Digitalization and innovation applied to the prevention and control of Foot-and-mouth And Similar Transboundary animal diseases (FAST)

Open Session of the EuFMD Standing Technical Committee

26-28 October 2022 - Hybrid event / Marseille (France)

European Commission for the Control of Foot-and-Mouth Disease

OS22
Book of abstracts

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European Commission for the Control of Foot-and-Mouth Disease

Welcome

Foot-and-mouth And Similar Transboundary (FAST) animal diseases pose a substantial threat to disease-free countries, where single incursions can have devastating outcomes, while controlling them in endemic areas can generate positive effects for national economies, livelihoods of livestock keepers, and animal welfare. Surveillance and control programs are often expensive and logistically challenging: in this context, developing integrated programs targeting FAST diseases with similar characteristics might improve use of resources, capacities and accelerate the achievement of animal health targets.

As many other sectors, veterinary services are experiencing a process of digital transformation characterised by the integration of new approaches, policies, and technologies into every aspect of disease surveillance and control. The COVID-19 pandemic has accelerated this trend: animal health professionals have to overcome many challenges, including travel restrictions and shortage of resources. This requires the use of new technologies and the application of creative strategies to reach stakeholders and achieve objectives in the most efficient way. How is digital transformation improving FAST capacity building, diagnostics, surveillance, and risk assessment? What cultural shifts, processes, and new technologies are changing the way in which we understand and control FAST diseases? What opportunities new technologies give for an improved FAST surveillance and control?

Research and innovation, digital tools and partnerships between public and private stakeholders in the veterinary domain can improve the control of FAST diseases and contribute to FAO's Strategic Framework in support of the 2030 Agenda through the transformation to more efficient, inclusive, resilient and sustainable agri-food systems for better production, better nutrition, a better environment, and a better life.

The OS22 will explore challenges and opportunities offered by digital transformation, innovation, and partnerships in the fight against FAST diseases.

Mr. Fabrizio Rosso

Deputy Executive Secretary of the European Commission for the Control of Foot-and-mouth Disease (EuFMD)

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Session I. Emergency preparedness and response

During the COVID-19 pandemic, emergency managers worldwide had to activate their emergency management plans in a virtual environment, and operate, at least partially, from virtual emergency operations centres. What lessons were identified from these experiences? Which parts of the emergency response could be managed virtually, and which still required face-to-face interaction? What systems need to be developed or improved to enable information exchange in the virtual environment? How has the engagement of stakeholders been affected by the use of virtual technology?.

Modelling to support contingency planning – Use of models has become essential to evaluate the impact of different response measures to FAST diseases. How can models contribute to improvements in contingency planning? What are the limitations of currently available models and how can they be overcome? How can models be used for real-time response planning?.

How can remote technology, such as unmanned aerial vehicles (drones), thermal imaging and artificial intelligence contribute to early detection of disease and surveillance in livestock and wildlife?.

Aim: To explore how digital transformation is supporting emergency preparedness and response and describe how new technologies can assist more efficient information exchange and timely decision-making in a response to a FMD and similar TADs incident.

FAST updates

Headline events from Global FMD surveillance activities (2020-2022)

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The WOAH/FAO FMD Laboratory Network was established in 2004 as a forum to exchange laboratory and epidemiology data for foot-and-mouth disease (FMD), as well as to harmonise and improve the quality of diagnostic testing carried out by international and national FMD laboratories. A key role of the Network is to monitor the spread of viral lineages that are maintained in the seven endemic pools distributed across the world, and continuously review the risks to livestock industries in countries that are free of FMD (with, or without vaccination). In addition to circulation of the pool-specific viruses, long-distance trans-pool movement of FMD viral lineages has been a common theme of recent reports generated by laboratories within the Network.

Since the last Open Session in 2020, particular attention has been focussed on the continued expansion of the O/ME-SA/Ind-2001e lineage which has become the dominant serotype O virus in Southeast Asia supplanting other lineages that were previously present (O/SEA/Mya-98 and O/ME-SA/PanAsia), and from where onward spread has caused extensive outbreaks on the Islands of Indonesia, a country that had previously maintained an FMD-free (without vaccination) status since 1990. Cases due to this

lineage have also been documented in Kazakhstan and Russia which are most closely related to viruses collected in Mongolia highlighting a new risk pathway for central Asian countries which is north of the Himalaya. In the European neighbourhood, FMD outbreaks occurring in the Eastern Mediterranean (Jordan, Israel and Palestine) have been caused by viruses from the O/ME-SA/PanAsia-2[ANT-10] sub-lineage, while in North Africa (Tunisia and Algeria), there have been new field outbreaks due to the O/EA-3 topotype which are most closely related to viruses collected in West Africa. The emergence of FMD in the Maghreb is a significant change of epidemiological status which may substantiate new trans-Saharan connections between North and West Africa (Pool 5). Elsewhere, the O/EA-2 topotype has spread into Southern Africa (Pool 6), where cases in Zambia, Namibia, Malawi and Mozambique represent the first time that this serotype has been detected in the region since 2000, when a virus of Asian origin (O/ME-SA/PanAsia) caused an outbreak in South Africa.

These unexpected events highlight the ease by which FMDV can cross international boundaries and emphasize the importance of the work undertaken by FMD Reference Laboratory Network to continuously monitor the global epidemiology of FMD and to assess the suitability of FMD vaccines to control outbreaks caused by these diverse viruses. Initiatives are underway to re-engage with field and labs teams in endemic countries to improve surveillance activities which have been impacted by the COVID-19 pandemic.

Session I. Oral presentations

More than technology: Experiences of virtual emergency operations centres (VEOCs) during the COVID-19 pandemic response in Canada

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Introduction

The aim of our research was to learn and discuss the personal experiences of Canadian emergency management professionals working in a VEOC environment during the COVID-19. The main research questions were;

What are emergency management professionals' personal experiences of working in a VEOC environment during the COVID-19 pandemic response?
What are the benefits and challenges emergency management professionals experienced working in a VEOC environment?
What lessons for VEOC planning, preparedness, and operations are available from these reflections on the COVID-19 response?

Methods

The International Association of Emergency Managers (IAEM) - Canada Professional Development Committee project team created a survey for data collection, and disseminated to all IAEM Canadian members and via social media. The survey consisted of 28 questions, collected over a 4-week period in September–October 2020. There were multiple-choice, open-ended, and short-answer questions. Each question was coded using an inductive method by two team members and then codes were compared. Where there was disagreement, the coders discussed the data and either incorporated the data into an existing code or created a new code.

Results

81 emergency management professionals from across Canada completed the survey. The findings highlighted VEOC challenges and strategies (both technical and non-technical), and explored working from home experiences before concluding with recommendations for future operations.

Discussion

More than half of respondents reported that COVID-19 was their first VEOC activation and working from home experience. Our research focused on the personal experiences of emergency managers. Respondents felt they were able to do their part in mitigating the spread of the virus, save time and money on travel, and increase productivity to juggle tasks and meetings. Coincidentally this resulted in organizational cost savings and fostering of change and innovation.

The benefits and challenges of working in a VEOC were both technical and non-technical. The most common strategies for technology were the use of familiar tools, ensuring sufficient bandwidth, and integrating a strong IT team into the EOC structure. The non-technological strategies included creating supporting processes for technical tools, providing 'just-in-time' and advance training, and encouraging the use of innovative solutions to increase situational awareness. Supporting staff's learning curve and caring for their mental health and well-being were deemed essential.

The findings highlight the fact that a VEOC is "more than technology" and existing tools cannot simply be migrated online. There is a need to incorporate three main elements into VEOC pre-planning and operations: Technology, Processes, and People. The process and technology is only as good as the people using it. Creating training and support for staff will help to develop skills required to work in a VEOC environment.

Digitising preparedness and response: case studies from Australia's biosecurity sector

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Introduction

In a sector that continues to witness increasing levels of risks that could disrupt our agricultural system, communities and economy, it is critical that we explore alternative means to preparing for and responding to emergencies. One such example has been the use of a virtual control centre (VCC) which has been considered here through a national (Exercise Network) and a state-based (QDAF VCC exercise series) example.

Materials and methods

Table 1 Comparative overview of Exercise Network and QDAF VCC exercise series.

	Exercise Network	QDAF VCC exercise series
Aim	Enhance the participants' preparedness to respond in a VCC.	Improve and formalise the implementation of VCCs for QDAF.
Timing	June 2021 Conducted over a two-week period	April 2022 – present Conducted over two days per exercise
System	Microsoft Teams	

Evaluation method	Observation, insights, lessons identified and lessons learned (OILL) process	

While these case studies were nuanced in their scope, both saw a strong focus on i) defining and testing processes for operationalising a VCC; and ii) developing capability in the use of a VCC. While both applied the OILL process for evaluation, the QDAF VCC exercise series also included double-looped learning that allowed a progressive integration of learnings.

Results

Table 2 Themed observations from Exercise Network and QDAF VCC exercise series.

Theme	Observations
People	Monitoring safety, health and wellbeing is hindered by limited visibility of body language and general performance. The range of digital proficiency is broader than anticipated.
Process	Establishing and managing information in an accurate and consistent manner is challenging. Processes for VCCs are in their infancy despite using 'business as usual' systems.
System and technology	Existing systems and technology, for the most part, are sufficient in meeting requirements of a VCC. IT infrastructure needs to be prepared and functional well in advance and repeatedly.

Discussion

While there have been challenges, the digitisation of responses has also offered some benefits. This includes having access to expertise regardless of location; activating responses within minutes; and minimising costs and disruptions when staff are 'deployed'. However, there remains much to be tested and refined in the establishment and management of a VCC.

Per Table 2, we no longer have the same level of visibility and connection. This, combined with the high-pressure and -paced environment and overlap between personal and professional circumstances pose risks of isolation, burnout and physical strains. This can be exacerbated by differences in digital proficiencies and access to 'enablers', such as equipment and support. Where resourcing allows, these risks ought to be mitigated through the provision of inductions, training, dedicated wellbeing and IT support, and establishment of a battle rhythm conducive to breaks.

Additionally, the implementation of processes, systems and technology require further attention. Fortunately, VCCs are cost-efficient in that existing resources appear capable to meet the needs of responding virtually. However, focus should be placed on establishing clear roles and responsibilities and guidelines for managing information (incl. approvals, confidentiality, sensitivity, common operating picture and version control), with an objective to complement response efforts, plans and existing structures. Iterative methods such as double-loop learning bolster the effectiveness of VCCs by providing a mechanism to identify gaps, barriers, and opportunities in capability, access, processes and systems and ultimately, integration and adoption.

The focus of the case studies has not been whether VCCs are better than a physical control centre. Rather, it has been to explore how we are able to optimise VCCs. The way we respond to emergencies has been redefined to be a spectrum between virtual and face-to-face. While physical control centres are recognised to remain the preference, alternative means must continue to be explored especially in preparing for major incidents, such as a foot-and-mouth disease incursion, which will undoubtedly demand support and resources beyond our borders.

New technologies to assist timely decision-making in a response and the use of modelling to support contingency planning.

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Models simulating spread of disease between animals, properties or countries have been used for decades in veterinary science. A disease transmission model is a simplification of the real world, build with the purpose of exploring and understanding the system, typically by answering "what-if" questions. Models are useful for evaluating scenarios that are difficult or impossible to carry out in real life due to e.g. economic or ethical constraints.

Especially after and during the large epidemics of classical swine fever (CSF) in the Netherlands in 1997 and foot-and-mouth disease (FMD) in the United Kingdom in 2001 and 2007, simulation models were used in veterinary contingency to investigate the efficiency of alternative control strategies. However, models should preferably be built and used in "peace-time"; though it is highly likely that risk managers will ask additional questions, requiring new model runs and model features, during an epidemic. Additionally, to compare control strategies, models can be used to investigate zone sizes, surveillance strategies, resource constraints and bottlenecks in the system.

New technologies to assist timely decision-making includes models built with the purpose of estimating the risk of disease introduction to certain countries or areas, based on outbreaks and transmission routes from neighboring countries. These types of models include models for horizon scanning and generic risk assessment models used to estimate risk of disease introduction.

By scanning the horizon, being aware of what will arise, investigating known transmission routes and having contingency plans ready for potential epidemics, it is possible to continuously optimize the control response system to fit the expected challenges. The rising questions are still; will the resources spent on being prepared outweigh the resources saved; can we easily tune the system as quickly as changes occur; and what happens when, despite all efforts, the experienced epidemic is unexpected?

Emergency vaccination as an additional measure to control a potential outbreak of FMD in Austria. Would it be useful?

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Introduction

Due to its potentially serious socio-economic impact, foot-and-mouth disease (FMD) remains one of the major threats to animal health and the livestock industry, drawing attention of veterinary authorities worldwide. Austria has not experienced an FMD outbreak over the past few decades

however, due to the current trends in globalisation, it must be assumed that there is a constant risk of FMD introduction into FMD-free countries. In the event of an FMD epidemic, Austria would follow the common European policy in eradication effort, where emergency vaccination is increasingly recognized as a useful additional control measure. A simulation study has been carried out to compare the effectiveness and the economic impact of conventional control policy (i.e. stamping out) with various vaccination strategies, aimed to identify the circumstances, in which emergency vaccination would be useful to control an FMD outbreak in Austria.

Materials and Methods

To simulate the hypothetical spread of FMD within and between herds, the stochastic spatial simulation model EuFMDiS (The European Foot-and-Mouth Disease Spread Model) was used. To evaluate the effectiveness of different vaccination approaches a range of initial outbreak conditions was selected. This included the region of the incursion, type of source herd, length of the silent phase and resourcing level. All initial scenarios were run until a fixed detection day (i.e. 14 or 21); the outbreak situation at first detection was saved as a 'snapshot'. Starting from this identical detection point, a number of alternative control strategies incorporating emergency vaccination, differing in terms of targeting species and start of vaccination, were compared. Such an approach ensures that each iteration of a simulation has an identical set of infected herds on the day of the first detection. The epidemiological results of these strategies, including the number of infected herds, the epidemic control duration, and the number of culled and vaccinated animals were compared with the conventional policy. In addition, the economic implications resulting from emergency vaccination scenarios were estimated by the EuFMDiS model (direct cost, i.e. cost of control activities) and by our own economic model (indirect cost, i.e. losses due to export bans and production losses resulting from business interruption). Wilcoxon rank-sum test was used to test the statistical differences between the implemented strategies and the stamping out policy.

Results

The preliminary results show that outbreaks of small dimensions (e.g. outbreaks initiated in low livestock density regions) can be effectively controlled by stamping out without vaccination. In cases of large epidemics, the magnitude of the outbreaks can be significantly reduced when implementing emergency vaccination. The extent of this reduction depends on various factors such as the trigger day of the vaccination, vaccination targeted species and the capacity of personnel resources. As a result of current international standards for regaining FMD-free status, trade impact under all vaccination strategies exceeds trade impact under the stamping out policy. Reduction of export losses can only be achieved when vaccinated animals are removed from the population. Our results show that targeted vaccination strategies can reduce the number of animals vaccinated and still control the outbreak effectively.

Discussion

Based on the simulation results, resources and effort during an FMD outbreak in Austria should first be placed on stamping out policy. However, emergency vaccination should be considered a useful option if there are indicators that might predict an extensive epidemic, such as a high number of infected herds at the beginning of the control phase or delayed first detection.

Simulation of FMD spread and mitigation measures in the Danish livestock population

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Introduction

As Denmark has not had an foot and mouth disease (FMD)-outbreak since 1983, the objective of this study was to use epidemiological modelling to compare the effects of a set of different mitigation measures on e.g. predicted number of infected and culled herds, and epidemic control duration1. The epidemiological impact of basic mitigation measures was compared to additional mitigation strategies on top of the basic measures. Additionally, the geographical influence and the impact of specific cattle production systems as index herds were analysed in terms of the predictive variables.

Materials and methods

To simulate the spread, detection, and control of FMD, the European livestock disease modelling framework (EuFMDiS) was used. In this model, 33,329 Danish herds (n= 28,748 farms) with in total 14.90 million livestock was incorporated, all susceptible to FMD. The proportions of infected animals within the herd determine the likelihood that a contact of source herds leads to an infection in destination herds. The model considers the spread between herds in daily time steps through direct contacts, market spread, indirect contacts, airborne spread and local spread. In farms practicing high levels of external biosecurity, we suspected a lower risk of becoming infected through the local spread and indirect contact pathways.

We modelled a hypothetical introduction of a Type O Pan-Asia strain in North Denmark, Central Denmark, South Denmark, and Zealand/Capital on the 29th of September 2022. We randomly selected 1,000 cattle index herds per region. In each iteration, a different cattle herd was chosen to include the production variation between the cattle herds in Denmark (Scenario 1). In another scenario, only commercial dairy herds (n=1,000) were chosen randomly in the entire Denmark (Scenario 2).

The model was run initially without any control measures until the end of Day 21, when the first FMD case was assumed to be detected. From the day of detections onwards, basic mitigation measures and/ or additional mitigation scenarios were investigated. These additional mitigation measures ranged from a larger protection zone (from 3 to 5km) and surveillance zone (from 10 to 15km) to implementation of a vaccination campaign.

Results

The model results indicated that the outbreaks size in Scenario 1 would most likely be relatively small (median infected farms: 1 in Zealand to 13 in South) and of short duration (range of median control1 days: 30 in Zealand to 44 in South). There were no significant differences within the regions between the different mitigation measures regarding infected farms. However, the control duration between the basic strategy and pre-emptive depopulation strategy varied within North, Central and South of Denmark (Scenario 1).

In case the first infection was detected in commercial dairy herd (Scenario 2) the average number of infected farms and control duration were 3.2 and 1.6 times higher, respectively, compared to results across all production system (Scenario 1). The enlargement of the zones and depopulation increased the control duration but did not reduce the number of infected farms significantly. When ring vaccination was implemented within 1 km radius around each infected herds 14 days after outbreak detection, there was a trend of reduced numbers of infected farms (Scenario 2).

Discussion

The comparison of Scenarios 1 and 2 in terms of the size and duration of the epidemic shows that the chosen index herd significantly influenced the course of an epidemic. Furthermore, the model indicated that the basic mitigation measures would be sufficient to control the FMD outbreak in Denmark with the assumed availability of human resources in these Scenarios.

Reducing producer losses in a FMD outbreak through implementing trading zones

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Introduction

Application of trading zones when managing livestock disease outbreaks has the potential to markedly reduce the economic impact of trade restrictions placed on countries. This involves establishing areas within a country, which are considered of negligible risk of transmitting disease through livestock and livestock product shipments to other areas of the country or internationally. The objective of this study was to estimate the economic benefits of trading zones as part of foot-and-mouth disease (FMD) control measures for limited duration outbreaks in Australia.

Materials and Methods

FMD incursion scenarios (n=11) were simulated with the Australian Animal Disease Spread model (AADIS). The simulations provided information on the size, geographic extent and the duration of outbreaks, while the number of animals culled due to disease provided supply shocks. Trading zones were based on state/territory borders. Following detection, a 3-day national standstill of susceptible livestock was assumed along with a 14-day national embargo on exports of susceptible livestock and livestock products. From day 15 of the outbreak, the national embargoes were replaced with trading zones formed by the unaffected state(s) resuming exports based on historical trade responses to FMD affected exporting countries. The export recovery duration data were combined with historical export data to estimate the share of Australian exports that could be embargoed. The market impacts of the potential export embargoes were simulated within the Australian Bureau of Agricultural and Resource Economics and Sciences' *AgEmissions* partial equilibrium model of Australian agriculture.

Results

Trading zones allowed unaffected Australian states to resume exports earlier. Under a national embargo, losses in producer returns (as measured by producer revenues) are between AUD 7 billion and 13 billion for limited outbreaks. Applying trading zones, reduced these losses to between $4 billion and $8 billion (21% to 80% reduction). For a larger simulated outbreak in Victoria, national producer losses were reduced by AUD 4 billion under a stamping out plus vaccination approach combined with trading zones applied in a stepwise progression, compared to an outbreak where stamping out alone is implemented with trading zones.

Discussion

An outbreak of FMD in Australia will result in large costs to both producers and the government with most of this due to trade-related economic losses. Although there is uncertainty about how long an exporting country might be excluded from international markets if an FMD outbreak occurs, large reductions in losses are possible if trading zones are able to be used to maintain trade from uninfected parts of Australia. Prior discussions with importing countries could facilitate acceptance of trading zones.

OutCosT-Rum, a tool to support countries in the evaluation of the economic impact of TADs affecting ruminants

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Introduction

The occurrence of transboundary animal diseases (TADs) causes serious socio-economic consequences, as it affects productivity, welfare, livelihoods, food security and trade. Communities that mainly depend on livestock are the most vulnerable, and the consequences of TADs may vary within and across countries/areas depending on the disease and its spread, the structure of the livestock sector, the social context and related control strategies. Therefore, it is often difficult to provide systematic estimates of their economic impact. The objective of this study was to develop a tool for the economic evaluation of any TADs affecting ruminants, by adapting and validating the already available tool for swine disease outbreaks, known as OutCosT-Pig.

Materials and methods

The OUTbreak COSting Tool for ruminants (OutCosT-Rum) is based on a deterministic model. It is built in Excel and composed by several spreadsheets: one for input data, three for results, and the last is dedicated to a qualitative assessment of indirect and non-monetary costs. Users can define up to eight different types of farms according to the country's specific definitions and classifications. OutCosT-Rum requires five main groups of input parameters: a) census, production parameters and prices; b) data on outbreaks and control measures in affected farms/areas; c) data on control measures in neighbouring and at-risk farms; d) data on surveillance and control activities in the livestock population, wildlife and /or vectors; and e) other activities that might be carried out, such as trainings, communication, or coordination tasks.

Results

As outputs, the model calculates the cost of 101 items related to: the disease and treatments (N11); diagnostic activities and control measures in affected farms (N29); measures in neighbouring and at-risk farms (N21); control and surveillance activities in general population (N20) and in wildlife/vectors (N10); trainings, communication, or coordination activities (N10). Results are shown for the whole area, and by farm type. Moreover, OutCosT-Rum allows differentiating between costs assumed by veterinary services, farmers, or other stakeholders. The tool can be used to calculate the cost of disease outbreak retrospectively, but also to estimate the potential cost of future outbreaks and alternative response strategies. The validation process is ongoing, and the tool is being tested through various case studies, i.e. real outbreaks of sheep pox and goat pox that affected Greece in 2013-2015 and 2016-2018, the real outbreaks of peste des petits ruminants (2018) and foot-and-mouth disease (2011) in Bulgaria, and a hypothetical scenario of future potential outbreaks of lumpy skin disease in Central Asia.

Discussion

OutCosT aims at supporting authorities to respond to TADs by estimating the associated costs and budgetary needs for diseases control. The results can be used for advocacy purposes to mobilize resources at national/international levels, ensuring that the response to outbreaks is not delayed, and to raise awareness on the impact of infectious diseases, promoting public trust in local government and collaborations with the private sector. Further development are ongoing to link the tool with the "European Foot-and-Mouth Disease Spread Model" (EuFMDiS) by automatically feeding some input values from the outputs generated by the EuFMDiS.

Modelling livestock infectious disease control policy under differing social perspectives on vaccination behaviour

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Introduction

The spread of infection amongst livestock depends not only on the traits of the pathogen and the livestock themselves but also on the veterinary health behaviours of farmers and how this impacts their implementation of disease control measures. Disease management practices employed by livestock owners can vary, due to differing responses to complex factors such as increased awareness of disease risks, pressure to conform to social expectations and the direct imposition of animal health regulations. Controls that are costly may make it beneficial for individuals to rely on the protection offered by others, though that may be sub-optimal for the population. Therefore, failing to account for socio-behavioural properties may produce a substantial layer of bias in infectious disease models.

Materials and methods

We investigated the role of heterogeneity in vaccine response across a population of farmers on epidemic outbreaks amongst livestock. Using a mathematical model we simulated the transmission of a pathogen with characteristics akin to FMD over spatial landscapes of farms for two counties in England (Cumbria and Devon). Under different compositions of three vaccine behaviour groups (precautionary, reactionary, and non-vaccination), we evaluated from population- and individual-level perspectives the optimum threshold distance to premises with notified infection that would trigger responsive vaccination by the reactionary vaccination group.

