

IMPLICATIONS FOR A SUCCESSFUL FMD CONTROL PROGRAM IN SRI LANKA

U. Gunasekera*

*Department of Veterinary Population Medicine
College of Veterinary Medicine
University of Minnesota, USA*

SUMMARY: Many discussions are ongoing as to the improvement of milk production in Sri Lanka from the selection of quality animals for breeding to nutrition management. This includes a lack of policies for the protection of local milk production and the improvement of animal health. It has been estimated that the loss of milk production was 73 million liters from 2018 to 2019 during the ongoing Foot and Mouth Disease (FMD) outbreak (DAFH key statistics). FMD is a major contagious animal disease that impacts milk production. There is a scope to improve dairy production in the country by supporting small-scale dairy farmers by controlling infectious animal diseases such as FMD. This review aims at identifying the areas where attention should be focused, to implement effective control measures against FMD.

INTRODUCTION

Foot and Mouth Disease virus

Foot and Mouth Disease (FMD) is caused by an RNA virus that affects cattle, goats, pigs, and other cloven-hoofed ruminants (*Aphthovirus*, *picornaviridae* family). The disease produces blisters in the mouth, tongue, hoof, and udder that affect the production of the animals (Arzt *et al.*, 2011b; Arzt *et al.*, 2011a; Arzt *et al.*, 2019a). This leads to economic losses for farmers. The viral genome contains a single open reading frame (ORF) encoding the entire genome, including structural and non-structural protein coding regions. The nonstructural proteins are used to differentiate the naturally infected animals from the vaccinated animals. The structural part of the virus is known as the VP1-VP4 protein capsid. Though it represents only 8% of the whole genome, FMDV serotypes and phylogenetic analyses have traditionally been characterized by sequencing the VP1 region (Boothroyd *et al.*, 1981; Bachanek-Bankowska *et al.*, 2018; Brito *et al.*, 2017; Brito *et al.*, 2018; de Carvalho Ferreira *et al.*, 2017). There are 7 serotypes of the virus, referred to as type O, A, C, Asia 1, SAT1-3. Infection with one serotype

does not provide cross-protection for a different serotype.

FMD classification overview

Like most RNA viruses, FMDV is highly susceptible to mutations during replication. As a result, the virus shows high genetic variation and rapid mutation rates that result in different viral phenotypes (Elena and Sanjuán, 2005). Serotypes are further divided into topotypes, lineages, sub-lineages, and strains. Viral topotypes are defined as groups of viruses that show >85% identity and typically show a restricted geographic distribution (Knowles *et al.*, 2005). Lineages are differentiated within a serotype based on a 5% difference in the genetic distance among viral clades. The strains are identified within the lineages. Because cross-protection amongst related strains (same serotype, different or same lineage) may only be partial, immune-driven interactions among co-circulating strains at the population level can lead to the replacement of existing strains with new strains. New strains can also emerge because the novel strain is more virulent than the existing strains.

For example, the lineage which was identified from Sri Lanka that belonged to serotype O, Ind-2001, emerged in India and later spread to Sri Lanka,

several African countries, as well as several parts of the Middle East and Southeast Asia out-competing the existing serotype O strains that were circulating. The lineage was divided through time into several sub-lineages (a,b,c,d) as it spreads across the world. In some countries, the Ind-2001 lineage gave rise to new and different sublineages that were genetically related such as those identified in the Middle East (O/BAR/2/2015) and Nepal (O/NEP/1/2014) (Bachanek-Bankowska *et al.*, 2018). Due to the change of lineage, sometimes the vaccine in use may not be effective for the outbreak strain. If the vaccinated animals show clinical signs of the disease after vaccination, that is known as vaccine failure. Because of this, it is difficult to select an appropriate vaccine for FMD in endemic countries and vaccine failures are frequent.

FMDV infection and the immunity

Not only does the virus keep mutating at the country level, but it has also been determined that the virus mutates at the animal level and herd level. This is true regarding both vaccinated and non-vaccinated animals (Fish *et al.*, 2020). When animals were infected with a variant combination of FMD virus inoculum simulating the field condition, different viral isolates of the consensus were isolated from the same animals at different time points throughout the infection period. Also, the virus keeps replicating *in-vivo* in different organs at different rates. In the same herd, animals in close contact were infected with the same clade of the virus from the consensus (Arzt *et al.*, 2019b). No extensive studies have been carried out to identify immunity acquired from natural infection. It has been discovered that immunity from natural infection will last for several years. Primarily B cells are involved in the acquired immunity and the role of T cells is controversial (Doel, 1996; Eschbaumer *et al.*, 2016). It is uncertain whether this acquired immunity can prevent reinfection or clinical infection in the animals.

VACCINATION AS A CONTROL MEASURE

FMD vaccination

The currently used vaccine for FMD is an inactivated vaccine that will produce immunity for up to 4-6 months duration depending on the

adjuvant (Parida, 2009). The FMD vaccine can reduce clinical signs, protect against clinical infection, and reduce the transmission of the live virus to susceptible animals (Brito *et al.*, 2011). Therefore, it is important to keep using a vaccine to reduce the economic losses for the farmers. Where multiple serotypes are circulating in the same country, when animals are protected against one serotype, a different serotype may emerge whereas when it is the same serotype that is circulating (ex: Serotype O only), animals will be protected against one lineage/topotype but a different lineage/topotype that can cross the immunity threshold will emerge to cause outbreaks.

Both targeted and emergency vaccination with an inactivated vaccine is practiced in endemic countries to control FMD. Even vaccination prior to one week of an outbreak with a homologous vaccine (emergency vaccination) along with movement control was identified as effective to control the outbreak. In this situation, an outbreak is defined as having detected at least one animal with clinical signs of FMD in a given herd (Brito *et al.*, 2011). A vaccine of a given serotype offers protection for the same serotype of FMDV, but heterologous intra-serotypic protection may still be variable and sometimes incomplete due to the genetic divergence of field strains from the vaccine strain. Therefore, vaccine matching to the circulating strain in the field is important when selecting a vaccine. Several steps should be considered for successful vaccine selection for a vaccination program such as quality, the efficacy of the vaccine in the field, vaccine coverage, maintenance of cold chain and sero-surveillance monitoring of the protective antibody titers after vaccination. Specific guidelines regarding vaccine selection are available in “Foot and mouth disease vaccination and post-vaccination monitoring” (<http://www.fao.org/3/a-i5975e.pdf>).

