach to ensure a stable and effective vaccine supply: the production of domestic vaccines and the licensing of selected imported vaccines. These include:

- **a. Aftogen Oleo Type O:** A highly purified oil-adjuvanted vaccine with antigen content exceeding 6 PD₅₀, free from non-structural proteins (NSPs), and designed to elicit rapid and long-lasting immune responses.
- **b. BioAftogen:** A multivalent vaccine formulated for use in both ruminants and pigs, containing serotypes O1 Campos, A24 Cruzeiro, and A2001 Argentina, each with antigen content ≥6 PD₅₀.
- **c. Aftovax:** An alum-based inactivated vaccine developed by Boehringer Ingelheim and distributed by Navetco in Vietnam. This vaccine contains type O strains such as O1 Manisa and O-3039, tailored to regional epidemiology and present at ≥6 PD₅₀.
- **d. AVAC-V6 FMD Emulsion (Vietnam):** A locally produced vaccine containing at least 6 PD₅₀ of the RAHO6/FMD/O-135 strain, which offers antigenic coverage across multiple sublineages of serotype O, including Mya-98, PanAsia, Cathay, and Ind2001.

These developments highlight Vietnam’s growing self-reliance and technical capacity in FMD control through vaccine innovation. The emphasis on genetic and antigenic matching of vaccine strains to circulating field strains represents a proactive and scientifically grounded strategy to improve FMD management nationwide.

IV. DISCUSSION

4.1. Evaluation of the Effectiveness of Control Measures Across Different Phases

In response to the complex and evolving epidemiological profile of foot-and-mouth disease (FMD) in Vietnam, the government has implemented control strategies across multiple phases. The Ministry of Agriculture and Rural Development has led the execution of comprehensive national programs for FMD prevention and control during four key periods: 2006–2010, 2011–2015, 2016–2020, and 2021–2025. These strategies include: (i) mass vaccination in high-risk and buffer zones; (ii) strict regulation of livestock transport, trade, and slaughter; and (iii) post-vaccination monitoring to evaluate immune responses and detect circulating strains.

These measures have effectively curtailed outbreak magnitude, reduced mortality, and mitigated virus spread. However, their overall efficacy has been constrained by the emergence of antigenically distinct field strains, underscoring the need for more adaptable and targeted interventions.

4.2. Clinical Pathology of FMD in Vietnam

The clinical presentation of FMD in Vietnam aligns with global disease manifestations. Infected animals typically develop high fever (40–41°C) and vesicular lesions on mucosal and thin-skinned regions such as the tongue, dental pad, lips, palate, interdigital spaces, and teats. Young animals are particularly susceptible to fatal myocarditis, contributing to significant economic losses and psychosocial distress among smallholder farmers.

4.3. Molecular Biology of FMDV in Vietnam

FMDV, a member of the *Picornaviridae* family, is a non-enveloped virus with an icosahedral capsid and a single-stranded positive-sense RNA genome (~8.5 kb). The capsid comprises four structural proteins (VP1–VP4), with VP1 playing a pivotal role in determining antigenic variability and host immune recognition.

Molecular surveillance in Vietnam has identified three major serotypes—O, A, and Asia 1—with serotype O being predominant. Most Vietnamese strains belong to the SEA/Mya-98 topotype, which exhibits limited cross-reactivity with some currently used vaccines. This antigenic divergence complicates efforts to achieve robust immunity through vaccination.

4.4. Prospects and Future Solutions

Although multiple FMD vaccines—both imported and domestically produced—are currently in use, their effectiveness is undermined by antigenic mismatch with local field strains. The development of next-generation vaccines that reflect the genetic and antigenic profiles of endemic Vietnamese strains is essential for the success of the current national FMD control program (2021–2025), with strategic goals extending to 2030.

Beyond vaccine innovation, other essential measures include: (i) enhanced disease surveillance systems for rapid outbreak detection; (ii) improvement of livestock breeding and husbandry practices; and (iii) expanded public awareness campaigns to promote compliance and early reporting. An integrated control framework that combines molecular epidemiology, vaccine customization, and community engagement will be pivotal to achieving sustainable FMD control in Vietnam.

4.5. Comparison of FMD Situation in Vietnam and Other Regional Countries

Vietnam's FMD landscape shares several features with neighboring Southeast Asian nations, particularly in serotype dominance and topotypic distribution. Regional reports, including findings from the 16th Meeting of the OIE Sub-Commission on FMD in Southeast Asia (Vientiane, Laos, March 2010), affirm the predominance of serotype O (SEA topotype) across the region.

In Vietnam, as in the broader region, serotype O (SEA/Mya-98 topotype) has been the most frequently reported lineage in recent outbreaks. However, experts such as Dr. Chris Morissy have highlighted the lack of archived samples from earlier outbreaks, which limits the comprehensiveness of molecular epidemiological assessments.

A notable parallel exists with the FMD outbreak in South Korea between November 2010 and January 2011, during which 97 confirmed outbreaks were reported across five provinces. The causative viral strains were identified as belonging to the O/SEA/Mya-98 lineage—the same as those detected in Vietnam. Genotypic confirmation by the FAO/OIE Reference Laboratory (Pirbright, UK) further validated the transboundary nature of this lineage.

These findings underscore the persistent circulation and wide geographic distribution of the SEA/Mya-98 topotype. Despite regional similarities, Vietnam continues to face significant obstacles in outbreak surveillance, diagnostic capacity, and vaccine effectiveness due to ongoing antigenic drift.

To improve long-term control outcomes, regional cooperation must be intensified through shared surveillance databases, joint vaccine development initiatives, and harmonized response frameworks. Collaborative regional strategies are essential for advancing toward the eradication of FMD in Southeast Asia.

V. CONCLUSION

Foot-and-mouth disease (FMD) continues to pose a complex and persistent challenge to Vietnam's livestock industry. Its endemic status is closely linked to structural characteristics of the sector, particularly the dominance of smallholder systems for ruminants and limited biosecurity in commercial pig farming. These vulnerabilities undermine control measures and contribute to frequent outbreaks, resulting in

high mortality rates, widespread culling, and considerable economic losses (Lee et al., 2020; Nguyen et al., 2023).

This study highlights the predominance of FMDV serotype O, especially the SEA/Mya-98 topotype, which remains the most widely circulating lineage across Vietnamese provinces. Phylogenetic analyses indicate close genetic relationships between local strains and those detected in neighboring countries such as China, South Korea, and Laos, underscoring the transboundary nature of FMDV transmission and the urgent need for regional collaboration in disease surveillance and response (Nguyen et al., 2020; Le et al., 2010).

One of the major barriers to effective vaccination in Vietnam is the antigenic mismatch between vaccine strains and the rapidly evolving field isolates. This underlines the importance of continuous molecular monitoring to detect emerging genetic and antigenic variations, thereby guiding timely updates to vaccine formulations (Le et al., 2016; Valdazo-González et al., 2012). The integration of molecular epidemiology with real-time outbreak data could enhance both preventive and reactive strategies.

In conclusion, a comprehensive FMD control strategy in Vietnam should involve: (i) strengthening genomic surveillance systems, (ii) improving the match between vaccines and circulating strains, (iii) enhancing biosecurity at both smallholder and commercial levels, and (iv) promoting regional coordination for cross-border disease control. These integrated efforts are essential not only for mitigating the impact of FMD in Vietnam but also for contributing to the broader goal of disease eradication in Southeast Asia and beyond.

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