Results

On our data-informed livestock systems, we demonstrate a divergence between population and individual perspectives in the optimal scale of reactive voluntary vaccination response. In general, minimising the population-level perspective cost requires a broader reactive uptake of the intervention, whilst optimising the outcome for the average individual increased the likelihood of larger scale disease outbreaks (Figure 1). On the other hand, when the relative cost of vaccination was low and most premises had undergone precautionary vaccination, adopting a perspective that optimised the outcome for an individual gave a broader spatial extent of reactive vaccination response.

Discussion

Mathematical models integrating epidemiological and socio-behavioural properties can identify instances of strong disagreement between the intervention stringency that is best from the perspective of a stakeholder responsible for supporting the livestock industry compared to a sole livestock owner. Under our assumed epidemiological context, these modelling insights can aid our understanding of how stakeholders may react to veterinary health interventions. If discord between perspectives was anticipated, the findings may inform those managing veterinary health policy of the requisite reduction in intervention cost and the required extent of nurturing beneficial community attitudes towards interventions.

Session I. Posters presentations

Developing a GIS-based decision support system to manage TADs in Mizoram, India.

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Introduction

Mizoram, a mountainous state nestling in the southern tip of the northeastern region of India, remains in constant threat of TADs, affecting the growth of livestock value chains. In recent years, the State suffered from Porcine Reproductive and Respiratory Syndrome (PRRS) outbreak. Subsequently, the first outbreak of African Swine Fever (ASF) emerged and is continuing.
The existing initiatives within the State primarily focus on emergency management cycle stages, viz. prepare, prevent, and detect. The expected outcome of the study is policy initiatives to enable the commissioning of a GIS-based decision support system (DSS) to support the implementation of action plans related to the 'response' and 'recover' phases.

Approach and methods

The study considered the following approaches to develop a technical design architecture for the GIS-based DSS
A landscape study covering policy, legal, and administrative aspects
Qualitative socio-economic risk analysis and mapping of illegal livestock trade routes
Aggregation, collation, and digitization of data

Besides desk review, the study supported expert consultation with the Government of India's space application center to explore local resource availability and develop a prototype. The following tools facilitated data collection:

Secondary data collection guide
Public infrastructure data collection guide
Data aggregation guide
Guide for Focus Group Discussions and Key informant interview

Result and Discussion

Based on the learning from the landscape study and socio-economic risk analysis, the study recommended a set of suggestions, mainly focusing on creating an enabling environment for the commissioning and using a planned DSS.
In the study, the technical design architecture of the DSS suggested a dashboard and a mobile application. The designed architecture applied the knowledge related to Good disease-related Emergency Management Practices (GEMP). It covered a series of logic under the following heads to help in decisions related to:

- Immediate notification/demarcation of infected and surveillance zone
- Resource allocation/demonstration of the success of control measures for private investment and trade facilitation
- Targeted actions (Preparedness, response)
- Resource mobilization/ utilization of infrastructure/institutions

- Livestock movement control
- Revival of the industry
- Management of operations by livestock producers (individuals and collectives)

The suggested logic under the above will use six data sets: disease outbreak data, geo-location data, natural data, census data, infrastructure data, and institutional data. Besides logic, preliminary digital datasets, including collected details of illegal trade routes, supported the development of a basic prototype by the North Eastern Space Applications Center (NESAC), Government of India.

The roadmap for implementation includes engagement with technical systems experts to scale up the basic prototype by deploying need-based GIS and other related spatial technologies.

A deep learning based approach for FMD detection

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Introduction

The research gives a new approach to the detection of foot and mouth disease (FMD) using deep learning techniques. The purpose of this study is to provide a timely and accurate early detection of FMD in cattle based on the symptoms. There is a shortage of veterinary specialists across the country due to brain drain which leaves farmer's cattle vulnerable, timeous advice for the detection of FMD as the disease leads to loss of production of livestock meats and also milk to farmers and also a major impediment as countries with foot and mouth faces trade restrictions moreover the disease is difficult and costly to control and eradicate.

Materials and methods

In this study images were acquired from the Internet, Veterinary department, European Union Foot and Mouth division (EuFMD), and also Pirbright Institute. Healthy cattle images were taken from the University of Zimbabwe farm with mixed cattle breeds. The healthy cattle dataset of JPEG images was taken with a Nikon D5300 24-MP digital camera. Foot and mouth images acquired are taken by different devices (cameras, smartphones) in variable conditions and have different resolutions. Images were classified into different classes since we are using supervised learning. Datasets are grouped into three data sets which are the Training directory, Validation directory, and also the Testing directory. Five classes of symptoms were assessed drooling, teat lesion, Gum lesion, tongue lesion, and feet lesion. Images were also preprocessed and different deep learning models were trained to learn features of both healthy and diseased cattle so that these features can be recognized for the classification of images never seen by the deep learning system.

Results

Different deep learning architectures using transfer learning were assessed and the Densenet 201 outperformed other models with an accuracy of 93.75%, precision 0.98, sensitivity 1.0, specificity 0.9916, AUC 0.99, and ROC of 0.9958. The model was able to detect images that it has never seen with Foot and mouth and thoses that are form healthy cattle.

Discussion

The results also showed the importance of color information and image focus in the identification of FMD. The deep learning system will be used for the development of a mobile application for the detection of FMD. The research under investigation is not intended to replace existing solutions for disease diagnosis, but rather to supplement them by early detection of FMD.

Understanding the level of preparedness to use emergency vaccination for FAST diseases in European countries

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Introduction

EuFMD is conducting a program of work to better understand the role of emergency vaccination for Foot and Mouth Disease (FMD) and similar Transboundary Animal Diseases (FAST) in Europe and its neighbourhood.

Materials and Methods

In 2022, EuFMD hosted two online workshops with participants from EuFMD member nations and other organisations. Participants used scenarios modelled in four European countries to develop a list of criteria for implementing emergency vaccination. Subsequent epidemiological modelling compared the effect of different emergency control measures, including different vaccination strategies, on hypothetical outbreaks of FMD in four different European countries. Scenarios were simulated using the stochastic spatial simulation model EuFMDiS (The European Foot-and-Mouth Disease Spread Model).

The scenarios modelled for these workshops were selected on the basis that they would lead to discussion and were not necessarily 'typical' of expected outbreaks in the selected countries.

Results and Discussion

There was considerable variation in effectiveness of vaccination as a control tool in the scenarios. The model outcomes indicated that emergency vaccination could reduce the chances of a large outbreak in some circumstances, particularly if response resources were constrained. Emergency vaccination appeared more applicable when an FMD outbreak occurred in densely stocked areas, and particularly if resources for control were constrained. The limited nature of the scenarios selected for demonstration purposes, meant that no general conclusions on the effectiveness of emergency vaccination can be drawn from this work.

For countries that export livestock and livestock products, negative trade impacts, associated with a longer interval to regain recognition of FMD freedom, are a disincentive to considering emergency vaccination as an economically viable control option for FMD.

The apparent complications of managing a vaccinated livestock population were also considered a constraint to using emergency vaccination, which might be mitigated if trade could continue from unvaccinated zones following completion of eradication activities.

The decision to use emergency vaccination in response to a FMD outbreak is based on many complex factors. While it may be technically feasible to manage an FMD outbreak in a previously free country with stamping out measures and pre-emptive culling, participants acknowledged that social and political factors may contribute to the decision implement emergency vaccination. It is therefore important that contingency plans consider the potential role of emergency vaccination, when and how to best implement it, and the management of vaccinated livestock populations.

The use of scenarios based on simulation modeling of country data was an engaging way for participants to consider the pros and cons of emergency vaccination for FMD. Use of modelling can

support development and review of contingency plans for FAST diseases.

Response system to outbreak of transboundary animal diseases with GPS and deep learning

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Introduction

A response system including outbreak investigation, emergency control measures, and risk assessment in the event of transboundary animal diseases such as foot-and-mouth disease (FMD), African swine fever (ASF), and highly pathogenic avian influenza (HPAI) in Korea, is describe in this presentation.

Materials and Methods

All data related to animal health in Korea are collectively managed by Korea Animal Health Integrated System (KAHIS). The big data platform was used to generate and manage epidemiological data for use in the event of disease outbreak in livestock farms. Signals emitted from device of global positioning system (GPS) attached to the livestock vehicles are tracked. The risk of disease outbreak in livestock farms is analyzed using deep learning techniques with information on farms and vehicle movement. Then reports are prepared using the robotic process automation (RPA) system.

Results

During last five years, from January 2017 to December 2021, 14 outbreaks of FMD, 21 ASF and 308 HPAI were confirmed in livestock farms in Korea. In each outbreak, as soon as a suspicious or infected animal was found, the livestock vehicles that visited the farm was listed, and farms visited by these vehicles were searched for. And the risk of the disease outbreak on these epidemiologically-linked farms was evaluated. The reports of the risk assessment were communicated to animal health institutes across the country. In case of detecting antigen of ASF or HPAI in wild animals, the risk of the outbreak in livestock farms was evaluated by tracking vehicles passed around the detection point. When conducting an epidemiological investigation at an outbreak farm, information (i.e., farms, satellite images, laboratory tests for surveillance, biosecurity inspections, visitors, and vaccinations, etc.) extracting from KAHIS in advance was accompanied.

Discussion

Various epidemiological tools are continuously being upgraded to effectively respond to outbreak of transboundary animal diseases. In Korea, research on data generated by the latest technology such as smart farm is being conducted for outbreak investigation. The digital transformation is playing an important role in improving effectiveness of animal health management.

Session II. Digital learning for veterinarians

Is access to digital learning tools creating barriers? Can we support those who do not have access to digital resources? How do we ensure that digitalization of learning does not increase the gap between learners from different settings?.

What are the digital skills needed to facilitate an effective and prompt response to animal health emergencies? How the growth on demand for new digital skills is envisaged in the near future and how can it be addressed?.

How can social learning improve veterinary capacity development?.

Are veterinarians equipped with the right digital tools that can enhance their work? Are animal health workers provided with the right digital skills to meet Continuous Professional Development and to meet the evidence of capacity development needed by countries?.

Aim

To discuss how equipping veterinarians with digital skills, enhancing the learning via digital and remote peers-to-peers modalities and increasing the access to digital learning tools represent an opportunity to develop capacity in the animal health sector for FAST disease control.

Session II. Oral presentations

Exploring the frontiers of digital possibilities - innovating for veterinary education and FAST disease control

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The rapid growth of consumer technology has increasingly played a huge role in shaping both expectations and motivations for adoption of new learning technologies. The COVID-19 pandemic led to an acceleration in the development and use of online technologies in education, as institutions found themselves forced to pivot to digital learning.
Training in the veterinary sector has not been exempt from the acceleration in digital innovation and there are growing numbers of technological developments in veterinary training and by extension, in the way in which veterinary services are delivered. These developments include mobile technologies, artificial intelligence and learner analytics, amongst a variety of others.
This presentation will explore various elements of digital innovation in veterinary education and consider the digital skills required and how these digital disruptors relate to FAST disease control, including potential barriers to access by learners.

Digital training as enabler for digital transformation of veterinary practice

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Introduction

Digital tools provide ample opportunities for fast communication, monitoring and quick risk assessment. A veterinary workforce that embraces new technologies and makes use of available tools can at large contribute to better preparedness and response to FAST disease outbreaks and beyond. Training, including digital training (DT), can hugely support the digital transformation of veterinary practice. DT in particular can increase outreach in a harmonized approach, facilitate access to more veterinary healthcare workers - even those established in remote areas, allow the individualization of the learning process and be cost-effective. It can also be an important tool for increasing resilience both in peace and crisis periods, such as in cases of FAST disease outbreaks. This review discusses opportunities and policy gaps related to the use of DT for continuous professional development (CPD) of the veterinary workforce.

Material and methods

Opportunities and threats related to DT are discussed against the latest European policy recommendations, such as the European Union principles for the design and issuance of micro-credentials, and the opinion of the European Coordination Committee on Veterinary Training on the impact of digital technologies & artificial intelligence in veterinary education and practice.

Results and discussion

Currently, more and more online courses and programmes are available worldwide, reaching out simultaneously to a big number of veterinarians and paraprofessionals located in many countries. Nonetheless, these advancements do not come with opportunities only. DT is not yet accessible for all. It requires special infrastructure, which is not for-granted everywhere. On top of it, digitalization requires some minimum skills and understanding, which happens often to be an indication of a generation or a societal gap. Professional ethics and deontology, validation of new technologies, data ownership and management are still largely unregulated even in the developed world, while issues like protection of personal data, data-sharing and data-manipulation are still not-well understood by individuals. When it comes to DT, issues related to quality of training and recognition of competences achieved that way are of major importance as well. Professionals need relevant education at first place and recognition of achieved skills as part of their professional development portfolio. DT shall cover these needs, thought it has to be anchored to the same set of standards applying for any kind of training, *e.g.* the European Union principles. That is to say that DT must subject to internal and external quality assurance; ensure transparency via the implementation of measurable, comparable and understandable (micro-)credentials linked to clear learning outcomes, workload, content, level, etc.; be relevant to lead to knowledge upgrade and professional development; follow a valid assessment against transparent standards leading to accreditation; be designed to be part of wider learning pathways; be recognized via standard procedures for recognizing foreign qualifications and learning periods abroad and be easily attached to the credential-holder portfolio to be used for academic or employment purposes.

In conclusion, DT does offer opportunities for an easy, informed, equal-opportunity and ethical digital transformation of veterinary practice provided that an appropriate framework is in place to cover the needs of all these professionals.

The application of virtual reality to FMD education

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Introduction

This presentation shows how Virtual Reality (VR) can be used as a biosecurity training tool to better equip animal industry workers to undertake emergency animal disease surveillance.
A pilot training application for foot-and-mouth disease (FMD) education using VR is being developed in 2 phases by Australian VR company Novus Res Pty Ltd in partnership with the Australian Department of Agriculture, Fisheries and Forestry (DAFF) and the European Commission for the Control of Foot-and-Mouth Disease (EuFMD). The aim is to determine how VR can be used as a cost-effective, scalable and realistic tool for FMD-related emergency training and response purposes.

Materials and methods

Phase 1 of the VR FMD pilot application used the Oculus Quest headset—a VR headset developed by Oculus, a division of Meta Platforms—with Australian-developed software, to examine the potential of VR in educating animal health workers conducting surveillance for FMD. The application comprised modules covering a range of FMD training concepts, each demonstrating elements of FMD biosecurity training that are well-suited to VR. The modules include establishing biosecurity control points, conducting FMD investigations on livestock, taking samples, and interviewing landowners. Users can then use their hands to perform a set of FMD surveillance-related training tasks while on a virtual farm.

Phase 2 further developed the pilot application to include the following enhancements:

greater realism to take advantage of the newer, more capable Oculus Quest 2 headset
additional content including a greater variety of FMD lesions and animal handling
assessment of user learning embedded within the module and multiplayer support, allowing multiple users to interact in the same virtual space.

Results

In evaluations of the Phase 1 experience by DAFF involving approximately 30 users, a high proportion (all users) reported that they would recommend the technology to colleagues, and users considered the technology would be useful as a supplement to other forms of learning for emergency animal disease response training.

Phase 2 will be evaluated during the second half of 2022.

Discussion

The VR technology's tracking, frame and refresh rates have improved since Phase 1 of the pilot program. The cost has reduced over time, and the technology now allows multiple users to share a single immersive environment.
In time, there is scope for VR training to become part of a veterinarian's (and other animal industry workers') educational experiences, and improve trainees' skills in examining animals for exotic diseases.

Trust and social learning in the veterinarian sector: Perspectives from the social sciences

K. Bardosh

Available upon request

Animal Health Service needs assessment study in Nigeria

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Introduction

This research was commissioned by the EUFMD and its partners, the Veterinary World Association and Health for Animals as part of the needs assessment to guide implementation of the project "Sustainable business in animal health through training of veterinary paraprofessionals. The project aims to increase livestock productivity among small holder farmers in Nigeria through competency and capacity development of veterinary paraprofessionals (VPPs). The goal of the research is to explore capacity building opportunities for Veterinary Paraprofessionals and suggest the most appropriate modes of delivery of such training.The study looked critically at the issues around barriers to inclusive delivery of online/digital based trainings especially from the gender perspective. training modalities.

Materials and Methods

The research used quantitative and qualitative methods to collect primary regarding business environment and access to continuous professional learnings. Data from VPPs in two pilot states in Nigeria (Kaduna and Oyo state). Both states have a big number of veterinary paraprofessionals and a thriving livestock industry, which creates commercial potential for the target demographic For the quantitative survey, 150 VPPs were interviewed via telephone surveys, While for the qualitative survey 78 VPPs were engaged in 12 sessions of focus group discussions (FGDs) in line with the principles of participatory rural assessments.

Results

The collected data revealed that VPPs generally appreciate blended training models that comprises online and offline methods. Although VPPs in rural areas prefer face-to-face training, urban based VPPs prefer online -based trainings. It was also found that female VPPs preferred the online training as it helps them overcome managing household responsibilities and meeting up with the training schedule. However, there is gender disparity in the responses regarding internet access as female VPPs tend to have lower access to internet due to financial constraint compared to their male counterparts. financially deficient females that cannot afford the bandwidth cost and rely on the text-based modules for self-study. In terms of access to digital learning devices, 96% have access to smart phones while only 26% have owned a laptop computer.

Discussion

The study was able to find the preferences of VPPs in Nigeria when it came to learning and training as well as areas of weakness and challenges they faced. Although access to devices and internet is generally high, there is a serious gender disparity as well as rural-urban digital divide and this poses a threat to inclusivity of digital learnings for veterinary paraprofessionals. Blended(online and offline) modalities is hereby recommended to solve the potential divide. Also, digital learning programs should consider incentivizing female learners to with internet data costs to encourage inclusiveness. However, while physical learning encourages networking, online learning tends to get more attention among

urban dwellers and female VPPs. It is easier to demonstrate training in different language learning styles for ease of access.

TOM a Training Management System

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Introduction

Member Nations and relevant stakeholders have asked EuFMD to provide an efficient solution to enable National Veterinary services to map the progression of the individual skills, monitor the development of capacity and incentivize veterinarians' education.
TOM aims to support National Veterinary authorities to develop capacity development, identifying the gaps in specific competencies and how to fill the gaps.

Materials and Methods

TOM has two main pillars:
A competency framework which identifies the behaviours or activities that someone needs to be able to perform based on their role in the organization. Frameworks were built using competencies pulled from EuFMD Get Prepared, PCP and PVS tools, OIE Day 1 competencies, CFIA competency framework , CDC and APHL and EuFMD course learning objectives. Frameworks were developed by identifying behaviours that were common and validated by internal experts.
A web based app that takes all the data and presents it in an easy to access format allowing National Veterinary Authorities and learners to independently identify training gaps and plan for capacity development.

Results

Within the web app learners can see the details of the competency framework, their current and required competency levels and the courses required to achieve a higher competency level.
National Veterinary Authorities can access the same individual learner level data for those within their organization. In addition they also have access to organizational position level data such as staffing levels and the competency levels for employees who hold a particular position in the organization (see Fig 1.)

Discussion

TOM can provide the information that can help both organizations and individuals be intentional and strategic in how they use their available resources to develop capacity.
Questions Tom can help answer include:

Do we have adequate staff levels?
Is there a particular role in our organization with a significant competency gap?
What is behaviours would staff display on the job with additional training?
What training should be prioritized for delivery at the organizational level?
What training should an individual request for career development

The WOAH innovation to the competency-based eLearning

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A competency-based approach able to incorporate the knowledge produced by the World Organisation for Animal Health (WOAH), is the basis of its new Training System. Organised around sixteen competency packages (CPs), the system aims at developing capacities in WOAH Members to facilitate the implementation of the international standards and guidelines and to strengthen Veterinary Services resilience, in the new contexts and expected roles.

Each competency-package is being developed respecting specific terms of reference that describe the technical domains, their links to the WOAH knowledge (standards, guidelines, strategies, and frameworks) and to the critical competencies that build the Performance of Veterinary Services (PVS) evaluation. Each domain includes the expected learning outcomes for three different levels of expertise, Day 1, Day 2, and expert level, as well as for the WOAH delegates. Thanks to a cross-reference system and based on a learner-centred approach, the digital training resources being developed are feeding the competency packages and can be used by learners to build their individual learning pathway and competency portfolio.

The digital resources are eLearning modules produced respecting specific guidelines – developed by the WOAH Platform for the Training of the Veterinary Services – defining core and advanced standards on the intended target audience, the learning objectives, the delivery methods, the learning assessment, the human resources involved in the module development, the module design, the learning approach, the technology used, risk management, and continuous improvement.

The ambition is to dispose of a solid training offer able to attract cross-sector professionals and build a learning community able to move from individual to peer-to-peer collaborative learning.
A priority competency package under development is CP2, dedicated to quality and management of veterinary service: three eModules on Leadership in Veterinary Services are expected to go live in late 2022.

A Common Content Box lead learners through the leadership theories and characteristics, with contextualized applications in Veterinary Services. The learning approach privileges a learning process that from the general concepts leads learners to specific situational experiences.

The module-specific learning activities adopt the opposite pathway: from specific situations, learners are asked to recognize the leadership characteristics and styles, take decisions, or evaluate behaviours. An experiential learning is facilitated by serious games based on video story telling representing realistic situations that veterinary staff encounter in their professional life. The video-stories describe facts and circumstances in times of peace and emergency, of gradual complexity, adapt to learners belonging to intermediate, expert and WHOA delegate/Chief Veterinary Office levels.

The management of a suspected outbreak of foot-and-mouth disease has been selected for the intermediate level, aiming at strengthening leadership capacity in crisis situations, through an immersive learning experience based on a story-telling that starts from an outbreak suspicion to its confirmation and communication. Other eight serious game complete the learning pathway.

The robustness of the competency-based training framework, the use of advanced learning methodologies based on quality standards and technological innovation, and a customised learning offer adapt to the different levels of expertise, are the basis of the WOAH training system, aiming at contributing to strengthen the capacities of the Veterinary Services and (as relevant) of the other components of the One Health Systems that countries are called to build and develop.

FAO elearning academy: Innovative learning methodologies and digital inclusion for sustainable animal health

C. Petracchi

The overall objective of the FAO elearning Academy is "universal education", for free, offered as a global public good, to anyone, at anytime and anywhere in the world... democratizing education, offering free learning opportunities, inclusivity, scalability, transparency in certification, with no greenhouse gas emissions, no limitations of physical presence, and competitiveness for inclusion in the professional market.

We promote digital inclusion in all its possible meanings: gender, youth, marginalized individuals, indigenous groups, citizens in conflicts and post conflict areas have the same educational rights and opportunities, and so far we have reached over 800,000 learners worldwide!.
We strive to fill the gap between formal and informal education, allowing professionals to easily and efficiently acquire the competencies they need to become more competitive and relevant https://elearning.fao.org/

The FAO elearning Academy offers over 500 multilingual certified e-learning courses, free of charge, as a global public good, for professionals working in animal health, food and nutrition security, social and economic development, and sustainable management of natural resources, and is the result of a collaborative effort involving over 400 partners throughout the world https://elearning.fao.org/mod/partner/view.php?id=4704.

The FAO elearning Academy is adopting the Digital Badges Certification System, to certify the acquisition of competencies, in order to progress talents within organizations and increase employment opportunities. Certification granted by FAO, by passing the final scenario-based performance evaluation, is now associated to the FAO elearning courses https://elearning.fao.org/mod/page/view.php?id=5179
To better understand our pedagogical models, learning solutions and initiatives: FAO elearning Guide on methodologies and good practices https://www.fao.org/3/i2516e/i2516e.pdf

To know more about our achievements: FAO elearning Academy: Major achievements for 2021: https://online.fliphtml5.com/juyqq/pqwv/

To select relevant courses browse the FAO elearning Academy Course Catalogue https://elearning.fao.org/course/view.php?id=715

An augmented reality experience to educate on how to recognise emergency animal diseases in sheep

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Introduction

 An Augmented Reality (AR) tool for mobile devices and the Hololens AR headset has been designed to help educate farmers, stock agents and students to identify key signs of some of the most important emergency animal disease (EAD) threats to the Australian sheep industry - foot & mouth disease, bluetongue, scrapie and sheeppox. The tool allows them to scan a room, paddock or any other space and place a virtual flock of sheep, identify symptoms being displayed and guess the disease. An information page is then shown describing the EAD and where to contact if they suspect they have an animal with

this disease.