It is equally important to vaccinate goats and pigs as it is to vaccinate cattle. Nonstructural FMD proteins were identified in a study done in “Odisha” in India from 38% of unvaccinated goats, indicating that the goats were infected with FMD (Ranabijuli *et al.*, 2010). Goats will show fewer clinical signs compared to cattle and pigs such as mild oral lesions, lameness, and pyrexia. Pigs are infected via the oral route and shed more virus in the aerosol route that is infectious to cattle and goats (Brito *et al.*, 2017, Arzt *et al.*, 2011a). Pigs develop severe foot lesions, pyrexia and vesicles at

pressure points (Arzt *et al.*, 2011). Some FMD strains such as serotype O Cathy topotype have been identified which affect only pigs that are not transferred to cattle (Brito *et al.*, 2017).

Selection of a suitable vaccine

When a vaccine is manufactured, safety, purity, and the efficacy of the vaccine are tested. Testing for safety is important to determine in the inactivated vaccine that the virus is properly inactivated. Testing for purity is important to determine the absence of extraneous agents and nonstructural proteins that differentiate clinically infected animals from vaccine protected animals when performing serological testing.

Vaccine efficacy provides an indicator of protection provided by the vaccine against the live virus. The live reference vaccine virus is available at the World Organization for Animal Health (WOAH/OIE) reference laboratories. The reference virus will be injected into two cattle over 12-months of age to harvest the challenge virus for further studies. Three groups of naïve cattle that have no history of FMD will be selected for vaccine injection and two more cattle will be selected as a control group. The vaccine will be injected in different doses in the vaccine group cattle and the control group will not be vaccinated. Animals in both groups will be challenged by the challenge virus by inoculating the virus in the upper surface of the tongue after 1 month of vaccination. The immune response of the animals will be measured, and unprotected animals are expected to show clinical lesions (Chapter 3.1.8 OIE). Based on the number of animals protected in each group, PD50 is calculated. PD50 stands for the dose of the vaccine that protects 50% of the animals in the vaccinated group. The vaccine that is used in the field is three times the amount that would be necessary to protect 50% of the animals at the vaccine trial. In FMD endemic countries, the 3PD50 vaccine is usually used. When an outbreak occurs in a FMD free country the 6PD50 vaccine is used (Knight Jones 2016). The duration of the immunity depends on the efficacy of the vaccine.

When this direct challenge test is not available, countries use the virus neutralization test (VNT) and Liquid Phase Blocking Enzyme Link Immunosorbent Assay LPB ELISA test in its place

(OIE Chapter 3.1.8). For the virus neutralization test, serum with antibodies from infected animals are diluted in twofold in the microtiter plates. The control standard serum is 21 days convalescent or post vaccination serum. The stock reference virus is added to microtitre plates containing diluted serum. This virus suspension contains about 100 TCID₅₀ (ie; 50% tissue culture infective dose). After 1 of hour incubation period, a cell suspension of BHK-21, IB-RS, lamb or pig kidney cells is added to each well and incubated again for 2-3 days. Microscopic readings are obtained after 2 days of intact blue stained cell sheets. These are recognized as positive wells where the virus has been neutralized by vaccine induced antibodies, and therefore no cell lysis has occurred by the virus. Interpretation of the test results varies between laboratories (OIE Chapter 3.1.8).

Vaccine potency is the strength of the vaccine measured as the antigen-antibody response by challenging the infected animal with vaccines under laboratory conditions (Chapter 3.1.8 OIE). Using a high potency vaccine may protect the animals even when the vaccine is suboptimal for the field strain (Knight-Jones *et al.*, 2016).

Cross protection for the field strain by a vaccine is evaluated by the vaccine matching study. Cross protection is defined as the immunity for a “one virus” strain induced by a different strain of the same serotype. Vaccine matching is an important step in selecting what vaccine is to be used in the country. The vaccine matching value is known as r_1 and is used to calculate the relationship between the vaccine virus and the field isolate. This is calculated as:

Vaccine serum protection against the field virus

Vaccine serum protection against the vaccine virus

The test can be carried out as an Enzyme Link Immunosorbent Assay (ELISA) testing or Complement Fixation Test (CFT). R-value <0.3 is considered as providing adequate protection against the field virus. Serum antibody titers also depend on the number of doses and the potency of the vaccine (Chapter 3.1.8 OIE).

Since the FMD serotypes, lineages, and sub-lineages keep changing frequently it is important to carry out vaccine matching regularly. The

WOAH/OIE recommendation is to carry out vaccine matching every two years. There are instances where the same serotype vaccine may not be protective against different lineages. Studies has shown that O/IND/R2/75 (vaccine used in Sri Lanka) provides adequate protection against O/ME-SA/Ind2001 lineage by vaccine matching using VNT (Dahiya *et al.*, 2020, Mahapatra *et al.*, 2015). One of these studies further demonstrates how ind-2001d lineage is being gradually replaced by an emerging lineage Ind-2001e (Dahiya *et al.*, 2020). The O/IND/R2/75 vaccine strain which was used in India and Sri Lanka was not able to prevent the outbreak occurrence that took place during the year 2013 and 2014 by the Ind2001d lineage (Subramaniam *et al.*, 2015).

Vaccine coverage

The level of vaccine coverage is calculated as the mean proportion of animals vaccinated in a selected population assigned to be vaccinated (Ferrari *et al.*, 2016).

Vaccine coverage = $\frac{\text{Actual number of the animals vaccinated}}{\text{Number of animals eligible for vaccination}} \times 100$

The WOAHO recommendation is to reach at least 80% coverage of herd immunity. Two consecutive rounds of mass vaccination with a 10-day interval of 80% coverage, in theory, will lead to 96% herd level immunity (80% of population first round+ 80% of the remaining 20% of the population i.e.: 80%+16%=96%) given that both doses are independent. Even doses are not independent (i.e., the same animal is vaccinated twice), there will be a booster effect for animals who were under effective vaccination initially which would extend their level of immunity. Giving two dose primary vaccination has been identified to reduce low antibody titer animals by 20-30% (Knight Jones *et al.*, 2016).

Due to many financial and technical difficulties, it is not always easy to achieve this target for the whole country. There has been a further reflection on methods to support the idea of short term local intervention for effective control of the disease minimizing the economic loss for the farmers (Cameron, 2019).

Effective reproductive number for FMD and vaccine coverage

For local intervention, it would be important to know the basic reproductive number (R_0) in high-risk areas for FMD. The vaccine coverage that is needed to stop the outbreak depends on R_0 . In a susceptible population, R_0 is the number of secondarily infected animals that are produced by a single primary case of the disease, (Anderson *et al.*, 1992). If the $R_0 < 1$ then the outbreak will not propagate further. The R -value changes from high to low as the disease progresses. If $R_0 = 1$ the disease will remain at equilibrium in the population.

R_0 can be calculated by:

$$R_0 = c \cdot p \cdot d$$

c-> contact rate between and infected and susceptible animals

p-> probability of transmission per contact

d-> duration of infectiousness

The contact rate depends on the management system and the route of transmission. The most successful virus transmission occurs via inhalation and oral route that reach the oropharynx mucosa (Stenfeldt and Arzt, 2020).

The probability of transmission varies with the number of days after the initiation of the outbreak with the change of population from susceptible to infected and recovered. The probability of transmission depends on the physiology of the animal as well. "p" can be reduced by reducing the number of infected animals and by vaccination. Early intervention is important to reduce the number of infected animals and to reduce the contact between farms. This is a variable parameter depending on the community. Vaccination reduces viral shedding even when the animals are infected. The duration of infection varies in different animal species and is identified as 8-11 days in cattle, pigs, and goats (Arzt *et al.*, 2019a). Duration of infection is also reduced by vaccination.

Therefore, R_0 differs among different populations and should be calculated separately. R_0 is calculated by means of the Susceptible, Infected, Recovered (SIR) model using transmission coefficient and other parameters in challenge studies, randomized control trials, or observational studies (Keeling, 2005).

In an FMD endemic country, the R_0 value can change due to already infected animals, related immunity (vaccination and natural infection), and the animals with maternal immunity. At such circumstances, effective reproductive number (R) is determined considering the above-mentioned factors. In a field situation, the effective reproductive number is the number of secondary animals in a herd to which the disease is transmitted. This can be calculated as:

$$R_{\text{effective}} = (1 - V_e) F$$

Where V_e is defined as the proportion of animals protected from clinical infection due to vaccination, maternal immunity, and previous infection. In India, it was identified that $R_{\text{effective}}$ has a value of 8.04 for an intensively managed farm (Hayer *et al.*, 2018) and 1.06 to 1.04 at sub district level in the Northern Thailand (Arjkumpa *et al.*, 2021).

Field epidemiological studies should be carried out to obtain these parameters for a given country. The proportion of the animals that needed to be vaccinated is given by $(1 - 1/R_0)$. Knowing the R_0 and effective R_0 in each population help to have an educated guess about the number of animals to be vaccinated and is cost-effective when it is difficult to vaccinate to reach 80% coverage in the herd that would stop the propagation of an outbreak (Perez *et al.*, 2004).

In the field, the vaccine should be transported between a temperature of 2 -8° Celsius. Records must be kept for cold chain maintenance, animal identification, and animal handling. It is advised to start a round of vaccinations at least 3 months before the beginning of the high-risk season (Ferrari *et al.*, 2016; Knight-Jones *et al.*, 2016). It was identified that the maximum animal interaction occurs from the beginning of April to end of September (Gunasekera *et al.*, 2017). WAOH/ OIE recommends administering an additional booster dose with at least 10 days gap from the first vaccination or 5 days after a booster vaccination before the commencement of animal movement (Ferrari *et al.*, 2016). The duration between two vaccine rounds afterward is determined based on the turnover of the herd, vaccine adjuvant, the potency and efficacy of the vaccine.

Vaccine effectiveness means, how well the animals are protected against undesirable outcomes. The effectiveness of the vaccination is calculated at the

field level by determining the incidence rate of the disease in the vaccinated and the non-vaccinated population (Ferrari *et al.*, 2016). India identified the most effective vaccine for Ind- 2001 strain as O/IND/R2/75 vaccine strain for the 2013-2014 outbreak (Mahapatra *et al.*, 2015) which was the strain of imported FMD vaccine in Sri Lanka. Despite using this vaccine strain in Sri Lanka, a wide-spread FMD outbreak occurred during the year 2013 and 2014. This outbreak is reported to be caused by the strain Ind-2001d (Abeyratne *et al.*, 2018).

New approaches in vaccine production that may prevent animals from getting infected are still being explored (Singh *et al.*, 2019). Viral vector vaccine, marker vaccine, virus-like particle vaccine, immune modulator vaccines, and DNA vaccine are proposed new approaches of vaccines.

POST-VACCINATION MONITORING

When a vaccine program is conducted it is equivalently important to identify the animals with protective antibody titers after each round of vaccination. Virus neutralization test (VNT) is the gold standard recommended by WOAHP for post vaccination monitoring. VNT can incorporate different virus strains but requires higher-level bio containment facilities. In the absence of VNT, serological tests that detect antibodies against structural proteins is also recommended (Ferrari *et al.*, 2016). The protective antibody titer of a given animal is measured by LPB ELISA (liquid phase blocking enzyme-linked immunosorbent assay) or Solid phase competitive (SPCE) ELISA to check the structural protein-related antibodies (Lim Kang *et al.*, 2018). The cut off value of the test is determined by the sensitivity and the specificity of the ELISA test and the prevalence of the disease in the field situation. A highly purified vaccine should not contain the nonstructural proteins. There are records that the vaccine produced in India, which was imported to use in Sri Lanka contains residual nonstructural proteins that interfere with the recognition of vaccinated animals from the infected animals (Mohapatra *et al.*, 2011). To differentiate the vaccinated animals from naturally infected animals by detecting nonstructural proteins 3ABC ELISA test is commonly used (de Carvalho Ferreira *et al.*, 2017, Brito *et al.*, 2017).