Materials and methods

Think Digital Studios, AHA and PIRSA worked together to design a storyboard concept to create an engaging learning augmented reality experience. Information and photographs about the EADs were gathered from subject matter experts; 3D models of sheep – both sick and healthy – were then designed and built specifically for this experience using a common breed of sheep seen on Australian farms (Suffolk) – see Figure 1. The 3D models were imported into Unity (development engine) and the functionality built to lead the user through an educating and crucially, a fun experience. The experience needed to be standalone and not requiring connection to the internet so a mobile app was the solution, as well as deployment onto an AR wearable for demonstration purposes. Following development, both functional and user testing took place prior to app release. A follow up review will take place three months after launch to incorporate any further user feedback.

Results

Feedback from user testing demonstrated that the app was easy to navigate, interesting and engaging to use and led to learning about the included EADs and action required if detected. The resulting 'Sheep EAD AR' app was launched on the App Store and Google Play in late June 2022.

Discussion

The included EADs in this AR experience have not been seen in Australia previously so primary producers and agents are not equipped to recognise them. The challenge was to create a way to educate and engage primary producers on the diseases and crucially what to do if they suspect they have a sheep displaying the signs and symptoms of one of these. An information page including a call to action, and the ability to refer back to the models of the sick sheep with signs were designed into the app as critical educational elements to take it beyond the 'fun' aspect of an AR game. As FMD has recently been detected in Indonesia (one of Australia's closest neighbouring countries), this educational tool now has even greater importance.
Although it is designed as an educational and not a diagnostic tool at this stage, there is potential to develop an AR tool for diagnosing EADs in future using Artificial Intelligence/ Computer Vision.

Session II. Poster presentations

"Lung inspector": An innovative 3D teaching app for interactive classroom and self-paced learning

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Introduction

The role of veterinarians in food safety and disease diagnosis (specifically detecting diseases of major animal and public health significance) is absolutely crucial. Current veterinary undergraduate teaching for veterinary pathology and public health is an essential component of the curriculum and relies heavily on a combination of lectures and practical classes using specimens, with issues including accessibility, significant time, labour commitment and pressure on regular sourcing of adequate material.

Material and methods

An existing and extensive bank of images from the department of Pathology and Public Health (University of Glasgow) was searched for relevant images of the most commonly diagnosed causes of lung pathology in sheep. Computed Tomography (CT) scan of healthy sheep lungs was performed and 3D Slicer (2017) was used to segment the data and producing a volumetric visualisation of them. 3D modelling and game development software (Unity, 2017) were used to create a working prototype app. Initial evaluation of the app was carried out through a student focus group, to evaluate the usability and the face validity of the app and a 10-point Likert-type rating scale post-testing questionnaire. The app was further tested during one of the regular teaching sessions (specimen description class) for all third year Bachelor of Veterinary Medicine students (approximately 120 students) for a total of 6 classes.

Results

An interactive app "Lung inspector" was built for use on Android devices (tablet and mobile) and a desktop version was also created for demonstration purposes. Healthy sheep lungs, three of the most common lung pathology in sheep (pasteurellosis, ovine pulmonary adenocarcinoma and lung abscess) and two of the most common categories 3 rejection at abattoir (lung blood splashing and parasitic pneumonia) were included. Feedback from veterinary students after testing the app was overall very positive ("An excellent teaching tool, second best only to physical specimens"), with all those who tested the app feeling that it was exciting and enjoyable to use, and that the face validity and user experience were of sufficient quality to allow the app to be used for interactive teaching and self-paced learning purposes.

Discussion

This work has shown that there is scope for enhancing veterinary pathology and public health teaching through adoption of novel teaching and learning methods such as mobile apps and simulations. The creation and testing of "Lung inspector", showed that veterinary students enjoyed using the app and felt it would be a useful addition to their curriculum. This work has also enabled better and further use of an existing bank of images as well as the reduction of animal specimens needed for undergraduate teaching. Aspects of the app and the lung model can be improved upon, but the initial test suggests that making these revisions and undertaking further testing and statistical analysis with a larger cohort of veterinary students, and perhaps those from a non-veterinary background for usability testing, can result in validation of the apps and models and the potential to adopt them formally into the veterinary curriculum.

SEACFMD portal: A central resource for FMD control and eradication in SouthEast Asia

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Introduction

The SEACFMD campaign is a large, complex, and ambitious undertaking that aims to boost livestock productivity and economic output by controlling and eradicating FMD in South-East Asia, China, and Mongolia. Throughout the Campaign, a variety of learning resource materials for communication have been developed in conjunction with national veterinary services and partners. Various means of dissemination have also been used.
The emergence of cloud computing has brought forth a variety of opportunities, such as knowledge

management. Utilizing the power of the cloud, Microsoft SharePoint Online, a feature of the Office 365 service, provides out-of-the-box support for implementing Knowledge Management as a Service. Here, we present the SEACFMD portal, a web-accessible archive of digitally available learning resources, as well as an interactive visualization dashboard of FMD situation in Southeast Asia.

Materials and methods

Following discussions on the structure and hierarchy of the information according to the categories of stakeholders in FMD control and eradication, the process of gathering, collating, archiving, and arranging of the resources began. The team initially relocated all resources relevant to FMD and SEACFMD to folders in an internal SharePoint. Then we saw a potential to build a SEACFMD portal for distribution on Microsoft SharePoint. Before deciding to proceed, the team thoroughly assessed the product's capabilities and constraints. The SEACFMD portal was introduced for the first time during the 26th SEACFMD Sub-Commission Meeting in March 2022 for the feedback. Then, it was distributed internally for peer review to other WOAH colleagues at the headquarters and regional offices.

Results

The SEACFMD Portal home page (Figure 1) includes widgets for the SEACFMD, SEACFMD toolbox, SEACFMD road maps, events, and a disease situation dashboard for FMD. There is also a section for news and future events. The relevant webpage of Global Framework for Transboundary Animal Diseases (GF-TADs) and WOAH (both HQ and regional) websites are linked with this as well.
The SEACFMD toolbox page includes collated materials for various stakeholders involved in FMD prevention and control, such as "Policymakers," "Disease control managers," "Field vets and veterinary para-professionals," "Community Animal Health workers," "Industry and commercial farmers," and "Researchers and academics".

Discussion

The SEACFMD portal is dynamic and has a collection of varied resources that have been classified for relevant users. While serving as a comprehensive library for FMD resources, it offers and facilitates effortless and secure cross-device collaborations. The Portal is dedicated to FMD and serves the need of the SEACFMD community.
Apart from having the option to download any of these resources for use, Members can use the platform to upload resources and share information in real time. Additionally, members can interact and discuss on any matters related to FMD control in the region to foster more conversation and participation.

Emergency toolbox: Digital solution for FAST diseases investigation

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Introduction

The Emergency Toolbox is a digital dashboard launched in January 2022 for the investigation and control of a suspected or confirmed outbreak of Foot-and-Mouth Disease (FMD), Rift Valley Fever (RVF), and Lumpy Skin Disease (LSD).

The objectives are:

to provide open-access online resources for veterinarians, epidemiologists, farmers, researchers, animal health officers, and anyone involved in the investigation and control of an outbreak of FMD, RVF,

and LSD;
to raise awareness on the impact of digital solutions applied to the control and prevention of FMD and Similar Transboundary animal diseases (FAST Diseases).

This research shows the impact of the introduction of digital solution applied to FAST Diseases investigation and control.

Materials and methods

An innovative approach has been applied for the development of the Toolbox.
The Emergency Toolbox is located in a Trello board, a project management tool. The usage of this platform has been remodelled in response to consultative needs. The adapted display has the main purpose to showcase media, resources, and assets that may assist the target audience involved in field investigation of animal diseases.

The three pillars of the Emergency Toolbox are: accessibility, usability, and inclusion. Going more specifically, resources are available in different media formats, i.e. videos, leaflets, podcasts, open-access courses, and knowledge bank learning assets. Navigation and displaying are user and mobile-friendly. The inclusive technology allows downloading with low bandwidth conditions and a color-blind friendly mode has been enabled.
To investigate the impact generated by the usage of the Toolbox, a quantitative and qualitative investigation has been conducted. An analytic function has been enabled to collect and aggregate data on accesses, sessions and consulted resources.

An online form has been developed and disseminated to gather qualitative data from a miscellaneous sample of veterinarians, epidemiologists, risk managers, communication and learning specialists, and in particular the form has been disseminated in two countries experiencing FMD outbreaks: the Republic of Indonesia, and the Republic of Tunisia.
For geographic and inclusive scopes, about where happenings occurred, the Toolbox has been developed in English, French and Arabic.

Results

The quantitative analysis shows that a range of 200 and 240 users access the Toolbox on a weekly basis. The totality of responders confirmed the usability and easy accessibility of the resources provided to investigate animal diseases. FMD was the disease most investigated (100%), jointly with LSD (50%), and RVF (10%) with the following geographical distribution:

Syrian Arab Republic: FMD, LSD
Republic of India: FMD
Arab Republic of Egypt: FMD
Republic of Tunisia: FMD, LSD, RVF
Federal Republic of Somalia: FMD, LSD
Republic of Indonesia: FMD, LSD

60% of the responders learnt about the Toolbox through FAO and Animal Health colleagues and network; 30% via social media; and 10% via newsletter.
The graph below shows some of the aggregated results.

FAST diseases investigation, qualitative study, online form.

Discussion

The Emergency Toolbox is an example of the impacts generated by digital and inclusive technologies applied to the investigation and control of FAST Diseases, and their crucial role in reducing socio-economic, political, and cultural barriers by providing direct, accessible, and useful assets.
As part of the digital transformation, the Emergency Toolbox needs to be intended as an ongoing process where improvements are constantly demanded and implemented according to the specific needs that FAST Diseases situations require from the animal health and scientific community.

Online teaching targeted at large cohorts through formative assessment and escape rooms

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Introduction
Consistency and reliability of official controls is fundamental for disease surveillance. The variability in backgrounds and age of those involved has a potential to lead to discrepancies in the baseline knowledge. Here, 2 types of online teaching are shown which are easily deliverable to large cohorts at remote locations. The first format is a CPD designed as formative assessment and delivered online to professionals undertaking official controls. Formative assessment (FA) allows for the participant to learn whilst tackling a challenge in a supported manner. This "enjoyable" challenge makes the activity more engaging and the anonymity removes worries of outside judgement. In addition, following feedback, the participant can assess their own knowledge build up and/or determine the areas where they would benefit from further study. The second format, is a virtual "escape room" using Microsoft One Note. This was a self-directed exercise where participants in the virtual session were divided into different breakout rooms and set tasks with a minor competition element of let's see who gets to the end first. Both of these formats are already being applied in further contexts showing their reproducibility and benefit.

Materials and methods

1st case: (A) Information cards revising conditions and recommended actions; (B) Formative assessment composed of online questionnaires, model answers and feedback
2nd case: Microsoft Onenote notebook with several sections' password protected. The various challenges were cases participants had to find the answer for before they could progress to the next scenario. In the platform they had access to info that would support those decisions but also to the facilitator. The facilitator could be called into a particular breakout room to guide/assist in the decision-making process. At the end the facilitator went through all the cases and explained these.

Results

The tools used for delivery of the virtual teaching and the available feedback from participants will be shown.

Discussion

Virtual teaching format such as the ones shown, are easily deliverable to large cohorts at the same time even if in very remote locations. In addition, no face-to-face attendance means there is more flexibility for the working professional which has many time constraints. Furthermore, the lack of necessity for a physical space means these formats are more affordable for the provider enhancing the ability of delivery to a wider audience. Training by the use of challenges in a supported manner makes the activity more enjoyable and is more likely to increase its uptake. On the other hand, the competition aspect of the "escape room" motivated participation in a less "friendly" virtual environment evidenced by the fact cameras were on during discussions in the breakout rooms but not in the main room. These collaborations are very important because it improves the understanding of the subjects and allows the sharing of different points of views which is fundamental for the development of practical knowledge.

Digital abattoir-enhancing veterinary public health learning and teaching

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Introduction

Abattoir activities are key components of veterinary training, however, accessing facilities can be difficult. The digital abattoir (DA) is a novel teaching tool that combines the advantages of blended learning and Virtual Reality to replicate and complement abattoir visits. The Digital Abattoir (DA) portrays five commercial establishments, including read and white meat species, delivering the content of a traditional visit. Students from universities across the globe have implemented this tool and data are being gathered.

Material and Methods

The DA is presented in a Web App and 3D Virtual Reality format. During a self-directed session, the students engage in a sequential tour with the Web App version. At the end of each section, a "Discussion Point "is introduced. To answer these questions, the students require to engage in lecture revision and/or literature research. The tutor facilitates a follow up discussion with the students in a face-to-face session. Having completed the teaching tour, the students are then invited to experience the abattoir environment. This is done using untethered virtual reality headsets and immersive 360-degree video with audio. Student feedback was collated via questionnaire at the of the 3D session.

Results

Common themes across the three developing universities have been collated. Student feedback indicates that the experience was useful, particularly the Web App. Also, the immersion in virtual reality increased students' spatial awareness. A proportion of the students that had not visited an abattoir prior to the activity believed that the digital tool would prepare them better to face the real visit. Students that have previously visited abattoirs reported that they found the tool to be "very informative" and "would have prepared them better to understand what happened during their placement". Anecdotally, one student reported more apprehension post-exposure than initially expected and some showed emotional reactions. Some students commented on the repetition of content from Web App to 3D and would prefer additional content on the same species. A proportion of students experienced some degree of dizziness, but none stepped out of the activity. Overall, students reported that the Web App component helped them to prepare the subject content and better understand techniques and procedures in the slaughterhouse.

Discussion

Although the Digital Abattoir was created prior to the pandemic, the teaching restrictions imposed by COVID-19 pandemic accelerated the demand for alternative solutions. Digital technologies that were once considered 'nice to have' have now become essential to business continuity.
Based on student feedback, our application enhances their education by complementing visits to real abattoirs in a safe and controlled manner. The virtual reality enables the students to engage stress free with the activity of an abattoir surrounding allowing them to focus on the subject content.
This ongoing study raises the immediate opportunities offered by blended learning and virtual reality in veterinary education and industry training in the areas of technical and emotional competence development, communication, and soft skill development. Advancements in networks and communication capabilities within virtual reality offer future opportunities in areas of remote consultation, collaboration, and teaching.

Gender responsive design for training veterinary paraprofessionals: findings from a needs assessment conducted in Nigeria, South Africa and Uganda.

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Livestock diseases have gender implications. Female livestock keepers who make up 60% of the world's poor livestock keepers (World Bank et al. 2009), can be particularly affected and are therefore an important target group for last-mile animal health services. In low-to-middle-income countries (LMICs), veterinary paraprofessionals (VPPs) play an important role for smallholder farmers (SHF) who often lack adequate access to veterinarians. Women VPPs, who are an important channel for reaching women SHFs, often make up only a minority of the VPP workforce and may face gender barriers to accessing training and upscaling their businesses.

To promote the provision of comprehensive and inclusive animal health services the "Sustainable Business in Animal Health Service Provision through Training of Veterinary Paraprofessionals" project, led by the European Commission for the Control of Foot-and-Mouth Disease (EuFMD) aims to develop and evaluate a gender-sensitive training model to improve VPP services in LMICs. This will be done through Continuing Professional Development (CPD) delivered through a blended learning approach that includes both virtual and practical in person training courses.

To guide the gender-sensitive development of the training program, a needs assessment for VPPs was conducted in two pilot regions within each project country (Nigeria, South Africa, and Uganda) in order to identify the preferred modalities for training and the priority capacities and competencies to be built. The needs assessment used a mixed-methods approach consisting of a qualitative Participatory Rural Appraisal (PRA) and a quantitative telephone questionnaire. This presentation provides an overview of the findings disaggregated by gender and explores challenges and potential solutions to overcome the identified gender barriers to blended training for VPPs in LMICs.

Session III. Virology and diagnosis

FMD is a persistent challenge for the livestock industry in many countries. Identification of virus-host interactions is critical for understanding the host defense against this virus infection and can provide insights for designing effective vaccines or drugs to prevent and control the spread of FAST diseases.
Progress in molecular epidemiology: how can the diagnosis and control of FAST diseases benefit from recent innovations in molecular diagnostic methods and platforms such as next generation sequencing?
Diagnosis of FAST diseases is still often negatively impacted by the challenges of sample collection and sample transport to national reference laboratories from remote areas and under adverse conditions. How can innovations in field-based diagnostics such as lateral flow immunoassays and biosensors contribute to improved diagnosis of FAST diseases?
How can digital technology through automated tools and dashboards contribute to more timely diagnosis and molecular analysis and information sharing of FAST diseases?

Aim

 To consider how modern technologies and digital transformation can support and improve the diagnostic capacity for FAST diseases and ensure availability of diagnostics, personnel, and capacities where they are most needed. Furthermore, to discuss how understanding the host defense can provide insights for designing effective vaccines or drugs to prevent and control the spread of FMD and similar TADs.

Session III. Oral presentations

Peste des Petits Ruminants and Rift Valley Fever events 2020-2022

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Introduction

Peste des petits ruminants (PPR) and Rift Valley Fever are examples of transboundary animal diseases having major consequences in terms of health and economics. PPR is a highly pathogenic viral disease infecting principally sheep and goats, but also some wild artiodactyls, camelids and suids. This disease circulates in large parts of Africa, Asia, Eurasia and Middle-East and it has recently appeared at the gates of Europe in Georgia (2016) and Bulgaria (2018). A vaccine sxiste and the disease is the target of an eradication campaign by 2030. RVF is an arbovirus also affecting small ruminants and camelids, but also cattle and can be transmitted to human. The virus is transmitted among ruminants through the bite of infected mosquitoes (belonging to the *Aedes* and *Culex* species) and to human through the direct contact with infected blood or tissues. The disease circulates mostly in most countries in North, East, West and Sahelian Africa as well as in the Arabian Peninsula. Despite the different way of transmission, transboundary animal movement is the most likely route of the spread of the two diseases. Even though the livestock trade is strictly regulated between endemic regions of the two diseases and most of the Mediterranean countries, regional, locally adapted strategies are needed to control the diseases efficiently. The aim of this talk is to provide a panorama of the epidemiological situation around Europe and provide some preliminary scenario for the introduction of the diseases, through animal movement, and risk of transmission due to the presence of competent vectors (only for Rift Valley Fever).

Materials and Methods

To this end we present results from recent publications on PPR and RVF circulation in UE neighboring countries. For RVF this information is completed by a literature review about the characteristics of the competent vectors in the Mediterranean basin. Data from UN Commtrade has been analyzed to reconstruct the mobility network from European countries and identify possible gateways for introduction.

Results

Both RVF and PPR are currently not circulating in EU, although PPR is present in limited area of Bulgaria.
For PPR, focusing on Eurasia region, there is a wide difference in the epidemiological status and risk among the different countries. In some of these countries there still poor reporting and real status is unknown. Despite efforts in vaccination, disease is circulating in wildlife in Turkey and Iran. In Turkey vaccination is carried annually and strict regulation on animal mobility from Anatolia is put in place. Although the prevalence in the region of Thrace is lower than in Anatolia, this region could still represent an entry point for PPR in Europa. Similarly another getaway of introduction is through Romania, with whom Turkey have several exchanges of livestock. Except for Israel, where outbreaks have been declared, and Syria, no data are available about the last 2 years in Middle Asia. In 2021 and 2022 several outbreaks of PPR occurred in North Africa, despite that most of movements are regulated between Northern Africa and Europe, the virus could be introduced through the movements between North Africa and Southern Spain.
During the last 2 years circulation of RVF has been reported in Senegal ,Mauritania, South Sudan and Libya (North and Western Africa) as well as in other African countries (Niger, Burundi, Kenya, Uganda Rwanda and Madagascar). Uncontrolled live animal trade routes exist from sub-Saharan to North African countries, and from there, similar paths to thos for PPR could allow the introduction in Europe (*work in progress*). For RVF, analysis confirms that five species of concern (*Ae. Caspius*, *Ae. Detritus*, *Ae. Vexans*, *Cx. Pipiens*, *Cx. Theileri*) could be involved in RVFV transmission in the Mediterranean Basin, and should prompt both further investigation into the risk of RVFV being introduced into what was previously an RVFV-free region, and reinforced surveillance in high-risk areas.

Discussion

While the two diseases have not yet appeared in EU, increase of regulated and regulated movements with endemic countries could increase the risk of introduction. Furthermore, changing in the environmental condition could widen the distribution of favorable habitats for competent vector species for RVF. Regional, locally adapted strategies are needed to control the disease efficiently.

Innovation in molecular diagnosis, next generation sequencing and molecular epidemiology for FMD and FAST disease

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Accurate and rapid diagnostic tests are an essential component of initiatives to control and eradicate transboundary viral diseases such as foot-and-mouth disease (FMD). Tests are deployed to confirm initial cases of diseases, monitor the spread of the virus, characterise the causative viral strain, and to provide evidence of disease freedom after outbreaks. Diagnostic testing in sophisticated state-of-the-art laboratories can be supplemented by point-of-care (POC) technologies (e.g. lateral-flow devices [LFDs], mobile PCR and isothermal tests) that can be deployed into scenarios where swift confirmation of clinical suspicion is required. Although index case diagnosis is always likely to occur in National Reference Laboratories (NRLs), these simple-to-use tests hold great promise to allow control decisions to be taken at the earliest possible time point in the midst of an outbreak; allowing new FMD cases to be rapidly identified. Furthermore, these simple-to-use methods might also enhance FMD surveillance in endemic settings where access to equipment or reagents is constrained.

This presentation reviews progress to develop new diagnostic tools that can be used to detect and

characterise viruses that cause important livestock diseases, including a "molecular toolbox" of new lineage-specific real-time RT-PCR assays that have been developed to quickly identify which FMDV lineage is present in samples. Away from laboratory testing, recent data demonstrates that simple sample preparation protocols and new equipment that utilize lyophilized reagents allow real-time RT-PCR or isothermal RT-LAMP assays to be performed in simple laboratories or in field settings in under 60 minutes. The analytical sensitivity of some of these molecular tests is similar to the established real-time RT-PCR assays employed for front-line diagnosis in NRLs. Therefore, these tests may provide an approach to rapidly negate suspect cases of FMD, with the prospect to reduce immediate risk-based slaughter of uninfected animals. Using field-tests (such as pan-serotypic and serotype-specific antigen lateral-flow devices), work has also explored novel cost-effective approaches that can be used to triage, and to safely ship specimens to FMD Reference Laboratories.

Once FMDV has been detected, nucleotide sequencing is used to compare field strains with reference viruses and to allow phylogenetic trees to be constructed. The MinION (Oxford Nanopore) is a portable, real-time device for DNA and RNA sequencing that identifies nucleotides by measuring the changes in electrical conductivity generated as DNA strands pass through a biological nano-sized pore. Results from on-going work to develop tailored approaches for FMDV and viruses causing other FAST diseases will be presented elsewhere at this meeting.

The impetus to develop these technologies has been largely influenced by the desire for more rapid diagnostic capability within Europe (and other developed countries); however, results from recent studies in East Africa (Kenya, Tanzania and Ethiopia) support the deployment of the POC technologies to enhance the surveillance for transboundary diseases in endemic settings.

Virus-host interactions in FMD virus infections

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The innate immunity represents an early innate host antiviral defense mechanism that takes place shortly after virus invasion and long before the development of adaptive immunity. Viruses must outcompete or subvert the initial antiviral innate immune response, allowing the establishment of persistent replication that leads to continuous stimulation of both the innate and adaptive immune components. Similar to other viruses, foot-and-mouth disease virus (FMDV), an etiological agent of severe and highly contagious viral disease, is reported to have evolved multiple strategies to evade and attenuate the host innate immunity to facilitate viral replication. In our lab, based on a subset of luciferase assays using promoter constructs of key components of the innate immunity coupled with IP-MS and Y2H, we decipher the mode of action of how viral proteins interact with host factors and further disrupt the host factor-mediated innate immunity, especially in the context of the type I interferon (IFN) system. It is well noted that FMDV proteins could interact with pattern-recognition receptors (PRRs) and key innate immune molecules (MAVS, TBK1 and IRF3), further resulting in inactivation of innate antiviral immune response.

Additionally, FMDV infection exhibited dramatic attenuation of signaling pathways important during the acute phase response, including the NF-ᴋB pathway and the complement pathway. Conversely, a diverse range of host antiviral factors are well characterized with respect to antiviral activity against FMDV. Broadly acting effectors including G3BP1, RPSA, TPL2 and JMJD6 were reported to either directly disrupt FMDV viral life cycle or indirectly regulate host innate immune response through multiple mechanisms to impair FMDV replication.

Finally, an anti-picornaviral strategy based on the crystal structure of FMDV 2C protein was developed. We determined the crystal structure of an FMDV 2C fragment to 1.83 Å resolution and designed an anti-FMDV peptide derived from PBL (PBL-peptide), which inhibited FMDV 2C ATPase activity, bound

to FMDV 2C with nanomolar affinity, and disrupted FMDV 2C oligomerization. In the future work, we will extend our focus to how FMDV evades and abrogates the acute phase response during FMDV replication. Our findings provides a new perspective for understanding what protection and prevention measures we will hold to eradicate FMDV infection.

IDENTYPATH: The genomic platform of ANSES for molecular detection and typing of pathogens

S. Delanoy

Available upon request

Complete genome sequencing of FMDV using Nanopore sequencing

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Introduction

The benefits of complete genome sequencing have become increasingly clear, for example the identification of emergent lineages with altered phenotypic characteristics or the fine scale tracking of virus movements. Indeed, in the UK in 2007 complete genome sequencing enabled the tracing of an outbreak of foot-and-mouth disease virus (FMDV), in turn allowing the identification of a missing premises.
Previously, we showed that it was possible to sequence the capsid-coding region of the FMDV genome using nanopore sequencing technology (Oxford Nanopore Technologies) following amplification of the P1 region by RT-PCR. Here, we designed a universal RT-PCR based amplification strategy for the amplification of complete FMDV genomes prior to nanopore sequencing using the MinION sequencer.

Materials and methods

The FMDV genome was split into 20 amplicons. One amplicon encompasses the S-fragment. The remaining 19 amplicons were approximately of equal size and were tiled across the L-fragment, each overlapping by approximately 100bp. Initially, primer sets were mixed according to the amplicon, resulting in 20 primer mixes. Subsequently, the primer sets were allocated to one of two pools of ten amplicons, enabling the amplification of complete FMDV genomes in two multiplex reactions. PCR products representing the genome of O/ZAM/11/2019 were generated using the primer sets and were subjected to nanopore sequencing using the MinION sequencer. Ligation-based libraries were prepared and run for 72 h. The resulting fastq files were subjected to reference assembly using the O/ZAM/2/2019 complete genome previously sequenced using Illumina MiSeq technology as a reference.

Results

Primer sets were screened against panels of virus isolates encompassing diverse FMDV lineages representing serotypes A, O, SAT1 and SAT2 in order to assess their cross-reactivity. As expected, P2 and P3 regions were broadly successful across all serotypes. The capsid regions of A, O and SAT2 were well amplified, whereas further modifications to primers are required to efficiently amplify all amplicons encompassing the SAT1 capsid region. Preliminary testing using Asia1 viruses suggests that the panel will also be successful for other serotypes.
Testing the products amplified in a multiplex format indicated that this format did not significantly

impair the amplification of the different amplicons, and nanopore sequencing indicated that O/ZAM/11/2019 is closely related to recently sampled type O viruses from Zambia.

Discussion

Nanopore sequencing using the ONT MinION offers the possibility of complete genome sequencing in decentralised and poorly resourced settings. Data generated here suggest that pools of primers can be used to amplify entire genomes prior to sequencing using the MinION. Further screening is required to establish the level of reactivity across diverse FMDV lineages. Additional sequencing runs are planned in order to further confirm the validity of this approach.

Interplay between FMDV 3D polymerase and the type I interferon response: A contribution to viral persistence?

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Introduction

One of the problems associated with Foot-and-Mouth disease is the ability of FMDV (Foot-and-Mouth Disease Virus) to persist in infected ruminants for several months. Despite considerable work done to date, the underlying mechanisms remain unknown. However, we have shown in a previous collaborative project that persistent infection in bovine primary cells is associated with a durable but attenuated and ineffective innate antiviral response that may rely on protein-protein interactions (PPI) between FMDV and its host. While FMDV persistence has been reported in ruminants, it has not been described in pigs. This differential persistence provides an opportunity to compare virus-host interactions between species, determine their host specificity and identify potential links between PPI and viral persistence.

Materials and methods

In this project we focused on the interplay between FMDV proteins and 16 cellular proteins belonging to the type I interferon (IFN I) pathway, which are described as involved in more than 75% of virus-host PPI. Plasmids expressing these 16 proteins from cattle, pig, sheep and goat, as well as expression vectors for the 15 FMDV O/FRA/1/2001 Clone 2.2 proteins were produced by Gateway method. PPI were identified under overexpression condition in HEK293T cells by NanoLuc-2-Hybrid screening and verified using affinity chromatography GST Pull-Down. The phenotypic impact of some FMDV proteins on the IFN pathway has also been investigated *via* luciferase reporter assays.

Results

The NanoLuc-2-Hybrid approach revealed numerous PPI between the IFN pathway proteins and the viral proteins tested. 3A, 3C and 3D are the viral proteins for which the greatest number of interactors were identified. The most promising results concern the 3D polymerase for which no interaction with the IFN pathway has been described so far. This protein was used to screen cattle, sheep, goat and pig NanoLuc plasmid libraries. When comparing the results of these screens, it appears that most of the interactors are shared with relative strength across species as illustrated in figure 1. The FMDV-host PPI, have been confirmed by affinity chromatography GST Pull-Down for the four species and functional validation of these PPI is ongoing. Furthermore, we have demonstrated by luciferase reporter assays the inhibitory effect of 3D polymerase on the induction phase of the IFN response.

Discussion

With this study, we have demonstrated novel interactions between some FMDV proteins, including 3D, and cellular proteins involved in the IFN pathway from four virus-susceptible species. A direct effect of 3D on the IFN pathway induction stage was also revealed. Combined, these results strongly suggest that 3D polymerase could play an unsuspected role in the FMDV escape from the host IFN response. A modulation of the antiviral response by the FMDV, through interactions with its host, is one of the hypotheses explored to understand FMDV persistence. Thus, it is entirely conceivable that the 3D protein, by interacting with certain proteins of the IFN pathway, may contribute to the establishment and/or maintenance of a virus-host equilibrium.

Epitope mapping of FMDV 146S specific single-domain antibodies by cross-linking mass spectrometry

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Introduction

We earlier isolated 10 single-domain antibodies (VHHs) that specifically bind intact (146S) FMDV particles but not the (12S) degradation products of serotype A strain A/TUR/14/98. Such 12S particles are much less immunogenic than 146S particles. As a result, the 146S particle specific VHHs are useful tools for quality control of FMDV antigens used in vaccines. Conventional monoclonal antibodies (mAbs) were shown to bind at least 5 independent antigenic sites by competition ELISAs and sequencing of mutants that are resistant to neutralization by mAbs. Escape mutants of serotype A binding 146S specific mAb 9 had mutations in VP3, near the 2-fold symmetry axis where separate 12S particles join into a 146S particle. This suggests that 146S specificity is caused by the epitope lying on two adjacent 12S pentamers that is separated by 146S particle dissociation. However, cryo EM structural analysis the serotype O 146S specific VHH M170 showed that it recognizes a loop on VP3 that has a different 3D structure in the 12S particle compared to the 146S particle. This change in conformation most likely causes the 146S particle specificity. To further understand the mechanism of 146S specificity, we mapped the antigenic sites of serotype A binding VHHs by competition ELISAs, VNTs and cross-linking mass spectrometry.

Materials and methods

A set of serotype A binding VHHs and mAb 9 were mapped into separate epitope bins by competition ELISAs using strains A/TUR/14/98 and A24/Cruzeiro/BRA/55. Virus neutralization titre and trypsin sensitive binding were also determined.
Cross-linking mass spectrometry (XL-MS) was done using VHHs M691F and M702F complexed with A24 Cruzeiro 146S particles. A bifunctional cross-linking reagent was added, and cross-linked peptides were identified after digestion with 5 proteases using liquid chromatography and tandem mass spectrometry. This allows identification of specific FMDV residues cross-linked to specific VHH residues. These residues were mapped onto the 3D structure of strain A22 IRQ.

Results

The VHHs formed four separate epitope bins (I, II, IV and V).

Bin	Number of VHHs			
	Total		146S specific	Remark
I	5	5	2	Includes VHH M8 with a known epitope on VP1

II	5	0	0	Many VHHs are 12S specific
IV	1	0	0	
V	10	9	8	Competes with mAb 9, includes VHHs M691F and M702F

The 146S specific VHHs were found in two epitope bins, one of which contained the two more broadly strain reactive VHHs M691F and M702F. The epitopes bound by these two VHHs was further mapped by XL-MS. It was found to bind primarily the same region of VP3 that overlaps the M170 binding site and contains the mAb 9 escape mutations. Both VHHs also recognize a number of adjacent VP2 residues. Remarkably some residues recognized by both M691F and M702F are not solvent exposed in the A22 IRQ 3D structure. Although many cross-linked residues were identified on VP3 close to the 2-fold axis it was unlikely that residues were cross-linked on the opposing VP2 molecule of an adjacent 12S pentamer.

Discussion

The 146S specific mAb 9 and VHHs M691F and M702F cross-link with the same or adjacent amino acids on VP3, close to the 2-fold axis. However, since it is unlikely that VP2 residues on the adjacent 12S pentamer are bound no clear proof was found that 146S specificity relies on the epitope being formed by two adjacent 12S pentamers. It is more likely that 146S specificity relies on altered conformation of this VP3 region upon dissociation into 12S particles, similar to VHH M170F. The crosslinking of both VHHs to the same residues that are internal in the 3D structure of A22 IRQ suggests that these regions are solvent accessible during XL-MS analysis. This suggests that FMDV 3D structures determined by cryo EM or X-ray crystallography are not reminiscent of the structure in solution, which is probably more flexible.

Preliminary validation of multiplex Eurasia lateral flow device for on-field identification and serotyping of FMDV serotype O, A and ASIA1

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Introduction

In foot-and-mouth disease (FMD) endemic regions, which often lack adequate transport systems and equipped laboratories, Lateral Flow Devices (LFD) represent the simplest tool for rapid on-site diagnosis. A commercially available pan-serotype LFD offers a user-friendly disease confirmation tool, but lacks serotyping capacity, whilst serotype identification is crucial to identify regional transmission patterns and to ensure appropriate vaccines selection in countries where multiple serotypes co-circulate. This study aims to depict the preliminary validation of the multiplex *Eurasia* LFD prototype, based on characterized monoclonal antibodies (MAbs), for FMD diagnosis and simultaneous serotyping of FMDV O, A and Asia1 in a single strip.

Materials and methods

Diagnostic sensitivity of *Eurasia* LFD was evaluated on 76 epithelium homogenates collected in endemic countries (33 serotype O, 31 serotype A and 12 serotype Asia1) and compared with IZSLER Antigen-ELISA (Ag-ELISA) kit results. Additionally, 70 tissue-cultured FMDV strains (40 serotype O, 23 serotype

A and 7 serotype Asia1) were tested to evaluate the ability of the devices to recognize the widest spectrum of FMD viruses. The result of each *Eurasia* LFD was assigned a value from 0 to 4 to reflect the intensity of the positive result line in the test window.

Results

Eurasia LFD performed on FMDV positive field samples serotype O and A showed a diagnostic sensitivity comparable to that observed with the Ag-ELISA. In detail, 88% of serotype O-positive and 81% of serotype A-positive were correctly detected with *Eurasia* LFD, whilst Ag-ELISA correctly serotyped 82% and 84% of serotype O and A, respectively. A lower sensitivity of *Eurasia* LFD (67%) was observed on positive samples serotype Asia1 often showing barely visible lines (scored as 1) confirmed by low Ag-ELISA OD values.
Conversely, all 70 tissue-culture isolates were correctly detected and typed by *Eurasia* LFD.

Discussion

The diagnostic sensitivity on field samples of the *Eurasia* LFD was comparable to that observed for Ag-ELISA, with a concordance between the two tests approaching 100%. Moreover, the *Eurasia* LFD confirmed to be able to correctly detect and serotype a very wide spectrum of FMDV strains, covering all the strains circulating in the 7 pools.

Full-length genomic RNA of FMDV is infectious for cattle

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Introduction

Ensuring the safe transfer of virus-positive diagnostic material is an important concern for FMD field studies. It has been proposed that the complex and expensive shipping requirements for infectious material should not apply to acid-treated FMDV-positive lateral flow devices (LFDs). The treatment with citric acid demonstrably abolishes virus infectivity, but it has been shown that acid-treated LFDs still contain full-length FMDV RNA that allows the subsequent recovery of infectious virus by chemical transfection of cell cultures. Whether full-length FMDV RNA alone can cause a productive infection in the natural host, however, has not been explored.

Materials and Methods

In this study, total RNA including full-length FMDV genomes was extracted from a virus culture using acidic guanidinium thiocyanate, phenol and chloroform. The RNA preparation was confirmed to be free of virus by inoculation of LFBK-ɑVɑ6 cultures. No CPE was seen after two blind passages. Six cattle were inoculated with the fresh FMDV RNA without any additives by injection into the tongue epithelium. In another six cattle, the FMDV RNA was only dripped onto the intact tongue epithelium and sprayed into the nasal cavity. After the exposure, swabs and serum were collected daily and the cattle were closely monitored for clinical signs of FMD.

Results

Within 24 to 48 hours after inoculation, the injected cattle developed clinical FMD with high fever. Large primary vesicles formed at the inoculation sites and secondary vesicles were found in the mouth and in the interdigital spaces. Viral RNA and infectious virus were detected in the serum and saliva of all

cattle. The cattle that were exposed to the FMDV RNA non-invasively, however, did not develop clinical disease and did not shed infectious virus or viral RNA.

Discussion

This confirms that FMDV RNA is highly infectious for cattle when injected, but the risk of infection is much reduced if the exposure is only superficial. Properly inactivated FMDV samples carry only a small risk of contagion, even if they contain full-length viral RNA.

Session III. Poster presentations

Design of a transport tool for inactivated FMDV on lateral flow device from the field to the laboratory diagnostic

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Introduction

Identification and characterization of circulating strains of Foot-and-Mouth Disease Virus (FMDV) is primordial for the control of the disease. However, shipment of FMDV infected samples to reference laboratories remains a challenge. In a previous study supported by EuFMD we have developed and validated a protocol for safe and low cost shipment of such samples (Romey et al. 2018). This protocol was based on the use of a lateral flow device (LFD) as support for shipment of positive samples after inactivation of FMDV by soaking the LFD in a citric acid solution. Although we have demonstrated the safety of this protocol and the ability to use these LFDs for virus detection and further characterization in the laboratory, a question remains: how to guarantee that the protocol is applied in the right conditions in the field? In the present project, we propose solutions to address this issue.

Materials and methods

A polylactic acid (PLA) filament 1.75 mm was used to produce the PLA tube with a 3D printer Artillery X1 Sidewinter. A 0.2% citric acid solution was prepared, and, LFDs provided in the Svanodip® FMDV-Ag kit (Boehringer Ingelheim Svanova, Sweden) were used. The stability of the 0.2% citric acid solution stored at 4°C, 21°C and 37°C for 36 months was monitored by measuring the pH every two weeks.

Results and discussion

The first idea was to include a pH indicator on the LFD. This indicator is expected to give proof that the LFD was soaked in the citric acid solution. The second idea was to provide a ready-to-use citric acid solution with the LFD in the antigen detection kit. To ensure the efficacy of this inactivating solution after storage, a stability study was conducted and indicated that its pH remains stable for at least 505 days with values between 2.3 and 2.7. Using a 3D printer, the prototype of a PLA sealed tube suitable for proper soaking of the LFD in the provided citric acid solution has been produced. This tube can be filled with 12 mL of citric acid solution, which is enough to cover the entire LFD. After performing the FMDV detection test on the LFD, the entire device should be introduced in the PLA tube and incubated for 15 min as it was previously established in the inactivation protocol (Romey et al. 2018). After incubation, the pH can be checked with the pH indicator present on the LFD to give proof of inactivation. Then, the citric acid can be discarded and the tube containing the LFD decontaminated before shipment. Another possibility could be to keep the LFD in the citric acid solution and to ship the tube after

its surface decontamination. This new transport tool and media could remove any doubt about the correct application of the protocol in the field and thus strengthen the biosecurity of inactivated LFDs shipments.

Reference

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Effect of Ruxolitinib on persistent FMDV infection in multilayered cells derived from bovine dorsal soft palate

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Introduction

More than 50% of FMDV-infected ruminants, even those vaccinated, carry the virus in the nasopharynx for a prolonged period and are thereby defined as persistently infected. Such carriers are considered as a potential source of infectious virus and represent an impediment for FMD control. The mechanisms underlying FMDV persistence are still not fully elucidated. However investigations performed so far suggest that the carrier state is mainly related to the host's immune responses. We have previously established an *in vitro* model of FMDV persistence in primary bovine dorsal soft palate (DSP) cells cultured as multilayers at the air-liquid interface (ALI). In this model, the analyses of the transcriptional host response during acute and persistent infection highlight a long-lasting stimulation of interferon-stimulated antiviral genes (ISG) that are ultimately ineffective to clear the virus. We hypothesized that the inhibition of the interferon response might modulate the level of replication of persistent FMDV and tested the effect of Ruxolitinib, a Janus kinase inhibitor, on persistently infected DSP in the ALI model.

Materials and methods

Bovine DSP cells isolated from 2 different animals ("A" and "B") were cultured on inserts (n= 105) for five weeks and were then infected with O/FRA/1/2001 Clone 2.2 (MOI 0.01), or inoculated with uninfected cell lysate. Infection was monitored until 35 days post-inoculation (dpi). Ruxolitinib was added to the culture medium from 7 dpi, 15 dpi, 21 dpi or 29 dpi onwards. Controls were FMDV-infected cells cultured in medium with DMSO (Ruxolitinib diluent) and non-infected cells cultured in medium with Ruxolitinib or DMSO. Samples collected throughout the experiment were analysed by viral isolation and titration, RT-qPCR (3D target) and immunohistochemistry (anti-3D mAb).

Results

FMDV inoculation resulted in lysis of cells in the upper cell layers, from 24 hpi (animal A) or 48 hpi (animal B) and until the end of the assay (D35). Interestingly, cell lysis appeared enhanced 7 days after the beginning of Ruxolitinib treatment, and more live FMDV and FMDV-RNA was detected in the supernatant in comparison to controls. Immunostaining also revealed an increased 3D expression in Ruxolitinib treated cells. The effect of Ruxolitinib was more marked when the treatment started on 7 dpi and 15 dpi, compared to 21 dpi and 29 dpi.

Discussion

Ruxolitinib caused an increase of viral replication and lysis of the persistently infected DSP cultures, that became obvious at 7 days after starting treatment and in particular, when the treatment started on 7 or 15 dpi. By showing a modulation of FMDV persistence, these data demonstrate that the inhibition of the JAK signaling of the type I IFN pathway leads to a disruption of the virus-host cell balance. These new findings give some clues towards a better understanding of FMD persistence mechanisms and can open for further evaluation *in vivo*.

Thoughts on environmental sampling: Methods to generate more information on FMDV using a simple sampling approach

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Introduction

Environmental sampling enables disease surveillance beyond regular investigation of clinical cases, extending data on the circulation of a pathogen in a specific area. Developing straightforward, low technology methods suitable for use in field conditions is key to the inclusion of such approaches alongside traditional surveillance techniques. Here we present methods to improve the collection and shipping of environmental samples, including recovery of infectious virus, pooling of samples and recovery of virus from dry swabs.

Materials and Methods

Pooling: Electrostatic dust cloths were used to swab surfaces (walls, floors, food troughs etc.) during cattle studies at the Pirbright Institute, UK and during field investigations in the Plateau state, Nigeria. Samples positive for FMDV RNA by rRT-PCR (experiment studies, n=44 and field investigations, n=27) were pooled at a ratio of 1:4 and 1:9 with negative samples. Sample pools were tested for the presence of FMDV RNA using rRT-PCR.
 Infectious virus recovery: Negative environmental samples were spiked with FMDV and supplemented with either 10% or 50% glycerol. Samples were tested up to 21 days and virus isolation on ZZ–R-127 cells were used to measure the viral titre over time. Transfections using the RNA were also attempted.
 Dry swab recovery: Cloth swabs were spiked with FMDV and left to dry for up to one month at 4 °C and at room temperature. rRT-PCR was used to detect FMDV RNA and virus isolation on LFBK cells were used to measure viability.

Results

Pooling: The results from the experimental studies showed detection of a single positive sample was possible unless the level of virus in that sample was low (> C_T 32). Conversely, the results from the field investigations showed there was little or no drop in viral titre when pooled.

Infectious virus recovery: At room temperature, the titre in all samples dropped considerably within 7 days and was negligible by the end of the study. For samples at 4°C infectious virus was still detectable after 21 days, and the highest titres were recovered from samples supplemented with 50% glycerol. Transfections using the RNA from environmental swabs were unsuccessful.
 Dry swab recovery: At room temperature, FMDV RNA was consistently detectable up to one day but the detection of low titres of virus was inconsistent hereafter. Low titres of infectious virus were recoverable from the swabs for up to 4 hours. Results from the 4 °C samples will be presented but are not available at the time of writing.

Discussion

The results suggest pooling could be applied at sampling sites with active outbreaks where high titres of virus are shed into the environment. Our results suggest supplementing media with glycerol would support the survival of FMDV in environmental samples, potentially providing a method for recovering infectious virus from field samples. However, using the RNA in transfection studies is not feasible. Preliminary results suggest the swabs could be used for sample collection and processed later in the day, but such an approach is not suitable for longer storage or transportation times.

Highly sensitive and user-friendly DAS antigen ELISA for the detection of a wide spectrum of FMDV serotypes and strains

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Introduction

Foot-and-Mouth Disease (FMD) is an international epidemic disease that infects cloven-hoofed animals such as cattle and swine. FMD is one of the most highly contagious viral diseases that causes devastating economic losses. There are seven FMD viruses (FMDv) serotypes, O, A, Asia1, C, SAT1, SAT2 and SAT3. The wide range of hosts, ability of small doses to infect, rapid replication, high levels of viral excretion and multiple forms of transmission make FMD difficult to control and eradicate. Since FMD can spread fast and cannot be differentiated clinically from other vesicular diseases such as vesicular stomatitis (VS) and swine vesicular disease (SVD), rapid and specific identification of the agent is of utmost concern. In regards with those international sanitary needs, Innovative Diagnostics has launched a Double Antibody Sandwich (DAS) antigen ELISA for rapid and specific multi-serotype FMDv detection.

Materials and methods

A panel of different monoclonal antibodies (MAb) against each of the FMDv types O, A, and Asia 1 was produced. Most of them could detect only a single-serotype antigen. However, some MAbs, named as *pan*FMD Mab, recognized multi-serotypes. The reactivity profile of each of these *pan*FMD MAbs was investigated by indirect ELISAs, with plates coated with inactivated viruses from different serotypes. The MAbs that showed the wider spectrum of recognition were selected and submitted to further testing for their ability to capture and reveal the different virus strains in DAS ELISA format. The *pan*FMD MAbs were labelled to Horseradish Peroxidase (HRP), and various combinations were tested by DAS ELISA using them either as trapping antibody or as HRP conjugate. Sensitivity was evaluated by testing the seven serotypes of FMDv and analytical sensitivity was tested under a reference panel from an international FMD reference laboratory. Results obtained with the new *pan*FMDv DAS ELISA were compared to commercially available techniques: a MAb –based ELISA kit produced by reference laboratories and a lateral flow device test based on the well described 1F10 MAb. The exclusivity was controlled by testing an SVD virus inactivated suspension.

Results

This new FMD Antigen *pan*Serotype Capture was able to accurately detect all seven serotypes of FMDV and all tested strains and does not cross-react with other viruses that cause vesicular diseases. The new FMD Antigen *pan*Serotype showed better analytical sensitivity than other techniques. Results lead to indicate there is a wider spectrum of detection, even on SAT antigens.

Discussion

This new FMD Antigen *pan*Serotype Capture, highly sensitive and user-friendly, gives results in less

than 90 min and allows for rapid and specific FMDv multiserotype detection. This is a promising tool for detecting and controlling FMDv outbreaks.