MOVEMENT CONTROL AS A CONTROL MEASURE

Legislations empower animal movement control during an outbreak by the Animal diseases Act No. 59 of 1992. Movement control will enable the prevention of animal movement from infected farms to non-infected farms. The Director General of the Department of Animal Production and Health (DAPH) or his delegate has the authority to appeal magistrate of the relevant area to enable movement control. Such a notice is valid for three months to prohibit the transfer of animal products, excreta, litter, grass, hay, or any other product without a permit signed by the responsible veterinary surgeon. The order will specify the species of an infected animal, specified disease, and the area width of limitation where the disease has occurred.

Where there is an intensive management system and movement of animals between farms can be traced, network analysis has been used to identify super spreader farms (farms that are more likely to spread infectious diseases) to apply movement control (Makaeu *et al.*, 2021). Once the farms with a high degree of contact with surrounding farms have been identified; restricting movement to and from these farms will reduce the disease spread by 80%. Simulation studies based on a farm system in the US has identified that this method would provide significant disease control. When animal identification methods are in place such as ear tagging, more detail level movement studies can be carried out as it enables identification of individual-level animals at risk and ability to trace back the animal movement related to disease spread (Kinsley *et al.*, 2019). Such farms concerning bovine tuberculosis have been identified in real-time in Uruguay (VanderWaal *et al.*, 2016). Still, this method is applicable in countries like Sri Lanka where animals intermingle freely considering the village as the unit of interest (VanderWaal *et al.*, 2017, Omondi *et al.*, 2021). By this method, if a village is initially identified as the super spreader/initial infection of an outbreak, then the movement control can be focused on that particular village. This way, the impact from FMD control on the economy of the farmers will be minimal and the cost for disease control measures will be minimal.

FMD in wildlife

It was identified from the studies carried out in Africa, where there is high interaction between cattle and wildlife, that the transmission of the viruses between cattle and wildlife is rare (Omondi *et al.*, 2018; Haydon *et al.*, 2002). The transmission between wild buffaloes and domestic cattle is identified in South Africa where cattle herds are almost completely free from FMD (Brito *et al.*, 2011), whereas in East Africa where FMD is endemic and outbreaks are frequent, the transmission is not significant. Therefore, exploration of the mode of transmission between wildlife and domestic animals becomes important when the countries attempt to make domestic cattle population free from FMD.

CARRIER STATE OF FMD

Both vaccinated and non-vaccinated ruminants can become persistently infected with the virus (Arzt *et al.*, 2018). Animals from which the live virus can be isolated from the oropharyngeal region of the cattle are known as carrier animals. There is a 10-day transitional period where infected animals recover from an infection or become carriers. Animals are most susceptible to get infected with a different strain of the FMDV during this period. Earlier, the carriers were identified when isolating the virus from oropharyngeal fluid was possible after 28 days. Later the carrier status in vaccinated animals was determined in 10 days and non-vaccinated cattle in 21 days (Arzt *et al.*, 2019b). Carrier animals can be further recognized as persistently infected with the same virus or serially infected with different viruses. Persistently infected animals have been identified in Pakistan, India, and Vietnam (Hayer *et al.*, 2018; Brito *et al.*, 2018; Farooq *et al.*, 2018). The reason why the carrier animals are serially infected is yet to be identified.

Cattle can become carriers for 13 months (Hayer *et al.*, 2018, Brito *et al.*, 2018) and the Asian buffaloes have so far been identified to be carriers for a minimum of 12 months (Farooq *et al.*, 2018). The viruses identified from carriers may be completely different from the vaccine strains and vaccines offer less protection for these new strains (Biswal *et al.*, 2019). Only evidence where carriers can initiate infection in naïve animals is found with African buffalo (Maree *et al.*, 2016). The IgA

antibodies in the oropharyngeal fluid will act as a barrier for carrier cattle becoming infected (Arzt *et al.*, 2011b). In an FMD endemic country, sub clinical FMD infection persists in the population in two forms, namely neoteric subclinical infection and persistent infection. Neoteric infection is defined as acute infection of vaccinated cattle or resistant to FMD due to natural infection (sympatric hosts) that do not show clinical signs and the persistent infection is defined as previously described. Neoteric animals shed greater amount of virus compared to persistently infected animals. It is not feasible to determine carrier vs neoteric animals at field conditions (Stenfeldt and Arzt, 2020).

FMD free countries do not import live animals from countries where FMD is endemic/free with vaccination since they have the potential threat to initiate a new outbreak causing massive economic losses and the role of the carrier in disease transmission is unclear. There are studies where they have identified similar strains in carriers similar to later emerged outbreak strains in Vietnam (Pauszek *et al.*, 2016, Britto *et al.*, 2017). Yet it has not been demonstrated under field conditions that a carrier can transmit the disease and cause an outbreak.

FMD CONTROL IN SRI LANKA

To provide guidelines on steps that endemic countries should take to reduce outbreaks to achieve eventual FMDV freedom, the FAO/WOAH outlined the Progressive Control Pathway for FMD (<http://www.fao.org/ag/againfo/commissions/docs/pcp/pcp-26012011.pdf>). At the FAO FMD regional conference, Sri Lanka was identified as in stage 1 of the progressive control pathway. Sri Lanka can reach stage 2 by having a strategic risk-based control plan and has nearly completed all the steps of stage 1.