Correlation between virus neutralization test and solid phase competitive ELISA on vaccinated animals. The impact of homology among FMDV strains behind vaccines and tests

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Introduction

Virus Neutralization Test (VNT) and Solid Phase Competitive ELISA (SPCE) are useful tools for a wide range of *in vitro* investigations, focused on serology studies in livestock and wild animals. After vaccination campaigns or immunogenicity studies, related to the control of Foot-and-mouth Disease (FMD), VNT and SPCE are usually performed to detect immune response of animals and, subsequently, the effectiveness of a vaccination. VNT remains the diagnostic gold standard, but various issues are related to this assay, first and foremost the manipulation of viable viruses and the related maintenance of an acceptable biosecurity level. Together with the complexity of test, mainly due to its affecting variables, this reason had often induced to find a correlation with SPCE, in order to substitute VNT with a safer and easier assay. In this study, comparing the data collected analysing sera from vaccinated animals, we evaluated the potential correlation between the two tests, focusing on the effect of homology/heterology of the strains behind the assays and those used during vaccination.

Materials and Methods

192 sera, previously collected from animals vaccinated against FMDV serotype A and O, were tested by VNTs and by SPCE IZSLER for the detection of antibodies against structural proteins of serotypes O and A. These tests were based on specific virus strains, which could be homologous or heterologous, depending on those contained in the used vaccines. Log_{10} of titers obtained with the two tests, were correlated with scatter plots. Titers of negative samples could not be calculated, thus for them only an estimation was assessed and plotted.

Results

Considering only animals receiving a vaccine including a single strain per serotype:

VNT and SPCE, based on FMDV homologous to the vaccine strains, showed good correlation between the tests, with R^2 0.6 and the 94% of related pos/neg results.
A lower, but still significative correlation was detected also between assays based on strains heterologous to those included in the vaccine, $R^2 \sim 0.55$ and 79% of pos/neg consistent results.
Comparing data obtained with heterologous SPCE and homologous VNT, the percentage of pos/neg consistent results decrease to 71% with a very uneven R^2 (between 0.62 and 0.26).
Data discrepancy increased comparing homologous SPCE and heterologous VNT, only 54% of pos/neg coherent results and low R^2 (0.37).
Overall, a clear increase of the percentage of positive samples missing the test based on the heterologous FMDV strain was detected. In detail, from homologous to heterologous VNT the ratio of positive samples missing the test grew from 3% to 46%, while considering the switch of SPCE, the percentage of positive samples missing the test increased from 4% to 28%.

When animals received a vaccine containing various strains per serotype, a similar situation was not observed.

Discussion

This study (i) proved that if harmonised, VNT and (IZSLER) SPCE have a good correlation between results, (ii) suggested that the performances of the tests may be related to the homology of strains behind the assays and the vaccines, (iii) revealed that tests based on heterologous strains show lower diagnostic sensitivity, if compared to analogous tests using homologous strains.

Development and evaluation of liquid-phase blocking Elisa for the detection of antibodies to FMD vaccine strain A/POCHEN/SKR/2010

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Introduction

Post-vaccination serological monitoring is an important method for control of foot-and-mouth disease (FMD). In particular, a liquid-phase blocking enzyme-linked immunosorbent assay (LPBE) is more accessible than the virus neutralization test (VNT) for a large-scale serological screening. A FMD A/ASIA/Sea-97-G1 sublineage virus occurred and was named A/Pocheon/SKR/2010 (A/Pocheon) in 2010 in Korea. A vaccine strain was developed using the A/Pocheon virus. In this study, the LPBE was developed and evaluated for the detection of antibodies to A/ASIA/Sea-97-G1 sublineage virus using the A/Pocheon virus as an antigen for post-vaccination monitoring.

Materials and methods

Virus supernatant of A/Pocheon strain was inactivated, concentrated and purified for LPBE antigen. Polyclonal hyperimmune sera against A/Pocheon strain were produced after immunizing rabbit and guinea pig with the purified antigen three times for capture and detector antibody, respectively. The panels of serum samples were collected from pigs vaccinated with monovalent A/Pocheon experimental vaccine and were tested in parallel by the VNT. Reciprocal $\log_{10}$ neutralizing antibody titers of ≥1.2 was considered as positive. The serum samples consisted of positive (n=69) and negative (n=40) sera based on the results of VNT. The LPBE was performed as described previously with some modifications and checkerboard titration was used for optimization of the LPBE. The results of LPBE were compared and analyzed with the those of VNT.

Results

Optimal dilution of the A/Pocheon antigen (0.5 µg/mL), rabbit IgG capture antibody (1/6400) and guinea pig IgG detector antibody (1/12800) was determined by testing serial two-fold dilution for LPBE. To evaluate the diagnostic performance of the LPBE, a total of 109 sera from pigs administrated with monovalent A/Pocheon experimental vaccine were tested and LPBE titers of ≥40 was considered as positive. The LPBE exhibited good performance with a high diagnostic sensitivity (98.6%) and specificity (90%) in comparison with the VNT. Scatter plots and linear regression curve based on the results of endpoint antibody titers of VNT and LPBE was further investigated for the correlation between both assays. The LPBE antibody titers of serum samples showed a high correlation with neutralizing antibody titers of VNT (r = 0.93).

Discussions

Since FMDV serotype A viruses is antigenically diverse, it is necessary to establish serological method to monitor antibody responses of each vaccine strain. The LPBE has been used as an alternative test method to the VNT to evaluate protective antibody responses induced by vaccine. Therefore, the LPBE was developed for the detection of antibodies to A/ASIA/Sea-97-G1 sublineage virus using the A/Pocheon virus antigen and high diagnostic performance of the LPBE was confirmed in this study. In the future, the LPBE will be applied to serological monitoring with the rapid detection of antibodies raised against FMD A/Pocheon vaccine strain.

Validation of digital RT-PCR: Sensitive and rapid detection of FMDV

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Introduction

 Foot-and-mouth disease (FMD) is a highly important disease of domestic and wild cloven-hoofed animals caused by the foot-and-mouth disease virus (FMDV). Among FMDV serotypes, serotype O and A are the most widely distributed serotypes in Asia and serotype Asia 1 occurs only in Asia. Rapid and accurate detection and serotyping of foot-and-mouth disease virus (FMDV) is essential for implementing control policies against emergent foot-and-mouth disease (FMD) outbreaks. Current serotyping assays, such as VP1 reverse transcription-polymerase chain reaction (RT-PCR)/Sequencing (VP1 RT-PCR/Sequencing) and antigen detection enzyme-linked immunosorbent assay (ELISA), have problems with increasing serotyping failure of FMDVs from FMD outbreaks. Digital PCR is a PCR technology where it generates a numerous reaction space and it allows to display the result values in O and 1. Even in only one well amplifies, the signal is detected. Because of this, digital PCR has highly sensitivity especially in ultra-low concentration samples. Therefore, this study was conducted to apply a digital RT-PCR for specific detection and differential serotyping of FMDV serotype O, A, and Asia 1 directly from field clinical samples.

Materials and methods

Primers and probes were designed based on the VP1 coding region sequences belonging to serotype O (n = 79), A (n = 88), and Asia 1 (n = 51) obtained from the GenBank database. Serotype-specific detection for field samples was evaluated using digital RT-PCR compared to VP1 RT-PCR/Sequencing for reference FMDV.

Results

Complete serotyping conformity between the developed digital RT-PCR and previous VP1 RT-PCR/Sequencing was demonstrated using FMDV field viruses prepared in cell culture. The developed digital RT-PCR demonstrated improved turn-around time (70min) and FMDV detection and serotyping capabilities for saliva samples when compared with 3D real-time RT-PCR and VP1 RT-PCR/Sequencing, during ten days of challenge infection with FMDV serotype O, A, and Asia 1

Discussion

Due to superior sensitivity, specificity and capability of absolute quantification, digital PCR is emerging as a next-generation PCR technique and is a potential platform that is continuously being developed by many diagnostic companies. Collectively, this study suggests that the newly developed digital RT-PCR assay may be highly useful for the detection and differential serotyping of FMDV serotype O, A and Asia 1 in the field.

Preliminary evaluation of lateral flow immunoassay for the antigen detection of lumpy skin disease virus

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Introduction

Lumpy skin disease (LSD) is a WOAH notifiable transboundary cattle disease caused by lumpy skin disease virus (LSDV), a dsDNA virus member of the Capripoxvirus genus, belonging to the Poxviridae family. LSD primarily affects cattle, causing fever, enlarged lymph nodes, lesions of the oral mucous membranes, of the respiratory, and digestive tract, abortions and a reduction in milk production. Considering the important economic impact on livestock, innovative and effective tools to detect the virus in fields would be of the greatest interest to speed up the diagnosis. Given its feasibility in field conditions and its easiness to use, lateral flow immunoassay (LFIA) could fulfil this goal. This study aimed at developing LFIA using monoclonal antibodies (mAb) produced against p32 LSDV structural protein and evaluating the preliminary specificity and sensitivity.

Materials and Methods

A panel of monoclonal antibodies (mAbs) was produced against the LSDV Neethling strain. Two of them (2F10 and 2C6) recognized two different epitopes of p32 protein and were selected to set up two different LFIAs: the first was preliminarily evaluated using a single antibody (single epitope, SE) as gold nanoparticles (AuNPs) conjugate and as coating mAb, and the second was evaluated using the two mAbs (double epitope, DE) reciprocally utilized as conjugate or coating mAb. Strips were composed as follows: sample pad, conjugate pad, detection membrane, and absorbent pad. To maximize the devices sensitivity, different parameters were considered. AuNPs of different sizes were synthesized and spectroscopically characterized, and several mAb-AuNPs conjugates were produced by varying the mAb-to AuNP ratio. The most performing device was selected based on the signal intensity using inactivated LSDV Neethling strain. Serial dilutions of the same viral strain were used to evaluate the analytical sensitivity, and the results were compared to those obtained with an ELISA sandwich using the same mAbs. Possible cross-reactions were evaluated by testing other viruses causing similar infectious diseases.

Results

The highest sensitivity was achieved from the DE devices (2F10 conjugate/2C6 capture), employing 32 nm-in-size AuNPs functionalized with 20 μg of mAb for each mL of AuNP and applied to the device as a solution of optical density 3 a.u.; these conditions were selected to develop the LSDV_LFIA.
The optimized LSDV-LFIA was tested with 10-fold serial dilutions of LSDV Neethling strain 10^6 TCID50/ml growth on ovine testis cell line (OA3.Ts), and the results were compared to the sandwich ELISA. The test line was still visible at 400-fold dilution of the viral culture corresponding to $10^{3.4}$ $TCID_{50}$/mL, whereas the ELISA cut-off was set up at 1/250 dilution (Net OD=0.1). No cross-reaction with other viruses was detected.

Discussion

The optimized LSDV_LFIA detected the virus in a wide dilution range and showed a better sensitivity compared to the ELISA test that exploited the same antibodies as a mechanism of virus recognition, corroborating the potential of this technique in controlling the spread of LSDV. It could be a promising tool that would improve the field surveillance of lumpy skin disease. The evaluation of the LSDV_LFIA on field samples is ongoing.

Development of Luminex technology for detection of antibodies against structural proteins of FMDV

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Introduction

Foot -and- mouth disease (FMD) is an acute, highly contagious disease of cloven-hoofed animals with impacts on farming and is responsible for major economic losses. Serological assays that measure FMDV-specific antibodies are used to monitor the presence of FMDV, for checking quality of FMD vaccine and levels of post-vaccination immunity. The aim of this work was to develop a multiplex immunoassay with recombinant empty viral capsids for FMD serological diagnosis using Luminex technology. Such a test could be used as an indicator of pre-exposure of FMDV or vaccination and to estimate immune protection in a single reaction and from a single sample against all 7 serotypes

Materials and methods

Recombinant FMDV O1Manisa and A22 antigens were prepared from vaccinia virus expressed as empty capsids (Porta C et al, 2013). These recombinant empty capsids O1M and A22 were directly coupled to Luminex magnetic fluorescent microspheres, for each serotype specific bead region is used. The Luminex immunoassays were performed using bovine sera for O and A serotype. which included sera that showed high cross reactivity in commercial or in house ELISAs. The biotinylated anti-bovine conjugate was used as detector; its binding to the fluorescent streptavidin-phycoerythrin protein allows tracking and quantification of the FMDV-specific antibodies present in the sera.

Results

In developing the Luminex assay, the first step was to optimise the concentration of the reagents including O1M or A22 FMDV capsid concentration, blocking solution, bovine sera dilution, quantity of coupled-bead per reaction, secondary biotinylated antibody dilution and streptavidin-phycoerythrin per reaction concentration. Encouraging results were obtained for single plex assay and then a multiplex test format for O1M and A22 was performed. Results were expressed as normalised MFI which was obtained after dividing the MFI of sample derived from capsid coated bead by the MFI of negative control (NC) for that sample. The preliminary cut off MFI for positive sera was determined as >10 and >13 for O1M and A22 respectively, where 80-90% sensitivity and 90-95% specificity was achieved. Also, reduced cross reactivity between serotypes is observed in multiplex format.

Discussion

 A preliminary comparison to other commercial or in house ELISAs showed reduction in cross reactivity between serotypes and the multiplex format of this test can be an additional tool for FMD diagnosis against different FMDV serotypes simultaneously in one single reaction, hence less time consumption. The future work is to adapt this model system for East African reference antigens (VLPs). i.e., O, A, SAT1, SAT2 serotype and develop an immunoassay for post vaccination monitoring and monovalent or multivalent vaccine quality assessment in East Africa.

Field application of novel solid phase blocking ELISA for antibody detection to FMDV type-A

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Introduction

A systematic vaccination program is ongoing in South Korea to control the two prevailing serotypes (A, O) of foot-and-mouth disease virus (FMDV). However, sero-surveillance to determine immune responses induced by vaccination was conducted using FMDV type O SP antibody ELISA due to the lack of reliable multispecies antibody detecting ELISAs for serotype A. Therefore, we have recently developed a novel recombinant protein-based solid-phase blocking ELISA (r-SPBE) with monoclonal antibody (Mab) for detection of antibodies to FMDV type-A. This study was conduced with an objective to compare simultaneously performance of other current tests in monitoring population immunity and to assess their fit-for-purpose attribute for sero-surveillance of FMD in Korea.

Materials and methods

A panel of 1,741 serum samples collected from cattle, pigs and goats vaccinated experimentally under vaccination regimen. In addition, 3,408 samples collected at random from field farms during biannual regular vaccination campaign in 2020 were tested simultaneously by the commercial FMDV type-A ELISA (PrioCHECK, ThermoFisher, USA) and virus neutralization test (VNT).

Results

Based on the testing of serial bleeds from experimentally vaccinated animals, the r-SPBE detected antibodies to FMDV Type A similar level to that observed using the VNT until 14 weeks post vaccination. When applied to 1,864 bovine, 1,492 pigs and 52 goat samples that were obtained from field farms for assessing the large-scale sero-surveillance, the r-SPBE identified more positive samples than did the PrioCHECK FMDV type A antibody ELISA. The sensitivity of the r-SPBE relative the VNT were 95.4% in cattle, 89.3% in pig and 84.6 % in goat respectively, and excellent concordance rate (kappa=0.91).

Discussion

This study concluded that the novel r-SPBE assay showed higher performance compare to the commercially available ELISA kit for detection of vaccine-induced antibodies in experimentally collected sera as well as field sera. Also, the assay thus retains the sensitivity of the VNT whilst being easier to use, more robust and specific, and therefore offers an improvement as FMD serological tool for post-vaccination monitoring under intensive vaccination.

Evaluation of the immunogenicity of three structural proteins of lumpy skin disease virus

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Introduction

Lumpy skin disease (LSD) is an infective cattle disease caused by lumpy skin disease virus (LSDV) belonging to the genus Capripoxvirus, Poxviridae family. LSDV has a linear double-strand DNA encoding for 156 genes, including 41 structural proteins. Two forms of the virion can infect the host with different mechanisms: the intracellular mature virus (IMV) and the extracellular enveloped virus (EEV), with EEV surrounded by an additional membrane containing several proteins. Although the infection mainly triggers a cell-mediated immune response, the humoral response also plays an important role in protecting the host, effectively allowing the detection of infected animals. Based on immunogenicity studies conducted on other Poxviruses, three LSDV structural proteins were selected and produced: two proteins are localized on the IMV envelope and one in the core, they are encoded by ORFs LSDV074, LSDV060, and LSDV095, respectively. The recombinant proteins were expressed in E.Coli, purified, and then they were used to develop three different ELISAs, one for each recombinant

protein. We tested sera from cattle experimentally infected by evaluating the specific immunogenicity of LSDV074, LSDV060 and LSDV095.

Materials and methods

The LSDV060, LSDV074 and LSDV095 ORFs were cloned in E.Coli expression vector using Golden Gate technology, in frame with a gene codifying for a fusion protein and a Histidine-Tag. After the expression, the proteins LSDV060 and LSDV095 were purified by metal affinity chromatography. They were preliminary titrated and three indirect ELISAs were developed. The purified LSDV060 and LSDV095 antigens were directly adsorbed to the plates, whereas the LSDV074 was immune-captured by the specific 2F10 monoclonal antibody (mAb). A panel of sera from 18 cattle experimentally infected with different LSDV strains and collected at 0, 7, 14, 21, and 28 days post-infection was tested. In addition, 198 LSDV negative cattle sera collected in Northern Italy were evaluated. The results obtained by the three ELISAs were compared to a previously developed indirect ELISA where the inactivated LSD virus was immune-captured by the 2F10 mAb.

Results

Cut-off values of the three ELISAs were assigned by testing the negative sera. All cattle sera tested with the viral antigen ELISA seroconverted at 14 dpi. The LSDV074 indirect ELISA identified the seroconversion at 14 dpi in 17 cattle; only one animal showed a weak positivity during the testing period, but when tested with LSDV060 indirect ELISA a clear seroconversion is detected. The latter assay detected the seroconversion at 14 dpi in 16 cattle, with remaining two animals showing a weak positivity. Noteworthy, the mild response was observed in cattle infected with Neethling strain. Only 6 cattle reacted against LSDV095 antigen and they corresponded to those infected with field strains.

Discussion

The LSDV074 and LSDV060 antigens reproduced the antigenic properties of the native viral protein and they can be used as a promising tool in ELISAs, replacing the virus in serological assays. The limited immunogenicity of LSDV095 antigen could be consistent with its function as core protein. However, its role during the host immune response needs further studies.

Field evaluation of a safe and cost-effective shipment of FMDV suspected samples to diagnostic laboratories using lateral flow devices

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Introduction

Foot-and-mouth disease virus (FMDV) causes a highly contagious vesicular disease in livestock with serious consequences for international trade. The control of FMD requires the identification of circulating strains in affected areas to implement effective control measures. However, restrictive regulations and high costs for shipping clinical samples to reference laboratories remain major obstacles. In our laboratory, we developed a cost-effective and safe protocol for shipment of FMDV samples based on the inactivation of the virus on lateral flow devices (LFD). This method allows molecular detection and typing of FMDV and rescue of live virus after RNA transfection into cells. The present study further evaluates this protocol on clinical samples freshly collected in endemic countries.

Materials and Methods

In Nigeria, Turkey and Pakistan, epithelium or vesicular fluid samples were collected on FMD-suspected clinical cases and tested in the field for FMD using LFD. LFDs were chemically inactivated or not, directly in the field, then submitted to reference laboratories for further molecular detection and virus rescue. In parallel, the protocol was tested on vesicular fluid collected from cattle experimentally infected with FMDV.

Results

The safety of the inactivation protocol was confirmed on field samples, as well as on vesicular fluid collected from experimentally infected cattle. On inactivated LFDs, molecular diagnosis was successfully performed allowing VP1 sequencing and molecular characterisation of strain involved. Transfection of RNA extracted from inactivated LFDs ensured virus rescue for some samples allowing thus further characterization, as sequencing of complete genome.

Discussion

This study demonstrates that this LFDs-based inactivation protocol, applicable directly in the field, is a safe way for room-temperature, dry-transportation of FMDV samples. It will substantially decrease the shipping cost, thus increasing field sample submission to contribute to a better FMD control.

Validation of disinfection by directed and non-directed processes in the BSL3 laboratory handling live FMDV

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Introduction

In laboratories handling live foot-and-mouth disease virus (FMDV), strict biosecurity measures are applied, including for the entry and exit of personnel as well as for the decontamination of all equipment and the various surfaces in the laboratory. Today, the most commonly used disinfectant for this virus is formaldehyde which is toxic for humans. The objective of our study is to validate FMDV inactivation efficiency by new less toxic products.

Materials and Methods

Depending on their use, the efficiency of disinfectant products was tested using different methods according to the French standard NF-T-72281 November 2014: (i) by spray for laboratory surfaces (directed disinfection process), (ii) by misting for large equipment or for the whole laboratory (airborne disinfection - non-directed process). Efficiency tests consisted in letting the virus in contact with the disinfectant product for a setted time, adapted to the product and the method used. The result was expressed as a reduction in the viral load determined by virus titration on cells. For the disinfection of the different surfaces, the virus was put in contact with a 0.5% citric acid solution for two minutes on a support. Six FMD serotypes were tested (O, A, Asia-1, SAT1, SAT2, SAT3) by this method. For airborne disinfection, the virus serotypes O and SAT2 were exposed to a 35% hydrogen peroxide solution for two hours.

Results

As 0.5% citric acid is not cytotoxic, the recovery liquid from the supports could be inoculated directly

on sensitive cells for virus detection and titration. For the highly cytotoxic 35% hydrogen peroxide, the recovery fluid had to be diluted and the large volume method was used. The results of both methods show an absence of virus in the recovery fluid after testing.

Discussion

In view of these initial positive results, we are continuing to test the effectiveness of these two products, which are less-toxic to humans under the right conditions of use. At the end of this study, these disinfection methods could be an alternative to other methods that use more toxic products.

Comparative evaluation of commercial ELISA kits for the detection of antibodies against FMDV structural proteins

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Introduction

 Post vaccination monitoring is essential to assess the effectiveness of vaccination campaigns against foot-and-mouth disease (FMD). There are several methods to screen FMD virus structural protein antibodies including Solid-phase competitive ELISA (SPCE), Liquid-phase blocking ELISA (LPBE) and Virus neutralization test (VNT). Among these, SPCE is widely used since VNT (gold standard test) has practical limitations. Commercially available SPCE kits which are serotype-specific do not have the same sensitivity for the detection of antibodies induced by the different vaccine strains. Here, we analyzed sera from animals vaccinated with O1 Campos, A24 Cruzeiro, and A2001 Argentina strains by Priocheck™, Izsler, and ID Screen™ ELISA kits (type O and A) and compared them with LPBE and VNT strain-specific methods.

Materials and Methods

 Sera from single vaccinated or revaccinated cattle, swine, and sheep were analyzed. All sera had antibody titers above protection values previously determined by LPBE or VNT for O1 Campos or A24 Cruzeiro.

Results

Results are summarized in Table 1 which shows the percentage of samples that were positive for each kit.
Serotype O: Priocheck O detected 100% and 93% of sera from single vaccinated swine and cattle, respectively; For Izsler O the percentage of positivity in single vaccinated animals was only 36% for swine and 20% for cattle; ID Screen O detected 100% of single vaccinated swine and cattle sera. All single vaccinated ovine and revaccinated animals were detected by the three kits.
Serotype A: Priocheck A detected 58% and 91% of sera from single vaccinated swine and cattle, respectively; Izsler A detected 0% and 50% of single vaccinated swine and cattle; ID Screen A detected 100% of swine and cattle sera. All revaccinated animals and most of single vaccinated ovine were detected by the three kits.

Discussion

Priocheck and ID Screen kit for O serotype have good sensitivity for the detection of antibodies against O1 Campos in all species analyzed, whereas Izsler O kit has low sensitivity in both swine and cattle. Priocheck A kit has acceptable sensitivity for the detection of antibodies against South American vaccine strains in cattle, although for swine the sensitivity is low. Izsler A kit has low sensitivity in both swine and cattle. Finally, ID Screen type A has very good sensitivity in both species. Most of the sera

from single vaccinated ovine were detected by the six kits.

In conclusion, it is recommended to use the appropriate tool to perform post vaccination monitoring according to the vaccine composition applied. In case of using vaccines composed by South American strains O1 Campos, A24 Cruzeiro, and A2001 Argentina, it is recommended to use VNT, LPBE using homologous strains, or ID Screen kit for cattle, swine, and sheep. Additionally, antibodies against O1 Campos are detected with adequate sensitivity by Priocheck O.

Identification of a cross reactive epitope within the G-H loop of FMDV

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Introduction

There are seven antigenically distinct FMDV serotypes; O, A, C, Asia1, SAT1, SAT2 & SAT3, with no cross protection between serotypes. There are five known antigenic sites on the FMDV capsid against which neutralizing antibodies bind to confer protection against the viral infection. VP1 contains the virus attachment motif (RGD) on the G-H loop that binds to the cellular receptor integrin for all the seven serotypes known and carries the serotype specific immune dominant epitope which is part of antigenic site 1. It has been shown that the RGD motif is not an essential constituent of peptides able to elicit neutralising antibody responses against the virus (Brown *et al.*, 1999). Monoclonal antibody (Mab) D9 is a neutralising Mab that binds to the linear immune dominant epitope of G-H loop, where for serotype O, its neutralising activities are affected by the changes at amino acid positions VP1 (L144, L148 and K154). In this study we hypothesised that there are two different types of epitopes on the G-H loop, one is conserved between serotypes, and non-neutralising, while the second epitope is neutralising and serotype specific.

Materials and Methods

To test this hypothesis, we have developed an indirect peptide ELISA using synthetic peptides representing the G-H loops from different serotypes present in East Africa including serotype O (O ETH/9/2019), serotype A (A SUD/9/2018, A UGA/28/2019), serotype SAT1 (SAT1 TAN/22/2013 and SAT1 TAN/22/2014) and serotype SAT2 (SAT2 ETH/16/2015 and SAT2 KEN/19/2017). The length of peptides used is between 31 and 35 amino acids including six lysine residues to ensure peptide solubility. A panel of neutralising, serotype specific Mabs previously characterised by IZSLER, Italy and known to bind to the G-H loop of VP1 were used to delineate the serotype specific neutralising epitope. In this study we will describe the profile of D9 cross reactivity as an example.

Results and Discussion

The preliminary results of this study showed that D9 which was previously thought to be serotype O specific Mab bound to serotype O, A and SAT1 G-H loops in a dose dependent manner but did not bind to SAT2 G-H loop peptides tested in this study (see above).D9 also cross reacted with the stabilised virus like particles (VLPs) corresponding to serotypes O, A, SAT1 but not SAT2 when the VLPs were used as antigen in the ELISA with integrin as a capture and D9 as detector. These preliminary data suggest the presence of conserved, cross-reactive epitopes on the G-H loop of FMDV on some of the viruses used in this study. The impact of this observation needs further investigation. Further characterisation of the conserved epitope is underway using alanine scanning, a panel of overlapping peptides and testing of D9 cross neutralization.

Session IV. Vaccinology

Innovative platform-based technologies offer real hope for the accelerated development of FAST vaccines that can be quickly and easily modified to combat evolving field strains. What are the most suitable technology platforms currently for priority FAST diseases?.

Innovative platform-based technologies offer many potential advantages over conventional vaccines. However, for any novel vaccine technology, there are also limitations to its application in the control of FAST diseases. How can we balance the advantages and limitations of each vaccine platform to direct research efforts towards the optimum technology for each FAST disease?.

How can the veterinary sector translate the experience gained with the development and commercialization of COVID-19 vaccines to fast-track similar development and commercialization of innovative technology platforms of FAST vaccines?.

What are the take home messages from projects (e.g., AgResults Foot and Mouth Disease Vaccine Challenge Project) aimed at encouraging the development and uptake of high-quality FMD vaccines tailored to meet the regional needs and how can we capture the best practices to establish similar schemes on other regions of the world?.

Are there innovative developments in cold chain logistics that can help improve the distribution and monitoring of FAST vaccines from the manufacturing site to the field to ensure the quality of the vaccine at the point of administration?.

What innovative developments in vaccination monitoring can help improve the management of FAST disease outbreaks?.

Aim

To explore innovative technological platforms for FAST vaccines, to identify options for their development and commercialization and to better understand their advantages and limitations compared to conventional vaccines; to identify innovative developments and digitalization applied to cold chain logistics and vaccine monitoring; to examine a real-life example of innovative vaccine projects to capture best practice principles that can be translated to other regional projects.

Session IV. Oral presentations

The application of new vaccine technologies to control high consequence animal diseases

B. Charleston

Available upon request

New vaccine technology: Hopes and fears

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The application of RNA and vector vaccines to combat the COVID-19 pandemic has shown that these and other new vaccine technologies have great potential to combat (emerging) diseases, but has also fuelled the discussion around their safety. Was the fear and scepticism among the global public of taking a COVID-19 vaccine realistic? In this talk I will briefly highlight the different vaccine technologies and some of their pros and cons. New vaccine technologies include antigens and antigen delivery methods, administration methods, and adjuvants. The impact of new vaccine technologies on large scale manufacturing, the cost of goods, and the product registration process will be address as well, with an emphasis on veterinary applications.

The need for an innovative framework for access and benefit sharing of FAST pathogens

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The Nagoya Protocol on Access and Benefit sharing is an international agreement that became effective in 2014, whose objective is "the fair and equitable sharing of the benefits arising from the utilization of genetic resources". It requires users to obtain authorization from the country of origin before accessing a genetic resource and to negotiate the terms and conditions of its use.

While the intention of the Protocol is to contribute to the sustainable use of biodiversity, its application to the field of infectious pathogens has resulted in increased bureaucracy, which makes it difficult to share strains and sequences. This red tape hampers innovation in the field of vaccines against FMD and other transboundary diseases (FAST) and it is ultimately detrimental for disease control and pandemic preparedness.

The Pandemic Influenza Preparedness (PIP) framework could be used as example of a framework that facilitates rapid sharing of virus strains, sequences and information. The veterinary scientific community and the international organizations needs to come together to define a similar innovative framework for FAST animal pathogens and ultimately exclude them from the scope of the Nagoya Protocol.

Replacement of FMD vaccine potency tests: What are the options?

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Introduction

Challenge of vaccinated animals for evaluation of foot-and-mouth disease vaccines will always be essential when new strains are implemented in vaccine production. To replace, reduce and refine animal experiments, producers are using alternative tests for batch release of vaccine. Producers either check the antibody response in standardised tests after vaccination or rely on GMP production and the quantification of 146S antigen in the vaccine.

Analysis of published data

There is a strong relation between antibody titre and protection but also a significant relation between 146S content and protection. Because the slope of the relation between antigen amount and protection is less steep the tolerance to error is much higher (Figure 1). This indicates that formulation of vaccine based on antigen dose is a better choice.

New techniques for determining antigen content before and after formulation have been developed, that potentially can replace sucrose or CsCl gradient analysis. Size exclusion chromatography or HPLC can be used to determine the antigen content, but recently also 146S specific antibodies (MAbs and VHHs) have been selected that can be used in ELISA. Also, several techniques have been described for extraction of the antigen from formulated vaccine, that allow the evaluation of formulated vaccines.

Conclusion

Potency tests on formulated batches of vaccines are currently not standard practice in FMD vaccine production sites. The PD_{50} study, however, is essential to document that a producer is capable to produce a good quality vaccine, but batch release can subsequently be based on serology in cattle vaccinated with the batch that has to be released, or by implementing GMP production and formulating in a standard way that has proven to produce 3 PD_{50}/dose vaccine with 95% confidence.

New insights in the humoral immune response following FMDV vaccination in pigs

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Introduction

Foot and Mouth Disease Virus (FMDV) vaccine efficacy is often evaluated by virus neutralizing titers (VNT) in serum after vaccination, as a proxy to evaluate protection through challenge. However, screening of new vaccines or adjuvants calls for additional tools to predict protection, since there is a grey zone where VNT may not fully correlate to protection. Our aim in this study was to decipher the functions of the humoral immune response as Fc-mediated protection should be also considered in addition to neutralization. The glycosylation profile of specific antibodies highly influences the interaction of the Fc fragment of the immunoglobulins with Fc Receptors at the surface of immune cell. The glycosylation pattern, in addition to immunoglobulins quantifications, were evaluated in pigs by addressing immunogenicity of O1Manisa (O1M) strain formulated in an oil-in-water adjuvant, combined with well-described immunostimulants targeting Pathogen Recognition Receptors (PRR).

Material and Methods

Conventional pigs were immunized once, through intramuscular route, on Day 0 (D0) with 5µg of O1 Manisa inactivated antigen formulated in an experimental single Oil-in-water-emulsion combined or not with immunostimulants targeting TLR3 (Poly I:C); TLR8 (CL097); TLR9 (CpG); Dectin-1 (□-glucan). A double-oil emulsion, Montanide ISA206 from SEPPIC, was also evaluated. Blood sampling was

performed in a weekly manner from D0, to D28, final day of the study. VNT and glycosylation profiles were measured on D28, whereas anti-146S particles FMDV antibodies (IgM and IgG by Indirect ELISA) or total Ab (serological blocking ELISA), were quantified all along the study.

Results
The anti-FMDV IgM response was quantifiable as early as D7, and still high on D28 though declining for all groups. The IgG response was delayed by one week compared to the IgM response, rising at D14, and did not reach the plateau by D28. Both IgM and IgG could distinguish the different groups, with ꞵ-glucan and CL097 giving rise to low titers and Poly I:C giving significantly increased IgM and IgG titers by D21 and D28. The serological blocking ELISA gave comparable results as the VNT and was already sensitive at D7 to distinguish the different formulations. When looking at the glycosylation profiles of the Fc portion of anti-FMDV IgG's, we could differentiate the formulations based on the patterns of fucosylation, mannose content, sialic acid content and G2FS2/G2FS1 ratio.

Discussion

Our data provide the first investigations on glycosylation in pigs, and for FMDV immune response. We developed tools enabling early measurement of the serologic response to different FMDV vaccine candidates. Additionally, our data are providing insights on the functions of these antibodies by characterizing their profiles of glycosylation, these ones shown in human and mice to be associated with Antibody Dependent Cell Cytotoxicity. The next step will be to assess these markers in a challenge study.

Agtech technologies supporting governmental diseases eradication programmes

C. Richaud

Smart farming technologies provide the farmers with their animal location and health status in real time. Equipped with these technologies, farmers can take immediate actions to improve the health and welfare of their herd and of every individual animal. The use of smart farming technologies provide a valuable time optimization in detecting and managing disease outbreaks. A connected global system to live track animals, allow secure localization and early detection. Once the time gap is closed, we advance towards transmissible diseases eradication.

Establishing a system for Prequalification of vacciness against FMD

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Introduction

Disease control authorities seeking to purchase FMD vaccines are frequently faced with the situation that there are no vaccines with marketing authorisations issued by the regulatory authority in their own country. In these situations, authorities may choose to use vaccines for which it is difficult to obtain assurance on the standards that have been applied for manufacture, testing and the granting of any marketing authorisation that might exist (also termed registration or licensing). An important function of EuFMD is to promote vaccine security for member nations in terms of helping to assure the supply of vaccines of suitable quality when needed. As part of the work plan 2019-2023 EuFMD is putting in place a system for prequalification of FMD vaccines with the objective of promoting the use of vaccines that comply with minimum international standards. Increased uptake of vaccines that

have been prequalified should also improve predictability of demand, thereby promoting investment by manufacturers and benefitting vaccine security for member nations. A system of prequalification is an important prerequisite for putting in place Assured Emergency Supply Options (AESOPs) for FMD, representing an alternative, or supplement, to conventional FMD vaccine banks. Under an AESOPs contract, the risks and costs of assuring the supply, when needed, of FMD vaccines of suitable quality would be shared between the manufacturer and the customer. The EuFMD has considered the experience gained by WHO in operating a successful prequalification scheme for human vaccines for many years, adapting the approach to reflect the wide differences that exist between the human and veterinary sectors with respect to vaccines and the practice of vaccination.

Materials and methods

Taking into account that EuFMD is not a regulatory authority, prequalification will be based on the principle of 'qualification assurance'. Only vaccines that have been 'qualified' by at least one national competent authority through the issue of a marketing authorisation will be eligible for prequalification. Applicants will submit a copy of the marketing authorisation together with additional information in the form of a prequalification evidence file (PEF) demonstrating that the vaccine complies with at least the minimum standards in the Manual of Diagnostic Tests and Vaccines for Terrestrial Animals of the World Organisation for Animal Health (the 'WOAH Terrestrial Manual'). Prequalification will not repeat the assessment performed by the national authority, rather a risk-based approach will be applied to evaluate the level of assurance that has been demonstrated for WOAH compliance in relation to the key properties of the vaccine that are essential for its safe and effective use – hence the term 'qualification assurance'. A phased approach to implementation will be followed as shown in Figure 1, below.

Results

A dedicated Prequalification Team has been established within EuFMD. Guidance on the technical requirements and administrative procedure has been developed through a Technical Advisory Group on Prequalification of FAST Vaccines involving experienced regulators, relevant experts and manufacturers as the main stakeholders. Having been through a process of public consultation, these guidance documents are currently being finalised and will be published on the EuFMD website once adopted by the Standing Committee on Prequalification which acts as the governance and oversight committee for the prequalification procedure. The Prequalification Team is now putting in place the operational systems and internal procedures so as to be in a position to receive expressions of interest to submit applications for prequalification for FMD vaccines as from January 2023.

Discussion

Even though there are many entities and authorities involved in assuring the quality of vaccines it can be difficult for risk managers in member nations of EuFMD to obtain the necessary assurance that FMD vaccines comply with the minimum standards of the WOAH Terrestrial Manual. EuFMD is establishing a system of prequalification to evaluate and publish information on the level of assurance that exists that vaccines meet these minimum international standards. In the first phase of operation the system will be based on documentary evidence provided by the manufacturer that is evaluated by independent experts experienced in the assessment of vaccines against FMD following a risk-based approach. At later stages of operation, the system will be extended to include testing of vaccines by suitably recognised reference laboratories and inspection of sites of manufacture for compliance with the principles of good manufacturing practice.

The AgResults FMD Vaccine Challenge Project as an Example of Innovative Vaccination Strategy

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Introduction

One of the most infectious livestock diseases in the world, Foot and Mouth Disease (FMD) presents a constant global threat to animal trade and country economies. To assist control measures, the global clustering of FMD viruses has been divided into 7 virus pools, where multiple serotypes occur but within which are topotypes that remain mostly confined to that pool. This clustering of viruses suggests that if vaccination is to be a major tool for control, each pool could benefit from the use of tailored/more specific vaccine formulations relevant to the topotypes present in that pool.

Discussion

The AgResults Foot and Mouth Disease (FMD) Vaccine Challenge Project (the "Project") is an eight-year, US$17.68 million prize competition that supports the development and uptake of high-quality quadrivalent FMD vaccines tailored to meet the needs of Eastern Africa (EA). The Project targets the following 'Pool four' countries: : Burundi, Ethiopia, Kenya, Rwanda, Tanzania and Uganda. The Project is being run in two phases: A Development Phase, to encourage the production of regionally relevant vaccines, and a Cost-Share Phase, designed to help to reduce the price of these vaccines in the marketplace to the end users, which is hoped will encourage broader uptake.

Manufacturers can submit quadrivalent FMD vaccines containing serotypes A, O, SAT1 and SAT2 which will be assessed as relevant for use in the region through a unique component of the Project requiring the screening of vaccines against the EA FMD Virus Reference Antigen Panel assembled by the World Reference Laboratory for FMD (WRLFMD), at the Pirbright Institute, UK, in collaboration with the WOAH/FAO FMD Reference Laboratory Network. To be eligible for the Project, sera from vaccinated cattle will be evaluated and confirmed as relevant for use in the region if they pass a determined neutralisation cut-off threshold titre against FMD virus strains in the panel. These vaccines will then be entered into the Project's Cost Share Phase.

This presentation provides an update of progress since the launch in early 2020 up to the present day and will discuss this unique approach enabling a regionally targeted FMD vaccine initiative.

Session IV. Poster presentations

The core group for vaccination advice, guidance and consultation - Middle East: Activities and perspectives

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Introduction

The Core Group for Vaccination Advice, guidance, and consultation – Middle East (Core GVA-ME) was established by the European Commission for the Control of Foot-and-Mouth disease (EuFMD). This group involves four regional experts and aims to assist countries in the region in the design and implementation of post-vaccination monitoring (PVM) activities and act as a platform to exchange experience and expertise on vaccination for FMD and similar transboundary animal (FAST) diseases.

Materials and methods

The Core GVA-ME group agreed to start on FMD, for the common importance of this disease to the target countries. In addition, the Core GVA-ME group considered the work on FMD as a template that can be adopted for future work on other similar transboundary diseases. Therefore, the Core GVA-ME group reviewed the concerned countries' responses to the survey on vaccination against FMD provided during the Fifth Middle East FMD Roadmap Meeting, which was held in December 2021. The Core GVA-ME group also attended the Second Virtual Meeting Group for Vaccination Advice, Guidance, and Consultation for FAST diseases in the Middle East, which was held in January 2022, where they presented their scheduled workplan starting from January until October 2022. Due to the countries' peculiarities regarding the vaccination strategies, the Core GVA-ME group adopted a country-by-country approach to proceed in reviewing the vaccination strategies according to each country's risk-based strategic plans (RBSP) for FMD control as well as evaluating their post-vaccination monitoring studies.

Results and discussion

During the first half of 2022, the Core GVA-ME group held seven meetings. One important virtual discussion panel was with the Egyptian Chief Veterinary Officer (CVO) on the vaccination strategy against FMD as well as a review of the two proposals for PVM studies in Egypt. Moreover, the Core GVA-ME group discussed and gave vital comments to improve the FMD-PVM proposal of Lebanon and deeply reviewed the progress of the ongoing PVM study in Northwest Syria. In addition, the officials in Jordan asked the Core GVA-ME group to help in results interpretation for the vaccine matching study performed by the Pirbright institute, and a meeting was held with a top scientist at the institute, EuFMD, and one of the members of the Core GVA-ME group which clearly helped Jordanian officials to submit a vaccine tender based on vaccine matching results. Currently, Libya is the subject of the Core GVA-ME group's activity to discuss the country's preparedness to enter the Progressive Control Pathway for Foot-and-Mouth Disease (PCP-FMD). Later, Sudan, Palestine, and Jordan will be scheduled to closely review their vaccination strategies as well as their PVM plans. The Core GVA-ME group represents an efficient approach and a good example to guide and implement the international initiatives on a regional level.

Early and long-lasting antibody responses in sheep after single dose and wto-dose course vaccination schedule with single oil emulsion vaccine containing O1 CAMPOS, A24 CRUZEIRO, A2001 ARGENTINA and ASIA1

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Introduction

Foot-and-mouth disease (FMD)-susceptible sheep's play an important epidemiological role in the spread of FMD. Outbreaks in sheep due to multiple serotypes FMDV O, A, Asia 1 have been reported in endemic regions such as the Middle East and North Africa. In the present study, we assessed the onset and duration of immunity (DOI) elicited by FMD single oil emulsion polyvalent Asia1 vaccine (FMDV O, A and Asia 1) and trivalent vaccine (FMDV O, A, A) in sheep after a single dose and two doses. The booster effect and the comparison in the immune response induced by the two vaccine compositions was investigated.

Materials and methods

The vaccines used in this study were manufactured by Biogénesis Bagó (Argentina) in accordance with GMP as water-in-oil single emulsion (PD50>6) and contained O1 Campos, A24 Cruzeiro, A2001 Argentina and Asia1/KZ/03 vaccine strains. The immunogenicity test was performed in two groups of 20 healthy FMDV antibody free sheep aged 3–6 months with no previous history of FMD vaccination.

Group 1 was vaccinated with 1 ml of polyvalent Asia1 vaccine, while Group 2 was vaccinated with 1 mL of trivalent vaccine by intramuscular route. In both groups ten animals received a second dose 28 days post primary vaccination (dpv). Two unvaccinated sheep were kept as controls. Serum antibody levels against each vaccine strains were determined by virus neutralization test (VNT) at different times between 0 and 210 dpv. Differences in VNT titers between animals receiving one or two doses of polyvalent Asia1 vaccine and between polyvalent Asia1 and trivalent vaccines at different times post-vaccination were assessed by the Mann-Whitney test (p-value<0.05 was considered statistically significant).

Results

After a single administration of FMD Vaccines in sheep, antibody response were developed from 15 dpv. Polyvalent Asia1 vaccine induced a peak of antibodies at 90 days, remaining at high levels up to 6 months after single vaccination. The administration of a second dose at 28 dpv, induced statistically higher neutralizing antibody titers against O1 Campos, A24 Cruzeiro, and A2001 Argentina vaccine strains between 90 and 210 dpv, while for Asia1, statistical differences were found at 56 and 120 dpv. No statistical differences in the immune response against O1 Campos, A24 Cruzeiro and A2001 Argentina vaccine strains were detected between groups receiving polyvalent Asia1 or trivalent vaccine at 210 dpv after one dose.

Discussion

The results indicated that sheep, elicited quick, high and persistent antibody response which were maintained in high levels, above 2 log10, up to six months even after single dose of Polyvalent Asia1 or Trivalent vaccines. The inclusion of Asia1 in the formula does not result in a detriment or enhancement in the immune response to the other strains. Moreover, both vaccines evaluated conferred satisfactory early and long-lasting immune response. Statistical differences in the immune response were observed in most bleeding times after revaccination at 28 dpv. Hence, the recommendation is to include a two-dose primary course (4 weeks apart) to guarantees higher antibody titers for the maintenance of satisfactory herd immunity levels at least for 6 months.

Protective capacity of vaccines containing O1 CAMPOS, A24 CRUZEIRO and A2001 ARGENTINA vaccine strains against FMD viral lineages circulating in East-SouthEast Asia, Middle East and North Africa

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Introduction

Foot-and-mouth disease (FMD) remains endemic in East-Southeast Asia, Middle East and North Africa causing significant economic losses; multiple variants of serotypes FMDV O and A are currently circulating. FMD vaccines from Argentina, are widely used in South America and in some countries in Asia and they have shown excellent efficacy in controlling FMD in these regions. Here we report satisfactory in vitro and in vivo vaccine matching studies of FMD vaccines formulated with O1 Campos, A24 Cruzeiro and A2001 Argentina vaccine strains against Type O and A field viruses circulating in endemic regions.

Materials and Methods

The vaccines used in this study were manufactured by Biogénesis Bagó (Argentina) in accordance with

GMP as water-in-oil single emulsion (PD50>6) containing purified antigens. The animals enrolled were vaccinated and bled by SENASA (OIE Reference Laboratory for FMD in Argentina) and serum samples were sent to perform vaccine matching studies at the World Reference Laboratory for FMD (WRLFMD) at Pirbright, UK. A Bovine Vaccinal Serum (BVS) pool derived from 5 cattle vaccinated with high potency O1 Campos monovalent vaccine, after single vaccination, was used. The antigenic relatedness of the O1 Campos vaccine strain and Type O field viruses (O/SEA/Mya98, O/ME-SA/PanAsia, O/ME-SA/PanAsia-2, O/ME-SA/Ind2001 and O/EA) was estimated according to the heterologous neutralization titer. Moreover, Virus Neutralization Test (VNT) on serum samples collected after vaccination of cattle with trivalent O1 Campos/A24 Cruzeiro/ A2001 Argentina vaccine was assessed against Type A field viruses (A/ASIA/Sea-97, A/ASIA/G-VII, A/ASIA/Iran05 and A/AFRICA). VNT titers greater or equal to 1.5 log10 were considered as an indicator of minimum heterologous cross-protection. Additionally, efficacy in pigs (50% Protective Dose) against heterologous challenge with O/ME-SA/Ind2001-e and A/ASIA/Sea-97 lineages were performed by SENASA.

Results

Protection threshold for heterologous protection has not been properly established yet. Therefore, we applied the value of 1.5 log 10 as it was previously discussed. Additionally, VNT titers were classified into three levels < 1.5, 1.5 to 1.8 and >1.8 log 10 to better characterize the cross reactivity induced by the vaccines. VNT titers against Type O field viruses were greater than 1.5, for all lineages evaluated. Heterologous VNT titers greater than 1.8 on 28 dpv were generated for 100% of viruses representing O/Panasia, O/PanAsia2, O/Ind2001d, and O/EA lineages. Titers between 1.5 - 1.8   were generated for some viruses of O/Cathay, O/Mya-98, and O/Ind2001e lineages, being in their greatest proportion higher than 1.8. VNT titers against Type A field viruses were greater than 1.5, for all lineages evaluated, showing high antigenic relatedness with A24/A2001 vaccine strains. Titers against A/G-VII and A/Iran 05 exceeded titers of 1.8 for all representing viruses. For A/Sea-97 and A/AFRICA, titers ranged between 1.5 - 1.8. Heterologous challenge tests resulted in a potency of more than 6 PD50/dose.