The PCP stage 1 includes value chain analysis, the hypothesis of virus circulation, estimating the socio-economic impact of the disease, identification of the virus, enabling environment, and regional corporation. The last value chain analysis in Sri Lanka was conducted by the Department of Animal Production and Health in 2008. Sri Lanka has a hypothesis of the circulation

of the virus, based on outbreak reports sent by veterinarians and serotypes and topotypes identification (Abeyratne *et al.*, 2018, Ranaweera *et al.*, 2019). Last vaccine matching was done in 2020 at the WOAHOIE reference laboratory (WRLFMD). According to the results, any of the vaccines O Manisa, O 3039 and O Tur 5/09 were identified as suitable vaccines matching the field isolates that belongs to lineage O/ME-SA/Ind 2001d (<https://www.wrlfmd.org/asia/sri-lanka#panel-5042>). WOAHOIE recommends use of above vaccines that are broadly protective against many circulating lineages as a measure to prevent emergence of more virulent strains at the field.

India has the FMD regional reference laboratory for South Asia. Sri Lanka has been using FMD vaccines (ex: O/IND/R2/75) from India and the local vaccine protective against on O/ME-SA/Ind-2001d lineage for FMD control. It would be beneficial for Sri Lanka to increase collaborations with India Regional laboratory to test the safety, potency, and the efficacy of the local vaccine at the field level.

The enabling environment in PCP stage 1 includes strengthening the veterinary services of the country. Sri Lanka has requested external evaluation of the veterinary system of the country by PVS (Performance of Veterinary Service) evaluation system of WOAHOIE. Many countries in South and East Asia have been evaluated by PVS. PVS is introduced by the WOAHOIE for the sustainable development of the veterinary program of a country to reach international standards. The PVS pathway investigates veterinary legislations, education, private/public participation, and developing laboratory capacities.

Sri Lanka participates in international collaboration workshops and updates information at the WOAHOIE WAHIS interface. It would be beneficial to extend collaborations as to the development of a strategic control plan for FMD control and improve on data sharing and capacity building. These steps will lead to developing a risk-based strategic control plan in stage 2 (<https://www.fao.org/3/cb1866en/cb1866en.pdf>). It is also important to have information evaluated at stage 1 of PCP separately at the province level. Estimating the individual immune status of the

animals and having a risk-based control program is important to be accepted in stage 2 of PCP.

Since the dairy system has changed over the last decade, the last value chain analysis conducted in 2008 may not be representative of the current socio-economic status of the country. Establishing a separate epidemiological unit for infectious animal diseases; and improving outbreak-reporting activities from paper based to electronic methods to increase surveillance and reduce the time for early detection of an outbreak warrants serious consideration by the responsible authorities.

In Sri Lanka, North Central and Eastern provinces were identified as the risk hotspots (Chandana 2008, Gunasekera *et al.*, 2017). In 2008, a Satscan analysis was conducted to detect clusters of FMD outbreaks (Chandana 2008). Common circulating strains identified in the country were traced back to strains identified from India (Abeyratne *et al.*, 2018). It is suspected that illegal animal movements occur between India and the northern part of the country. North, North Central, and Eastern provinces should be given special attention in FMD control activity when determining a risk-based strategic control plan. A recent study conducted in the Eastern part of the country has identified that more knowledgeable the farmers regarding FMD, better they adhered to implementation of FMD control measures such as vaccination (Atambawa *et al.*, 2021). Another option is to target high production areas (ex: Central province) to actively maintain the FMD free status. These activities will facilitate establishing FMD free zones at a later PCP stage. It is evident that it is difficult to control FMD with vaccination alone, as the vaccine does not offer real protection from acquiring the infection but will reduce the transmission of the virus to non-infected animals. Since the disease-causing virus is a highly mutating RNA virus, it would take time for the manufacturers to come up with a vaccine that would provide full protection to the disease. Combination of movement control and vaccination has helped to establish FMD free zones in South American countries. Having a strategic control plan that will incorporate methods to increase surveillance, control outbreaks with appropriate vaccination, movement control and inputs from stakeholders pertaining to the economic loss may

help Sri Lanka to move forward towards freedom from FMD.

REFERENCE

- Abeyratne, S. A. E., Amarasekera, S.S.C., Ranaweera, L.T., Salpadoru, T.B., Thilakarathne, S.M.N.K., Knowles, N.J., Wadsworth, J., Puvanendiran, S., Kothalawala, H., Jayathilake, B.K., Wijithasiri, H.A., Chandrasena, M.M.P.S.K., Sooriyapathirana, S.D.S.S. (2018). The phylogenetic analysis of VP1 genomic region in foot-and-mouth disease virus serotype O isolates in Sri Lanka reveals the existence of “Srl-97”, a newly named endemic lineage. *PloS One* **13**, e0194077. <https://doi.org/10.1371/journal.pone.0194077>
- Arjkumpa, O., Picasso-Risso, C., Perez, A., Punyapornwithaya, V. (2021). Subdistrict-Level Reproductive Number for Foot and Mouth Disease in Cattle in Northern Thailand. *Frontiers in Veterinary Science*, **10**, 8:757132. doi: 10.3389/fvets.2021.757132. PMID: 34859089; PMCID: PMC8631321.
- Anderson, R.M., May, R.M., Anderson, B., (1992). *Infectious Diseases of Humans: Dynamics and Control*, Revised edition. ed. Oxford University Press, Oxford.
- Arzt, J., Baxt, B., Grubman, M.J., Jackson, T., Julleff, N., Rhyen, J., Rieder, E., Waters, R., Rodriguez, L.L., (2011a). The Pathogenesis of Foot- and- Mouth Disease II: Viral Pathways in Swine, Small Ruminants, and Wildlife; Myotropism, Chronic Syndromes, and Molecular Virus–Host Interactions. *Transboundary and Emerging Diseases*, **55**, 305 0.1111/j.1865-1682.2011.01236.x.
- Arzt, J., Belsham, G.J., Lohse, L., Bøtner, A., Stenfeldt, C. (2018). Transmission of Foot-and-Mouth Disease from Persistently Infected Carrier Cattle to Naive Cattle via Transfer of Oropharyngeal Fluid. *mSphere*, **3**. <https://doi.org/10.1128/mSphere.00365-18>
- Arzt, J., Branan, M.A., Delgado, A.H., Yadav, S., Moreno-Torres, K.I., Tildesley, M.J., Stenfeldt, C., (2019a). Quantitative impacts of incubation phase transmission of foot-and-mouth disease virus. *Scientific Report*, **9**, 2707. <https://doi.org/10.1038/s41598-019-39029-0>
- Arzt, J., Fish, I., Pauszek, S.J., Johnson, S.L., Chain, P.S., Rai, D.K., Rieder, E., Goldberg, T.L., Rodriguez, L.L., Stenfeldt, C., (2019b). The evolution of a super-swarm of foot-and-mouth disease virus in cattle [WWW Document]. *PLoS ONE*, **14**.

<https://link.galegroup.com/apps/doc/A583563657/AONE?sid=lms> (accessed 9.18.19).

Arzt, J., Julleff, N., Rodriguez, L. (2011b) The pathogenesis of foot-and-mouth disease I: viral pathways in cattle. *Transboundary and Emerging Diseases*, **58**, 291–304.

Athambawa MJ, Kubota S, Kono H. (2021) Knowledge affecting foot-and-mouth disease vaccination behavior: traditional dairy farmers in the dry zone of Sri Lanka. *Tropical Animal Health and Production*, **7**, 88. doi: 10.1007/s11250-020-02501-5. PMID: 33415503; PMCID: PMC7790336.

Bachanek-Bankowska, K., Di Nardo, A., Wadsworth, J., Mioulet, V., Pezzoni, G., Grazioli, S., Brocchi, E., Kafle, S.C., Hettiarachchi, R., Kumarawadu, P.L., Eldaghayes, I.M., Dayhum, A.S., Meenowa, D., Sghaier, S., Madani, H., Abouchoaib, N., Hoang, B.H., Vu, P.P., Dukpa, K., Gurung, R.B., Tenzin, S., Wernery, U., Panthumart, A., Seeyo, K.B., Linchongsubongkoch, W., Relmy, A., Bakkali-Kassimi, L., Scherbakov, A., King, D.P., Knowles, N.J. (2018). Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage. *Scientific Report*, **8**, 14693. <https://doi.org/10.1038/s41598-018-32693-8>

Biswal, J.K., Ranjan, R., Subramaniam, S., Mohapatra, J.K., Patidar, S., Sharma, M.K., Bertram, M.R., Brito, B., Rodriguez, L.L., Pattnaik, B., Arzt, J. (2019). Genetic and antigenic variation of foot-and-mouth disease virus during persistent infection in naturally infected cattle and Asian buffalo in India. *PloS One* **14**, e0214832. <https://doi.org/10.1371/journal.pone.0214832>

Boothroyd, J.C., Highfield, P.E., Cross, G.A.M., Rowlands, D.J., Lowe, P.A., Brown, F., Harris, T.J.R., (1981). Molecular cloning of foot and mouth disease virus genome and nucleotide sequences in the structural protein genes. *Nature* **290**, 800. <https://doi.org/10.1038/290800a0>

Brito, B., Pauszek, S.J., Eschbaumer, M., Stenfeldt, C., de Carvalho Ferreira, H.C., Vu, L.T., Phuong, N.T., Hoang, B.H., Tho, N.D., Dong, P.V., Minh, P.Q., Long, N.T., King, D.P., Knowles, N.J., Dung, D.H., Rodriguez, L.L., Arzt, J., (2017). Phylodynamics of foot-and-mouth disease virus O/PanAsia in Vietnam 2010–2014. *Veterinary Research*, **48**, 24. <https://doi.org/10.1186/s13567-017-0424-7>

Brito, B.P., Mohapatra, J.K., Subramaniam, S., Pattnaik, B., Rodriguez, L.L., Moore, B.R., Perez, A.M. (2018). Dynamics of widespread foot-and-

mouth disease virus serotypes A, O and Asia-1 in southern Asia: A Bayesian phylogenetic perspective. *Transboundary and Emerging Diseases*, **65**, 696–710. <https://doi.org/10.1111/tbed.12791>

Brito, B.P., Perez, A.M., Cosentino, B., Rodriguez, L.L., König, G.A. (2011). Factors associated with within-herd transmission of serotype A foot-and-mouth disease virus in cattle, during the 2001 outbreak in Argentina: a protective effect of vaccination. *Transboundary and Emerging Diseases*, **58**, 387–393. <https://doi.org/10.1111/j.1865-1682.2011.01217.x>

Cameron, A.R. (2019). Strategies for the Global Eradication of Peste des Petits Ruminants: An Argument for the Use of Guerrilla Rather Than Trench Warfare. *Frontiers in Veterinary Science*, **6**. <https://doi.org/10.3389/fvets.2019.00331>

Chandana, D. (2008). Use of GIS as a Management Tool in Monitoring, Surveillance and Control of FMD in Sri Lanka. University of Peradeniya, Sri Lanka MSc dissertation

de Carvalho Ferreira, H.C., Pauszek, S.J., Ludi, A., Huston, C.L., Pacheco, J.M., Le, V.T., Nguyen, P.T., Bui, H.H., Nguyen, T.D., Nguyen, T., Nguyen, T.T., Ngo, L.T., Do, D.H., Rodriguez, L., Arzt, J. (2017). An Integrative Analysis of Foot-and-Mouth Disease Virus Carriers in Vietnam Achieved Through Targeted Surveillance and Molecular Epidemiology. *Transboundary and Emerging Diseases*, **64**, 547–563. <https://doi.org/10.1111/tbed.12403>

Dahiya, S. S., Subramaniam, S., Biswal, J. K., Das, B., Prusty, B. R., Ali, S. Z., Khulape, S. A., Mohapatra, J. K., Singh, R. K (2021). Genetic characterization of foot-and-mouth disease virus serotype O isolates collected during 2014–2018 revealed dominance of O/ME-SA/Ind2001e and the emergence of a novel lineage in India. *Transboundary and Emerging Diseases*, **68**, 3498–3508. doi: 10.1111/tbed.13954. Epub 2020 Dec 19. PMID: 33305514.