Discussion

Vaccine matching based on VNT titers showed the suitability of O1 Campos, A24 Cruzeiro, A2001 Argentina South American vaccine strains in controlling FMD viral lineages circulating in endemic regions. Moreover, in accordance with in vivo results, the high potency vaccines used in this study induced protection against O/ME-SA/Ind2001e and A/ASIA/Sea-97 threats.

Evaluation of FMD vaccine quality: Lights and shadows of the small-scale immunogenicity studies

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Introduction

In countries endemic for Foot-and-mouth disease (FMD), routine or emergency vaccinations are strategic tools to control infection; according to WOAH/FAO guidelines, a prior estimation of vaccine effectiveness is recommendable to optimize control plans. The aim of this work is to determine the benefits of the small-scale immunogenicity studies (SSIS) and the issues that may arise during its performance, based on the results of previous studies.

Materials and methods

Polyvalent vaccines from different manufacturers, and including FMDV serotypes O, A, Asia1 and SAT2, were evaluated during six SSIS carried out in as many countries and using large and small ruminants as model animals. The sera collected by vaccinated animals were tested with Virus Neutralization

Test (VNT) against FMDV strains homologous and heterologous to those included into the vaccines themselves.

Results

The most common information obtained analysing sera collected during a SSIS is the effectiveness of the FMDV vaccine selected and used during the study, itself. To come to this important conclusion, the seroconversion of involved animals was assessed, both after a single and a booster dose administration, focusing on the seroprevalence of the whole sample population or concentrating on the variation of immune response on every single animal. Moreover, VNT against heterologous strains also suggested the possibility that the investigated vaccines might be cross-protective against other FMDV strains, for instance, those recently circulating in neighborhood countries. Nevertheless, some critical issues may arise during a SSIS, that could undermine the correct execution of that study, such as the unavailability of the vaccine strains to be used in the VNT, the inaccessibility to information on vaccine strain, the unexpected death of animals, some problems in the samplings or even a sudden incursion of an FMDV field strain in the experimental population.

Discussion

Taken together, the results of this study confirmed the strategic importance of SSIS to determine the effectiveness of an FMDV vaccine, even with respect to the epidemiological situation of the region where it was administered. They also highlighted the importance of carefully following the sampling design, clearly outlining some of the gross errors that should be avoided.

Efficacy study of FMD vaccines against the challenge of the O/CATHAY isolate for the efficient control in pigs

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Introduction

Foot-and-mouth disease (FMD) O/CATHAY lineage virus is a known porcinophilic virus that has caused devastating damage to the pig industry. In vaccine matching and efficacy results by other FMD reference laboratories, there have been concerns that many commercially available vaccine could not confer effective protective immunity against O/CATHAY lineage viruses. In this study, we conducted the *in vivo* efficacy tests to find the applicable regimen for three commercial vaccines (O_1/Manisa+O/3630, O_1/Campos, and O/Primorsky/2014) and one experimental vaccine (O/Boeun/SKR/2017, O/ME-SA/Ind-2001e lineage) to confer the protective immunity against heterologous challenge with the O/CATHAY field virus, O/VN/30/17, in pigs.

Materials and methods
Two efficacy trials were performed. In each trial, nineteen FMD sero-negative pigs were randomly divided into six experimental groups; four vaccinated groups (n = 4 per group, O_1/Manisa+ O/3039, O_1/Campos, O/Primorsky/2014, and O/Boeun/SKR/2017) and one unvaccinated control group (n = 3). For trial 1, the pigs vaccinated twice at 14-day intervals and unvaccinated controls were challenged by intradermal inoculation at two sites in the tongue with the O/CATHAY virus inoculum 7 days after booster vaccination. All animals were monitored for 7 days to inspect signs of FMD. Sera and oral swabs were collected daily after challenge. For trial 2, the pigs vaccinated twice at 7-day intervals and unvaccinated controls were challenged with the same way.

Results

Every pig vaccinated twice at two-week intervals was protected against the heterologous challenge

with the O/CATHAY lineage virus, while some pigs in other vaccinated groups and all pigs in the control developed typical FMD clinical signs. In this study, comparing the efficacy results between trial 1 and trial 2, the protective immunity induced by vaccination increased over time, as a matter of course. Interestingly, all pigs in trial 1 were protected against the challenge with the O/CATHAY lineage virus, probably due to the highly induced heterologous virus neutralisation (VN) titer. The results of heterologous VN titer in trial 2 indicated the poor immunization in some pigs against the challenge.

Discussions

Our study indicated that the heterologous VN titer against the challenge virus would be the indicator of the protection. As the results of these clinical trials, it might be concluded that the proper modification of the vaccination regimen could be the alternative measure to control the possible future FMD outbreak more efficiently.

Evaluation of the efficacy in pigs by vaccination of commercially available FMV vaccines against heterologous challenge with A/ASIA/G-VII lineage viruses

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Introduction

Vaccination is an important measure for prophylactic control of foot-and-mouth disease (FMD) in endemic countries. One of the main factors for successful disease control is to select the most suitable vaccine strain, which will protect against currently circulating viruses. The aim of this study was to evaluate the efficacy in pigs by vaccination of commercially available FMD vaccines against heterologous challenge with A/Asia/G-VII lineage viruses, which have exhibited insufficient cross-protection.

Materials and methods

In each efficacy test, nineteen FMD sero-negative pigs were randomly divided into six experimental groups; five vaccinated groups (A_{22}/IRQ/64, A_{24}/cruzeiro + A/Argentina/2001, A/Zabaikalsky/2014 and A/ARRIAH/2015; n=4 per group) and one unvaccinated control group (n= 3). At 28 days post-vaccination, pigs were challenged with A/Asia/G-VII lineage viruses by tongue inoculation (2×10^6 $TCID_{50}$/200 µl). After that, clinical outcomes, viral shedding, and FMDV-specific immune responses were evaluated. Animal testing was performed twice independently using two viruses, A/BHU/03/2017 (animal testing-1) and A/TUR/13/2017 strain (animal testing-2).

Results

Animal testing-1: Except for two out of four pigs vaccinated with A/Zabaikalsky/2014 and all in the unvaccinated control, none of pigs showed secondary lesions, which demonstrating vaccine-mediated protection against the heterologous challenge. In real-time RT-PCR results, there was very low viral titers detected from bloods of some vaccinated pigs, which indicating that vaccination might prevent and reduce viremia. This might be due to the vaccine-induced immune response beyond the threshold level of 1.2 (log_{10}) for heterologous neutralizing antibody (NAb) titer conferring possible protection. Animal testing-2: None of pigs vaccinated with group A24/cruzeiro + A/Argentina/2001 and A/ARRIAH/2015 developed secondary lesions, which demonstrating vaccine-mediated protection against the challenge. These groups exhibited very low viral titers in clinical specimens, which indicating that the vaccine-induced heterologous neutralizing antibodies recorded over the threshold level of 1.34 (log_{10}) might reduce virus replication. In contrast, three and two pigs vaccinated with A22/IRQ/64

and A/Zabaikalsky/2014, respectively developed secondary lesions after primary lesion was observed at the site of inoculation. However, the clinical severity and viral RNA titers in infected pigs within A22/IRQ/64 and A/Zabaikalsky/2014 group were lower than those of unvaccinated control group, which demonstrating that vaccination has a somewhat effect on the prevention and reduction of virus replication.

Discussions
Our results showed some vaccine strains used in this study have the cross-protective potential against A/Asia/G-VII lineage viruses, A/BHU/03/2017 and A/TUR/13/2017 strain in pigs. However, some pigs having lesions at site of virus inoculation tested positive for viral RNAs in oral swabs, which indicating the possibility of releasing infectious materials into environment from sub-clinically infected pigs.
To further quantify the level of protection in pigs, it will be necessary to perform a standard vaccine potency test (i.e. 50% protective dose (PD_{50}) method) using the vaccine showing cross-protective potential.

Development of FMD vaccine for intradermal inoculation for swine

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Since outbreak of the foot-and-mouth disease (FMD) in South Korea in 2010, the Korean government has enforced a mandatory vaccination policy, and has recently implemented a bivalent (type O and A) vaccination. Although FMD outbreak was suppressed by vaccination, side effects caused by intramuscular(IM) injection emerged into a new problem in pig industry. Intradermal (ID) injection is known to have a low incidence of side effects and good antibody-forming ability. In present study, we compared the efficacy of FMD ID vaccine. Antibody was tested using the SP ELISA and neutralizing antibody titer was determined by homologous virial neutralization test (VNT). In the guinea pigs, the ID group showed an average antibody value of 40% or more at 14 day post vaccination (dpv). However, the IM group showed less than 40% immune efficacy at 14 dpv. After that, both groups showed more than 50% (positive value). As a result of serological analysis of the ID, it showed immune efficacy equal IM. A similar tendency was obtained in the target animal (the swine). In addition, the result suggests that ID induces faster antibody titer. Besides, there were lower side effects in all ID than IM group. In conclusion, ID can be suggested as an alternative to the existing IM route, in which side effects frequently occurs. In the case of an experiment comparing adjuvant, three adjuvants showing high immunity were selected for long-term comparison. Adjuvant A initially showed a relatively low antibody titer. However, after the mid-term, the antibody titer showed a remarkably high level. Adjuvant B initially showed a high antibody titer of 40% or more. And even after the mid-term, it maintained a high antibody titer of 80% or more. In conclusion, it seems that adjuvant B is suitable as an adjuvant that maximizes the effect of ID injection that induces high immune efficacy in the early stage. In the future, it could be necessary to study the optimal conditions through additional experiments to confirm several compositions for the FMD vaccine.

Session V. Risk assessment and modelling

What innovative approaches and data-driven technologies can advance disease modelling, risk assessment and forecasting?.

How can risk information be shared in a timely, efficient, and effective manner?.

How to integrate different data sources into useful information to assist decision making processes to prevent and control FAST diseases?.

How can models be used to inform policy and decision makers for FAST disease prevention and control? What are the best practices for using modelling to inform policy and decision makers?.

What are the limitations and challenges of using data to model and assess risk? How can we overcome these challenges? How can we deal with uncertainty?.

How can we explain the outcomes of risk assessments and models to the general public if needed?.

How can risk analysis and model tools be made available to developing countries? How can we make research results understandable, useful, and available to veterinary services and other stakeholders that could benefit from them?.

Aim

To showcase advances and innovations in risk analysis and modelling as suitable tools for using data and transforming it into meaningful information to assist decision-makers to manage the risk of FMD and similar TADs.

FAST updates

Key aspects of the current Sheeppox, Goatpox and Lumpy Skin Disease Virus Epidemiology

N. De Regge

Sciensano, Scientific direction of infectious diseases in animals, Service exotic and vector-borne diseases, EURL capripox viruses

Lumpy skin disease, sheeppox, and goatpox are notifiable transboundary diseases of cattle, sheep, and goats, respectively, caused by viruses of the Capripoxvirus genus. They are responsible for direct and indirect financial losses, origination from animal mortality, morbidity (including fever, reduced milk production, characteristic pox lesions, etc), cost of vaccination, and trade restrictions of animals and their products.
Sheeppox virus (SPPV) and goatpox virus (GTPV) are mainly spread by direct contact between animals. Since these viruses can survive in the environment, indirect transmission may also occur through fomites such as human movement, vehicles, wildlife and trade of hides when insufficiently treated. These viruses are widespread in Africa (north and west of the Sahara) and Asia. During the last decade, they have also emerged in Europe, with a few outbreaks in Greece between 2013-2018 and in Bulgaria in 2013. Mid-September 2022, a new outbreak was reported in the province of Granada, Spain. This was the first notification of SPPV since the virus was eradicated in Spain in 1968. In the meanwhile (by October 9th), the presence of the virus has been reported in 9 foci, 2 additional ones in close proximity of the initial farm and 6 in a cluster in the province of Cuenca, about 200km north of the first cluster.

Lumpy skin disease virus (LSDV) is a vector-borne disease in cattle that has been endemic in large parts of Africa for a long time, and since the beginning of the years 2000 gradually spread through the Middle East and Turkey, into the Balkans, Russia and the Caucasus. Since 2019, the disease also spread to Asia, with notifications from China, Bangladesh and India, being countries having the largest cattle populations worldwide. The virus continued spreading southwards, reaching Indonesia in 2022. While the genome of circulating strains had remained rather stable during the LSDV spread in Africa, the Middle East, Europe, and first outbreaks in Russia , Russia reported in 2017 the detection of clinical LSDV cases caused by a vaccine-like recombinant LSDV strain carrying genetic signatures from both Neethling- and KSGP-based LSDV vaccines. Full genome sequences of LSDV strains isolated from outbreaks in several Asian countries show that these recombinant strains spread through south-east Asia. Recent data indicate that the recombinant strains are the result of recombination events that occurred during a badly controlled vaccine manufacturing process and that the emergence of these strain is the result of a spillover from vaccinated animals. These recombinant LSDV strains which behave as wild type strains undermine available diagnostic testing strategies since they are missed or recognized as vaccine strains by so called DIVA PCRs that are normally used to discriminate LSDV vaccine strains from wild type field strains. Preliminary indications of increased virulence and potential non-vector-borne transmission of the recombinant strains urgently need to be studied in more detail, just as the efficacy of available vaccines against these strains.

Session V. Oral presentations

Harnessing technology to collect and integrate data and convert to useful information for decision makers

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Data-driven innovations to inform disease control and prevention: Successes and pitfalls in applying model results to policy

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The intersection of science and policy remains a challenging space, perhaps highlighted most clearly in the world's efforts to address COVID-19 and leverage rapidly evolving scientific information. For foot-and-mouth disease (FMD) and similar transboundary animal diseases (FAST), the need to prevent, detect and respond to shifting disease threats highlights the need for data-driven tools that can be used to collect critical health information, explore policy alternatives, anticipate consequences, and evaluate impacts. A variety of modelling tools are often used to evaluate alternative approaches to the control of FAST diseases; however, the use of these tools is not without pitfalls, and the dangers of

"garbage in, garbage out" are increasingly present.

This series of paired talks explores recent examples of the successful use of modeling results to shape and inform policy while highlighting key issues that need to be addressed across the community of field epidemiologists and modelers to develop trusted, sustainable modeling partnerships and applications. We will also take a deeper dive into challenges around data collection to support modelling and the communication of modeling results to policymakers with the goal of highlighting possible solutions, as well as the areas where the modelling community still has work to do. Join us as we dive into recent advances in modeling tools and approaches, success stories of modeling applications, and a discussion of common pitfalls that limit the impact of modelling on policy.

Risk monitoring tool for FAST diseases (RMT-FAST): a semi-quantitative framework to estimate the risk of disease introduction

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Introduction

The cross-border movement of animal pathogens can lead to dramatic social and economic consequences. Therefore countries implement prevention measures (e.g. surveillance, border controls and trade restrictions) to reduce the probability of entry of new pathogens. However, resources available for such risk mitigation measures are limited, especially considering the large number of potential source areas and different pathways of entry of the pathogens. We propose a simple and easy-to-use tool to monitor the risk of introduction of foot and mouth and similar transboundary (FAST) animal diseases (Peste des Petits Ruminants, Lumpy Skin Disease, Rift Valley Fever, Sheep and Goat Pox) with the aim of assisting health authorities to identify the most likely routes and source countries for the introduction of these diseases.

Materials and methods

The Risk Monitoring Tool (RMT-FAST) is a risk ranking framework that assesses the potential introduction of FAST diseases to a 'target country' from neighbouring countries ("source countries"). Briefly, data collected by EuFMD regarding the epidemiological situation and the mitigation measures in place are used to attribute a score to each source country. Then, the possible connections (i.e. live animal trade, geographic proximity, etc...) between the target and source countries are evaluated by the user on the basis of the available information. The model combines all mentioned scores to rank the relative likelihood of pathogen introduction in the target country through six pathways (airborne, live animal contact, product of animal origin trade, vectors, fomites, wild animals). A pilot with the participation of experts from Spain was carried out to test the tool using the most recent available data.

Results

The application of the proposed framework indicated that, from the potential source countries, Spain is most closely connected to Morocco, Algeria and Tunisia. Considering the disease status and risk pathways, entry of FMD to Spain was most likely from Tunisia, Mali and Mauritania and mainly associated with the illegal introduction of animal products or fomites. In contrast, Morocco seemed to dominate the risk for PPR and SGP entry and both Mali and Mauritania were the most risky countries regarding LSD and RVF. The results of the case-study were considered plausible by the participating experts.

Discussion

RMT is a rapid, easy to use and practical aid to produce a preliminary risk assessment for FAST diseases, and could be periodically used by central veterinary or border Control Authorities to monitor risk situations and identify risk questions for a more thorough risk assessment. The tool could be easily extended to cover more countries and diseases. As with any model, the quality of the results is dependent on the accuracy of the data input. Whilst high quality and accurate data are available for some parameters (e.g. legal trade in animals and products), accurate data regarding illegal movements of animals and animal products are not available. Disease status and effectiveness of mitigations measures are dynamic and similarly prone to uncertainty. Notwithstanding these limitations, the tools is useful for countries to perform a rapid ranking of the risks of disease incursion.

Mapping the risk of spread of Peste des Petits Ruminants in the Black Sea basin - A knowledge-driven approach

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Introduction

Peste des petits ruminants (PPR) is a highly contagious viral disease affecting small ruminants and threatening farmers' food security and sustainable livelihoods across Africa, Asia, and the Middle East. After the successful eradication of Rinderpest, PPR was targeted as the next animal disease to be eradicated. Nonetheless, in the last two decades, PPR has continued spreading, including into countries where it had never been reported and in others that had already been officially recognised as PPR-free. In the Black Sea Basin, the disease is endemic in Turkey and emerged for the first time in Georgia and Bulgaria. These and other occurrences led to increasing concerns over the reintroduction of PPR into Europe. In this project, we aim to identify areas with a high risk of PPR spread within the Black Sea region.

Materials and methods
We applied a knowledge-driven approach (Spatial Multi-Criteria Decision Analysis/GIS-MCDA) to produce a risk map that identifies the most suitable areas for PPR spread in the region. This method uses the opinion of experts to weigh the importance of risk factors (RFs). First, through an extensive literature review, we identified RFs for PPR spread and, jointly with PPR experts, defined the most relevant ones for the study region. The selected RFs included: small ruminant density, smallholder farming, movements to seasonal pastures, proximity to animal markets, and proximity to previous PPR outbreaks. Spatial data for each of the RFs were gathered by national consultants and the FAO Statistical Database (FAOSTAT). Opinions were elicited through an RF pair-wise comparison matrix, which was presented in a regional PPR workshop organized by the FAO REU and the FAO PPR Secretariat and filled in by experts (with knowledge of small ruminant production and/or PPR epidemiology).

Results
RF data was collated, analysed and mapped and all maps were standardized on a scale of 0 to 1. After analytical hierarchical process calculations, 21 matrices were found consistent and, for each one, RF weights were calculated. A final suitability map for PPR spread was produced through a weighted linear combination of the standardized maps and the RF weights given by each expert (Figure 1). The illustrated results showed a higher suitability index (SI) in Anatolia (Türkiye), the border of Bulgaria with Thrace (Türkiye) and Eastern Georgia, a medium SI in Romania and a lower SI in Belarus, Ukraine and Northern Bulgaria. The risk map was validated with PPR outbreaks from 2019 to 2021 and the ROC analysis had an AUC of 67.6% (61.9-73.2%).

Discussion
These results highlight the usefulness of GIS-MCDA for integrating available knowledge about PPR and free spatial data. Despite limitations related to data quality and its harmonization, and the uncertainty implied with the expert opinion, our risk map had a reasonable predictive accuracy. This implies that the method is a useful tool to map the suitability of PPR spread in the study region. Our results can potentially be used to support decision-makers on the prioritisation and implementation of control and surveillance activities, thus facilitating more efficient risk-based use of resources.

Determinants of livestock mobility in Senegal

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Introduction

Livestock mobility plays an important role in the dissemination of major diseases in West Africa, including Foot-and-Mouth disease, Rift Valley Fever, and Peste des Petits Ruminants [1]. There is a need to identify reliable predictors of livestock movements. So far, a majority of studies have focused on the analysis of static movement networks [2]. We aimed at modelling the temporal dynamics of cattle and small ruminant movements in Senegal using a set of predictors: livestock market prices, rainfall, and biomass production.

Materials and methods

Official registrations of cattle and small ruminant movements across departments (the administrative units of Senegal) were supplied by the Senegalese Veterinary Services. We fitted a generalized additive model with a latent hurdle Poisson distribution to predict the number of herd movements registered between departments at each months on the years 2014 and 2019 [3]. The use of a hurdle Poisson allows an explicit modelling of the probability of missing observation. Pairs of departments – department of origin and department of destination - were considered as fixed effects. Explanatory variables were the values in the previous month as well as the difference between values in the current and previous month of departmental aggregates of environmental variables - biomass production and rainfall – and regional average market prices of cattle and small ruminants. The effects of these variables, along with the specific effect of calendar months, were modelled with thin plate spline functions.

Results and discussion

The effect of calendar month was significant except for small ruminants in 2014. The likelihood of livestock movement was increased around the time of religious holidays during which the consumption of cattle (Magal de Touba) or sheep and goat (Tabaski) plays an important role in the celebrations (Fig. 1). Among the used explanatory variables, biomass production had the most consistent effect across species but with slight variations between periods. In 2014 the likelihood of movement was negatively correlated with the biomass production at the department of origin while in 2019 the likelihood of movement was increased when the biomass production substantially changed from one month to the next in the department of origin. The effect of market prices differed between species: an increase in the market price at origin decreased and increased the likelihood of movements for cattle and small ruminants respectively.

We demonstrate that both environmental (biomass) and economic variables (market prices) can be used to predict the temporal dynamics of livestock mobility. Ruminant owners are incentivized to sell or displace their animals in periods of substantial changes in livestock market prices or in the level of grass or crop production where they live.

VADEMOS: Applications of vaccine demand estimation tool for managing FAST diseases

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Introduction

FAST diseases, in particular Foot-and-mouth disease (FMD), are recognized as the most important livestock diseases worldwide due to their large economic impact. Vaccination is central to most national control strategies. However, often a vaccine supply and demand mismatch exists with limited understanding of current and future vaccine requirements. VADEMOS is able to predict the FMD vaccine demand in endemic settings. New upgrades have been recently released, as detailed, and more features will be available in the near future including consideration of other FAST diseases.

Materials and methods

VADEMOS is a stochastic quantitative model developed considering changes in livestock populations, progress of disease control policy linked to the projected FMD Progressive Control Pathway (PCP) stage, and related vaccination regime in each livestock sector. The WOAH WAHIS and FAOSTAT databases, as well as country-specific data on current FMD outbreaks, livestock population and density were used along with experts' opinion sought to determine the extent of vaccine coverage, as well as the reduction in number of outbreaks for each PCP stage.
A web-based format with an interactive interface allows the user to modify parameters and therefore run simulations for "*ad-hoc*" scenarios.

Results

The tool provides estimates by year regarding the expected number of vaccine doses required for a wide range of endemic countries over a ten-year-period. As variability and uncertainty have been captured, VADEMOS not only returns the most likely value but also confidence intervals visualized via tables and graphs. The new version allows aggregation of estimates by region (i.e. Middle East countries) or continent (i.e. Asian countries). In addition, the model splits vaccine demand into two categories, prophylactic and reactive vaccination (i.e. number of doses used for the expected number of outbreaks). For large ruminants, the overall number of doses is detailed by sector (beef, dairy or smallholder) as well as population proportion of young and adult stock (to allow for age-related variation in vaccine dose schedules). Modifications to inputs can be seen instantly in the model output and data can be downloaded in a spreadsheet to permit comparisons or further investigation.

Discussion

VADEMOS is the first worldwide tool able to predict FMD vaccine demand. Policy makers might use the tool to better plan vaccination campaigns and to allocate in advance the resources needed for the adopted strategy. Industry may use it to predict market demand and consequently limit the risk of over- or under-production. Although VADEMOS is currently set for FMD, minimal modifications would be necessary to cover other vaccine-controlled diseases such as lumpy skin disease, peste de petit ruminants, sheep-pox and goat-pox.

Real-time decision making - Appropriate use of infectious disease models during outbreaks and in endemic settings

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Introduction

In the event of an outbreak of infectious disease, models can be used to assist policy makers to establish the risks associated with the disease and the potential role of interventions in reducing the future impact of the outbreak. However, during outbreaks there is often significant uncertainty regarding the true nature of disease spread, with not all data available that may be required to parameterise disease models. It is therefore crucial to explore the accuracy of models and the underlying uncertainty in predictions when utilised during ongoing outbreaks. In this presentation we will present findings from research carried out on both Foot-and-Mouth Disease (FMD) and from the ongoing SARS-CoV-2 (COVID-19) pandemic.