Doel, T.R. (1996). Natural and vaccine-induced immunity to foot and mouth disease: the prospects for improved vaccines. *Revue scientifique et technique*, **15**, 883–911. <https://doi.org/10.20506/rst.15.3.955>

Elena, S.F., Sanjuán, R., (2005). Adaptive Value of High Mutation Rates of RNA Viruses: Separating Causes from Consequences. *Journal of Virology*, **79**, 11555–11558. <https://doi.org/10.1128/JVI.79.18.11555-11558.2005>

- Eschbaumer, M., Stenfeldt, C., Rekant, S.I., Pacheco, J.M., Hartwig, E.J., Smoliga, G.R., Kenney, M.A., Golde, W.T., Rodriguez, L.L., Arzt, J. (2016). Systemic immune response and virus persistence after foot-and-mouth disease virus infection of naïve cattle and cattle vaccinated with a homologous adenovirus-vectored vaccine. *BMC Veterinary Research*, **12**. <https://doi.org/10.1186/s12917-016-0838-x>
- Fish, I., Stenfeldt, C., Palinski, R. M., Pauszek, S. J., Arzt, J. (2020). Into the Deep (Sequence) of the Foot-and-Mouth Disease Virus Gene Pool: Bottlenecks and Adaptation during Infection in Naïve and Vaccinated Cattle. *Pathogens*, **9**, 208. <https://doi.org/10.3390/pathogens9030208>
- Farooq, U., Ahmed, Z., Naeem, K., Bertram, M., Brito, B., Stenfeldt, C., Pauszek, S.J., LaRocco, M., Rodriguez, L., Arzt, J. (2018). Characterization of naturally occurring, new and persistent subclinical foot-and-mouth disease virus infection in vaccinated Asian buffalo in Islamabad Capital Territory, Pakistan. *Transboundary and Emerging Diseases*, **65**, 1836–1850. <https://doi.org/10.1111/tbed.12963>
- Gunasekera U. C., Sivasothy, A., Wedasingha N., Thayaparan, S., Rotewewa, B., Muralithas, M., Baumann, M. P. O., Punyapornwithaya, V. (2017). Analyzing the Foot and Mouth Disease outbreak as from 2008 to 2014 in cattle and buffaloes in Sri Lanka. *Preventive Veterinary Medicine*, **1**, 78-88. doi: 10.1016/j.prevetmed.2017.10.008. Epub 2017 Oct 18. PMID: 29157377.
- Ferrari, G. (2016). Foot and mouth disease vaccination and post-vaccination monitoring: Guidelines. Food and Agriculture Organization of the United Nations, [Rome]
- Haydon, D.T., Cleaveland, S., Taylor, L.H., Laurenson, M.K. (2002). Identifying reservoirs of infection: a conceptual and practical challenge. *Emerging Infectious Diseases*, **8**, 1468–1473. <https://doi.org/10.3201/eid0812.010317>.
- Hayer, S.S., VanderWaal, K., Ranjan, R., Biswal, J.K., Subramaniam, S., Mohapatra, J.K., Sharma, G.K., Rout, M., Dash, B.B., Das, B., Prusty, B.R., Sharma, A.K., Stenfeldt, C., Perez, A., Delgado, A.H., Sharma, M.K., Rodriguez, L.L., Pattnaik, B., Arzt, J. (2018). Foot-and-mouth disease virus transmission dynamics and persistence in a herd of vaccinated dairy cattle in India. *Transboundary and Emerging Diseases*, **65**, e404–e415. <https://doi.org/10.1111/tbed.12774>
- Kang, YL., Jeong, JY., Choi, HY. et al. (2018). Evaluation and optimization of a conventional SPCE for FMD post-vaccination monitoring. *BMC Veterinary Research*, **14**, 371. <https://doi.org/10.1186/s12917-018-1686-7>
- Keeling, M.J., (2005). Models of foot-and-mouth disease. *Proceedings of the Royal Society B: Biological Sciences*, **272**, 1195–1202. <https://doi.org/10.1098/rspb.2004.3046>
- Kinsley, A.C., Perez, A.M., Craft, M.E., Vanderwaal, K.L. (2019). Characterization of swine movements in the United States and implications for disease control. *Preventive Veterinary Medicine* **164**, 1–9. <https://doi.org/10.1016/j.prevetmed.2019.01.001>
- Knight-Jones, T.J.D., Gubbins, S., Bulut, A.N., Stärk, K.D.C., Pfeiffer, D.U., Sumption, K.J., Paton, D.J., 2016. Mass vaccination, immunity and coverage: modelling population protection against foot-and-mouth disease in Turkish cattle. *Scientific Report*, **6**, 22121. <https://doi.org/10.1038/srep22121>
- Knowles, N.J., Samuel, A.R., Davies, P.R., Midgley, R.J., Valarcher, J.-F. (2005). Pandemic Strain of Foot-and-Mouth Disease Virus Serotype O. *Emerging Infectious Diseases*, **11**, 1887–1893. <https://doi.org/10.3201/eid1112.050908>
- Mahapatra, M., Yuvaraj, S., Madhanmohan, M., Subramaniam, S., Pattnaik, B., Paton, D.J., Srinivasan, V.A., Parida, S. (2015). Antigenic and genetic comparison of foot-and-mouth disease virus serotype O Indian vaccine strain, O/IND/R2/75 against currently circulating viruses. *Vaccine*, **33**, 693–700. <https://doi.org/10.1016/j.vaccine.2014.11.058>
- Maree, F., de Klerk-Lorist, L.-M., Gubbins, S., Zhang, F., Seago, J., Pérez-Martín, E., Reid, L., Scott, K., van Schalkwyk, L., Bengis, R., Charleston, B., Juleff, N., (2016). Differential Persistence of Foot-and-Mouth Disease Virus in African Buffalo Is Related to Virus Virulence. *Journal of Virology*, **90**, 5132–5140. <https://doi.org/10.1128/JVI.00166-16>
- Mohanty, N.N., Subramaniam, S., Rout, M., Sarangi, L.N., Bisht, P., Pandey, L.K., Mohapatra, J.K., Panda, H.K. (2015). Serosurveillance of foot-and-mouth disease in ruminant population of Coastal Odisha, India. Beni-Suef Univ. *Journal of Basic Applied Sciences*, **4**, 279–283. <https://doi.org/10.1016/j.bjbas.2015.11.002>
- Mohapatra, J.K., Pandey, L.K., Sanyal, A., Pattnaik, B. (2011). Recombinant non-structural polyprotein 3AB-based serodiagnostic strategy for FMD surveillance in bovines irrespective of vaccination. *Journal of Virological Methods*, **177**, 184–192. <https://doi.org/10.1016/j.jviromet.2011.08.006>

- Omondi, G., Gakuya, F., Arzt, J., Sangula, A., Hartwig, E., Pauszek, S., Smoliga, G., Brito, B., Perez, A., Obanda, V., VanderWaal, K. (2018). The role of African buffalo in the epidemiology of foot-and-mouth disease in sympatric cattle and buffalo populations in Kenya. *Transboundary and Emerging Diseases*, 10.1111/tbed.13573 PMID: 32303117
- Omondi, G. P., Obanda, V., VanderWaal, K., Deen, J., Travis, D.A. Animal movement in a pastoralist population in the Maasai Mara Ecosystem in Kenya and implications for pathogen spread and control. *Preventive Veterinary Medicine*. 10.1016/j.prevetmed.2021.105259.
- Pauszek, S.J., Eschbaumer, M., Brito, B., de Carvalho Ferreira, H.C., Vu, L.T., Phuong, N.T., Hoang, B.H., Tho, N.D., Dong, P.V., Minh, P.Q., Long, N.T., Dung, D.H., Rodriguez, L.L., Arzt, J., (2016). Site-specific substitution (Q172R) in the VP1 protein of FMDV isolates collected from asymptomatic carrier ruminants in Vietnam. *Virology Reports*, **6**, 90–96. <https://doi.org/10.1016/j.virep.2016.10.001>
- Perez, A.M., Ward, M.P., Carpenter, T.E. (2004). Control of a foot-and-mouth disease epidemic in Argentina. *Preventive Veterinary Medicine*, **65**, 217–226. <https://doi.org/10.1016/j.prevetmed.2004.08.002>
- Ranabijuli, S., Mohapatra, J.K., Pandey, L.K., Rout, M., Sanyal, A., Dash, B.B., Sarangi, L.N., Panda, H.K., Pattnaik, B. (2010). Serological Evidence of Foot-and-Mouth Disease Virus Infection in Randomly Surveyed Goat Population of Orissa, India. *Transboundary and Emerging Diseases*, **57**, 448–454. <https://doi.org/10.1111/j.1865-1682.2010.01161.x>
- Ranaweera, L.T., Wijesundara, U.K., Jayarathne, H.S.-M., Knowles, N., Wadsworth, J., Mioulet, V., Adikari, J., Weebadde, C., Sooriyapathirana, S.S. (2019). Characterization of the FMDV-serotype-O isolates collected during 1962 and 1997 discloses new topotypes, CEY-1 and WCSA-1, and six new lineages. *Scientific Report*, **9**, 1–10. <https://doi.org/10.1038/s41598-019-51120-0>
- Parida, S. (2009) Vaccination against foot-and-mouth disease virus: strategies and effectiveness, *Expert Review of Vaccines*, **8**, 347-365, DOI: 10.1586/14760584.8.3.347
- Subramaniam, S., Mohapatra, J.K., Das, B., Sanyal, A., Pattnaik, B. (2015). Genetic and antigenic analysis of foot-and-mouth disease virus serotype O responsible for outbreaks in India during 2013. *Infection Genetics and Evolution*, **30**, 59–64. <https://doi.org/10.1016/j.meegid.2014.12.009>
- Singh, R.K., Sharma, G.K., Mahajan, S., Dhama, K., Basagoudanavar, S.H., Hosamani, M., Sreenivasa, B.P., Chaicumpa, W., Gupta, V.K., Sanyal, V., (2019). Foot-and-Mouth Disease Virus: Immunobiology, Advances in Vaccines and Vaccination Strategies Addressing Vaccine Failures-An Indian Perspective. *Vaccines*, **7**. 10.3390/vaccines7030090
- Stenfeldt, C., Arzt, J. (2020). The Carrier Conundrum; A Review of Recent Advances and Persistent Gaps Regarding the Carrier State of Foot-and-Mouth Disease Virus. *Pathogens*, **9**. <https://doi.org/10.3390/pathogens9030167>
- VanderWaal, K., Gilbertson, M., Okanga, S., Allan, B.F., Craft, M.E., 2017. Seasonality and pathogen transmission in pastoral cattle contact networks. *Royal Society Open Science*, **4**, 170808. <https://doi.org/10.1098/rsos.170808>
- VanderWaal, K.L., Picasso, C., Enns, E.A., Craft, M.E., Alvarez, J., Fernandez, F., Gil, A., Perez, A., Wells, S., (2016). Network analysis of cattle movements in Uruguay: Quantifying heterogeneity for risk-based disease surveillance and control. *Preventive Veterinary Medicine*, **123**, 12–22. <https://doi.org/10.1016/j.prevetmed.2015.12.003>
- http://www.daph.gov.lk/web/images/content_image/publications/annual_reports/AnnualReport2018.pdf
- https://www.oie.int/fileadmin/Home/eng/Health_standards/tahm/3.01.08_FMD.pdf
- http://www.daph.gov.lk/web/images/pdf/animal_diseases.pdf
- <http://www.fao.org/ag/againfo/commissions/docs/pcp/cpcp-26012011.pdf>