Materials and methods

We utilise an existing farm-level FMD model that has previously been developed for the UK 2001 FMD epidemic, whereby the risk of spread between premises takes into account farm location, size and species composition. The model is sequentially fitted to data as an outbreak progresses to explore how model predictions change as more data are available. We also present findings from a compartmental model of SARS-CoV-2 that was developed in early 2020 and utilised by the UK government to advise regarding the spread of COVID-19 and the effect of interventions.

Results

Our results show that during the early stages of outbreaks, the inherent uncertainty in the underlying disease data can result in substantial uncertainty in predictions regarding the future spread of disease. This uncertainty resolves as more data are accrued, but lack of data in the early stages can impact the ability of models to accurately predict the role of interventions. We discuss the implications for livestock disease in endemic settings where data are often not as readily available.

Discussion

This research emphasises the need for rapid surveillance and monitoring during emerging outbreaks in order to reduce uncertainty regarding how pathogens are circulating. Whilst models can play a role in decision making even during the early phase of outbreaks, modellers must communicate uncertainty in model outcomes to ensure that models are pararameterised to take into account the most up to date data available. In conclusion, close communication between epidemiologists, modellers, veterinary/ public health experts and policy makers is crucial to minimise the impact of future outbreaks of infectious disease.

Session V. Poster presentations

Using livestock mobility data to inform surveillance system: Application to the Senegal case

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Introduction

Livestock mobility is a key element of both production and trade systems in West Africa. Animals are frequently moved looking for better grazing areas or to be traded alive, to provide to familial needs or festivity-related consumption. As animals move so do pathogens, therefore livestock mobility is one of the principal factors contributing to the spread of transboundary animal diseases in the region. Due to the seasonality of these movements, the risk of disease introduction changes over the year, and the role of the different locations in the disease propagation varies consequently, making it difficult to optimise control and surveillance measures. Where a system for mapping movements exists, like in Senegal, some estimations of the risk of disease introduction and spread could be done and control measures could be put in place [1, 2, 3].

Materials and methods

In this study, we analysed 2020 livestock mobility data of Senegal to describe the temporal variation of mobility structure, and to identify different areas that could be potentially involved in the pathogen spread at different times of the year, and therefore be used as sentinel nodes. Data were collected in the form of Laissez-Passer Sanitaire (LPS), a sanitary mobility pass issued by the Directorate of Veterinary Services every time herders move their animals, and aggregated at different temporal (month or week) and spatial (department) scales, to provide a network representation for each species analysed (cattle, small ruminants, cattle and small ruminants without distinction).
We analysed mobility data using a complex network approach: the nodes corresponded to the departments of origin and destination; a direct link existed between two nodes if at least one animal was moved from the department of origin to the department of destination.
After a preliminary descriptive analysis to identify general spatial and temporal patterns, we simulated the spread of a direct contact animal disease (PPR or FMD-like) through the three livestock mobility networks, to study the influence of temporality on disease propagation. We considered a simplified network transmission SI model, with the departments of Mali and Mauritania as disease source nodes at different times of the year. We used the temporal path formalism [4] to identify potential Senegalese departments that could be involved in the spatial spread. To explore the effect of temporality on disease spread, we compared the results of the temporal mobility network with those of an aggregated static representation, to finally assess how reliable were predictions done if only a static network representation was used. Finally, we used CART method to identify possible network characteristics that could help the identification of most vulnerable areas.

Results and discussion
Our analysis showed that a static approach could widely overestimate the speed and the extent of disease propagation. On the other hand, the temporal analysis revealed that reachability and vulnerability of departments change along the year (Fig 1). Furthermore, preliminary analysis showed that the weeks around Tabaski (31st of July, week 31 in Fig 1) and Grand Magal of Touba (6th of October, week 41 in Fig 1), two important Muslim festivals associated with large consumption of livestock, corresponded to periods of major trade and disease diffusion. Furthermore, we showed that a static approach could widely.
These results highlight the importance of including temporality effect on surveillance measures to identify sentinel departments, and could improve disease surveillance systems by optimising the distribution of personnel and resources along the year.

FMD in Northern Nigeria: Risk factors and spatial distribution in small ruminants

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Introduction

Foot-and-mouth disease (FMD) is endemic in Nigeria, which has an estimated population of more than 128 million small ruminants mainly concentrated in the northern part of the country. Most small ruminants infected with FMD are asymptomatic, creating the conditions for silent viral spread and posing a threat to other domestic species, yet their role in the epidemiology of FMD is generally neglected. Studies looking at seroprevalence, spatial patterns and risk factors for exposure in small ruminants are limited. The objectives of the study were thus to (1) determine the true seroprevalence of FMD in backyard small ruminants in northern Nigeria, (2) identify factors associated with FMD virus antibody detection at animal and household level, and (3) identify spatial patterns for FMD virus exposure, with the aim to guide future animal health interventions.

Materials and methods

A cross-sectional study was conducted in northern Nigeria (Bauchi, Kaduna, and Plateau States) (Figure 1a, 1b). Data collected using a standardised questionnaire, and results from serological tests for antibodies against non-structural proteins (NSP) of FMD virus, were analysed at animal and household level. True prevalence was estimated stochastically to account for variability in the test sensitivity and specificity previously reported. The association between variables and FMD seropositivity was assessed at animal level using mixed-effects logistic regression with household as a random effect, and at household level using Poisson regression with adjusted (robust) variances and the number of animals sampled per household as offset. A choropleth map of Bayes smoothed ratios was generated to show the distribution of FMD seropositivity (Figure 1c). The Anselin Local Moran's I and the Getis-Ord Gi* statistics were used to identify significant spatial autocorrelation.

Results

The overall true seroprevalence was 10.2% (95% CI 0-19.0). FMD seropositivity was widely distributed across the study area with more than half of households presenting at least one seropositive animal (n=182; 60.7%).
At animal level, an interaction between State and species was detected, highlighting that Plateau sheep had almost four times the odds of being seropositive compared to goats (OR=3.78, 95% CI 2.08-6.87, p<0.001), while goats in Kaduna and Bauchi had higher odds compared to goats in Plateau (Kaduna: OR=2.97, 95% CI 1.89-4.67, p<0.001; Bauchi; OR=1.83 95% CI 1.13-2.97, p=0.01). At household level, State and herd size were the main risk factors identified in the multivariable model. Kaduna had higher prevalence ratios (PR) compared to Plateau (PR=1.89, 95% CI 1.40-2.55, p<0.001) and herds with >20 animals had higher PR compared to herds of up to 10 animals (PR=1.30, 95%CI 0.96-1.78, p=0.09). One hot spot was detected in Kaduna, and a cold spot was identified in Plateau (Figure 1d, 1e).

Discussion

This study confirms that FMD is endemic in northern Nigeria and exhibits spatial heterogeneity across the study area, and highlights the importance of small ruminants in the overall epidemiology of FMD. These findings provide a baseline for the development of cost-effective, risk-based interventions targeting areas at higher risk of infection, as required to progress on the control of FMD in the country.

Modelling the transmission routes for FMDV within a cattle herd

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Introduction

Outbreaks of foot-and-mouth disease (FMD) in disease-free countries can lead to millions of animals being culled and can cost billions of pounds. To control an outbreak, rapid detection and application of control measures are required to contain the spread. To do this it is essential to understand the transmission dynamics within a farm to determine the number of infected animals over time and the levels of environmental contamination.

Materials and methods

We present an individual based model of foot-and-mouth disease virus (FMDV) within a cattle herd incorporating transmission through direct contact and via environmental contamination. The model is parameterised using results from transmission experiments estimating the level of viral shedding by cattle, the transmission rates and the rates of environmental contamination and decay. Further fitting is undertaken using data from farms affected during the 2007 epidemic in the UK using approximate Bayesian computation sequential Monte Carlo (ABC-SMC). We compare the simulated number of cattle showing clinical signs per day to the age of lesions from cattle to quantify model accuracy. ABC-SMC is also used for model selection to determine the most important routes of transmission (i.e., direct, environmental or both).

Results

Results show that most infections arise through direct transmission between cattle, but the accumulation of environmental contamination can also cause infections within a herd. Furthermore, model selection indicated that a model incorporating direct transmission (with or without environmental transmission) captured the data better than a model with environmental transmission only. Although environmental contamination cannot sustain an outbreak on its own, it can continue to be a risk of infection after all animals have recovered or been removed unless the premises is properly decontaminated. The model also shows that the mean time of infection and the herd generation time are larger for environmental transmission than direct transmission, indicating that the route of between herd transmission can be inferred by the herd generation time.

Discussion

We have demonstrated how ABC-SMC can be used to estimate the importance of two possible routes of transmission of FMDV. Although environmental contamination may play a small part in within-herd transmission, it can still produce infections and is a risk for new susceptible animals or between herd transmission. This methodology also has the potential to be used for any other FAST diseases with multiple routes of transmission.

FMD control strategy in the United Arab Emirates - Spread modelling and progress towards eradication

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Introduction

Foot and Mouth Disease (FMD) is a notifiable disease to the World Animal Health Organization (OIE). FMD is one of the most contagious zoonotic diseases, with important economic losses. FMD causes a low mortality rate in adult animals but often causes a high mortality rate in young animals due to myocarditis. United Arab Emirates (UAE) intensifies the effort in line with the Progressive Control Pathway for Foot-and-Mouth Disease (PCP-FMD) developed by FAO and EuFMD and further endorsed by the OIE, guiding endemic countries through a series of incremental steps to manage FMD risks better. This study aims to assess the impact of control strategies, including early detection, movement control, surveillance, and vaccination. The benefit of this study is to inform the policy maker on required actions for making progress towards eradicating FMD from the UAE.

Material and Methods

Data on the population database of livestock holdings were obtained from the Abu Dhabi Agriculture and Food Safety Authority (ADAFSA) Animal Health Division. Data were collected on animals from 24,836 holdings and farms. The total population of the animals considered in this study was nearly 3 million. Most of the farms, 14,914 f representing 60% of the farms in the country, harbored either sheep or goats or both sheep and goats at the exact location. There were 8,410 small mixed sheep and goats farms, representing 34% of the total; a small number of dairy farms in the country are owned by private companies.

The methodology in this study applies a customized UAE ecological setting, the North America Diseases Spread Model, named NAADSM-UAE. NAADSM is a stochastic, state-transition simulation model designed to simulate the spread and control of highly contagious diseases in a population of susceptible animals. NAADSM is a spatially explicit, herd-based model that simulates disease spread and proposed control strategies.

Results

The benchmark simulation, with all control measures excluding vaccination, showed that the disease duration would be 81 days. The number of newly infected farms would maximum reach 350 farms, including 220 commercial farms of sheep and goats, or 63 % of the total infected farms. Meanwhile, a comprehensive, intensive with-vaccination campaign scenario would reduce the disease duration to 28 days. The total number of newly infected farms would stay as it is in the benchmark scenario at 350 farms. However, the number of newly infected commercial sheep and goats farms would be reduced to a maximum of 180 farms.

Discussion

Animals' disease spread modeling and simulations can be valuable tools for designing optimum disease control strategies. In the United Arab Emirates, the FMD strategy has reached Stage 2 – Figure 1. This study recommended a comprehensive campaign against FMD in the country, including early detection and diagnosis, tracing backward and forward, developing an Animals ID system to carry out an FMD surveillance program, and an intensive vaccination program. Furthermore, it is worth noting the country launched an initiative to involve research institutions and all other relevant stakeholders to increase awareness about the FMD and its socioeconomic impacts.

Assessing endemic FMD control strategies in the Republic of Türkiye using a mathematical metapopulation model

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Introduction

Foot-and-Mouth Disease (FMD) is a widespread and economically important livestock disease endemic in large regions of the world, including most of Asia and Sub-Saharan Africa. Despite this computer modelling of FMD spread generally focuses on areas free of the disease. Modelling of disease spread is useful to assess the benefits and drawbacks of potential control strategies prior to their implementation, which is of specific importance to resource-constrained endemic countries considering eradicating the disease within their borders.

Materials and methods

High quality data from the Republic of Türkiye was used to develop and populate a mathematical metapopulation model of endemic FMD. Model parameters were fitted to the observed FMD incidence data and control strategies were simulated to assess their effect on disease reduction and likelihood of eradication. The sensitivity of these control mechanisms to relevant parameters was then assessed.

Results

Our model results indicate that reactive ring vaccination and prophylactic mass vaccination were highly effective in controlling the spread of FMD in provinces where it was previously endemic. Movement bans had little effect alone or in combination with other control policies. Only prophylactic mass vaccination had the potential to completely eradicate the disease, and biannual mass vaccination in combination with reactive ring vaccination was found to be most effective at eradication.

Discussion

This work suggests that there is no substitute for regular mass vaccination in countries that wish to eradicate FMD, although ring vaccination provided a highly effective and cheaper measure to control the disease. The fact that movement bans were less effective highlights the fact that control for FMD in endemic areas is not the same as in epidemic contexts. These results may inform future policy decisions for the control of FMD in regions where it is currently endemic.

Epidemic modelling at the livestock-wildlife interface: Insights from a case study to the African swine fever pandemic in Romania

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Introduction

Transboundary animal diseases pose a continual threat to the health of livestock and the welfare of livestock producers, with foot-and-mouth disease and similar transboundary (FAST) animal diseases (including peste des petits ruminants, Rift Valley fever, and *capripoxvirus* diseases) being of exceptional concern. The role of wildlife in maintaining or propagating these diseases is an area of active research, and should epidemic incursions occur into formerly disease-free regions, achieving disease control can require measures targeting both the domestic and the wild compartments. Understanding how transmission dynamics and applied control measures in one compartment can influence dynamics in the other compartment may be key to enacting optimal strategies, and parameterized models that account for this interface could play an important role in such decisions. Using the current African swine fever pandemic as a case study, we've created a model to mechanistically explain these

transmission dynamics in an environment with suspected disease spillover.

Materials and Methods

A multihost spatiotemporal stochastic simulation model was designed and fitted to current outbreak data. Backyard domestic pig farms were represented at the village scale due to the ubiquity of backyard farming in villages, commercial farms were represented by their point coordinates retrieved from national veterinary registries, and wild boar habitat was modelled as home-range suitability using CORINE land cover satellite data. Transmission rate parameters were estimated using approximate Bayesian computation – sequential Monte Carlo (ABC-SMC) methodology. Following parameterization of our model, the relative contribution of hosts to epidemic propagation was determined.

Results

We were able to quantify the role that a reservoir species plays in explaining infection dynamics among low-biosecurity livestock herds. While herd-to-herd contacts were responsible for the majority of infections in the domestic compartment, wild-to-domestic spillover played an essential role in epidemic spread. Roughly 20% of cases among livestock came from wildlife, except in the area of initial transmission (Tulcea county) where wild boar were responsible for 80% of the infections among domestic pigs (Fig. 1).

Discussion

Unravelling transmission processes in a multi-host environment is paramount to designing integrated and efficient surveillance and intervention strategies. Here we demonstrate the ability to model disease transmission at the domestic-wildlife interface through combining livestock coordinates, publicly-available ecological data, and epidemic data to produce a fitted epidemic simulation. Model outputs allowed the quantification of relative transmission rates between wild and domestic hosts and will continue to be used to assess the effectiveness of additional control strategies during the initial phase of the epidemic.

The role of animal movements during the high risk period in the 2001 FMD epidemic in Urugay

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Introduction

The movement of livestock between farms was one of the main risk factors for infection at the farm level during the high-risk period (HRP) of the 2001 FMD epidemic in Uruguay. This corresponds to the period where the virus was present but not yet detected in the country and the movements between livestock operations facilitated contact between infected and susceptible farms.
The aim of this study is to describe and quantify the transmission network of animal movements between farms during the initial phase of the 2001 FMD epidemic in Uruguay. These results are crucial to identify targets for surveillance and control measures.

Materials and methods

A directed network was developed by using the observed data on cattle and sheep movements during the HRP of this epidemic. The network included farms that were infected during the early stage of the epidemic, as well as any farms connected to them via animal movements during that time, except for

moves involving slaughterhouses.

The in and out-degree for each node was calculated. Other measures were also computed such as the network density and the betweenness of each node. The R igraph package was used for network analysis.

Finally, an acquaintance model was fitted to the data to estimate the basic reproduction ratio (R_0) based on the probability of getting infected given the number of acquaintances (k) and the average probability that a contact leads to infection (q)

Results

The network consisted of 201 nodes (180 farms and 21 livestock markets or dealers) and 191 links among nodes (176 cattle movements, 13 sheep movements and 2 including cattle and sheep). The network was weakly interconnected with an average of 1.05 links per node and a density of 0.5%.

The distribution of out and in-degree are presented in Figure 1 (A & B). The network at the end of the HRP contained 84 infected farms (42%) and 117 negatives farms (58%) (Figure 1 D). Therefore, we assumed that the probability of infection was ▯ – = 0.42 and the estimated basic reproduction number between herds was 2.29.

Discussion

The estimated Ro was similar to estimations obtained by using other methods such as the exponential growth rate method (2.26) and a SIR model assuming a homogeneous population (2.72).

The finding revealed a high heterogeneity of contacts among livestock operations with only a few nodes having higher number of contacts than most of the other nodes in the network. The node with the highest betweenness was a livestock market that had a key role in the dissemination of FMD during the HRP. A farm had the second highest betweenness, indicating that these types of farms that frequently lies in the shortest path between other nodes in the network can also play a role in the spread of the disease.

The detection of livestock operations that are central in the flow of animals in the network and operations with high in-degree and out-degree values should be important components of contingency plans for guiding surveillance and disease control measures.

Network and risk analysis of Iran's livestock movement in 2020 and 2021

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Introduction

Network analysis is a set of integrated techniques to depict conections among factors and to analyze the structures that emerge from the recurrence of these relations. When large amounts of data related to livestock transport are available, network analysis helps users to understand the flow and direction of movement, therfore, help you to make better decisions to reduce the risks posed by livestock transportation. In addition you use these data and results for implementing better control measures and surveillance in national plans. In this survey, network analysis was performed on ruminants movement data between provinces of Iran, then, risk analysis was performed to detect provinces with high input and high output.

Materials and method

 network analysis was performed on the data of ruminants that were moved in 2020 and 2022. These

data mainly were divided into two categories [large ruminants (cow, buffalo, camel) and small ruminants (sheep, goat)] which entered or exited from thirty-one provinces of Iran. Each group was divided into two categories of input and output and each category was divided into four parts. R studio software, QGIS, SPSS, and Excel were used to perform the analysis.

Results

Large ruminants group inputs were divided into four sections based on the population of imported animals. The first part includes a quarter of Iran's provinces, whose animal imports were between 371 and 2698 heads. The second quarter includes provinces that between 2698 and 11121 heads of animals were imported. The third quarter includes provinces that between 11121 and 20277 heads of animals were imported. The fourth quarter includes provinces that between 20277 and 42878 heads of animals imported. Accordingly, Tehran (129891) and Khorasan Razavi (64486) were two provinces that had the most import of animals .Due to the high volume of the number of incoming animals, they are considered as outliers data. Regarding, export of animals in provinces, it is illustrated that Khorasan Razavi province with a number of nearly 90,000 large ruminants has the highest output, followed by the provinces of West and East Azerbaijan. For export of animals, the first quarter includes provinces that have an output of 1005 to 4521 heads of large ruminants. The second quarter includes provinces that have an output of 4521 to 7279 heads of large ruminant. The third quarter includes provinces that have an output of 7,279 to 20034 large ruminants. The fourth quarter includes provinces that have an output of 20034 to 368888 head of large ruminants. Tehran province with the number of nearly 2500,000 heads of small ruminants importation, had the highest input for small ruminants. For small ruminants movements data, the first quarter includes provinces that have the input of 6414 to 16186 heads of small ruminants. The second quarter includes provinces that have the input of 16,186 to 50,278 heads of small ruminants. The third quarter includes provinces that have the input of 50,278 to 294,188 small ruminants. Fourth-quarter contains the country's provinces that have the inputs of 294,188 to 599,218 heads of small ruminants. Note: The two provinces of Tehran and Isfahan with the number of 2485424 and 1067207 heads of animals, respectively, due to the high number of incoming animals, have been considered as provinces with higher animal output. The three provinces of Khorasan Razavi, West and East Azerbaijan with 89425, 86934, and 45267 heads of livestock, respectively, have been considered as outliers data due to a large number of outgoing livestock. West Azerbaijan province with about 1300,000 head of smal ruminatns has the highest output, followed by Khorasan Razavi and Lorestan provinces in the next positions. The first quarter includes provinces that have an output of 1782 to 6555 heads of small ruminants. The second quarter includes provinces that have an output of 6555 to 42058 heads of small ruminants. The third quarter includes provinces that have an output of 42058 to 317490 heads of small ruminants. The fourth quarter includes provinces that have an output of 317490 to 761875 heads of small ruminants. The three provinces of West Azerbaijan, Khorasan Razavi, and Lorestan with 1327901, 1191095, and 972770 heads of output livestock, respectively, have been considered outliers data due to the high volume of output livestock (fig1).

Discussion and Conclusion

According to network analysis and risk analysis, Khorasan Razavi province has the highest risk of disease incidence, followed by East Azerbaijan, Semnan, Yazd, Gilan, Golestan, Mazandaran, and Tehran, respectively, have the highest risk of disease spread (fig2). The final risk map was preaperd by assigning different weights to different risk factors (transfer network in the population of large ruminants (cattle), transfer network in the population of buffalo, transfer network in the population of small ruminants, transfer network in the population of camels, transmission network in the population of other animals, transportation network of the country and rivers of the country. Using maps obtained from the analysis of livestock transfer network, as well as maps prepared from various scientific sources such as the official website of Harvard University, etc., various risk factors with a specific weight that we consider in the risk analysis model. In this way, prioritization between high-risk and low-risk provinces and cities is determined, which will help us in making decisions to appropriate control measures in the hot spots. Finally using network analysis and risk analysis can greatly limit the spread of the disease within the country by controlling of entrances of livestock in provinces that have a high risk of spreading the disease.

Identification of the determinants of animal mobility to better anticipate the spread of infectious diseases in West Africa

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Introduction

Livestock mobility plays a pivotal role in the spread of animal and zoonotic infectious diseases. Understanding the patterns of livestock mobility is necessary to improve surveillance and control. This is particularly true in the West African region, where mobility is fundamental for livestock production and trade and mobility data are difficult to collect. The aim of this study is to describe mobility patterns in West Africa (Nicolas *et al.*, 2018) while identifying the driving socio-economic and environmental factors to better anticipate the spread of infectious diseases in West Africa.

Materials and methods

We analysed livestock (cattle and small ruminant) movement data within and between two West African countries: Senegal and Mauritania. Data were obtained through the aggregation of sanitary certificates collected by the Veterinarian system in these two countries in 2014. Information was aggregated at the department level (administrative level 2), and each department in each country was considered as a node of a directed network. The reconstructed network represented a sub-portion of a larger network involving North and West African countries (fig 1). Network analysis tools were used to provide a description of the network through the evaluation of some essential network and centrality metrics such as density, diameter, betweenness, and connectivity. We used Exponential Random Graph Models (ERGM) (Belkhiria *et al.*, 2019) to identify possible drivers for small ruminant and cattle movements separately.

Results and discussion

The resulting network is poorly connected (density 3%) and has a small diameter (9), meaning that locations geographically far apart can be reached in a few steps. The network forms a single connected component, which increases the risk of disease being able to reach any node in the network. Several international communities containing nodes of Senegal and Mauritania have been identified. In this region, Bignona, Nioro du Rip, Louga in Senegal, and Kaédi in Mauritania are the most central nodes and are on the main axis of livestock movements between Mauritania and Senegal.
Environmental factors (like Dry Matter Product (DMP), elevation), that are related to livestock production, as well as anthropogenic factors (Human density, accessibility, urbanization type (desert, rural, semi-urban, urban and hyper-dense), Gross Domestic Product (GDP) that are related to livestock trade and human activities, were used to inform ERGM models for the different species. The final ERGM model suggests that the factors influencing mobility structure are different between small ruminants and cattle. For small ruminants, the difference between the type of urbanization at origin and destination drives the creation of links between different departments in the area; In contrast, average GDP at the department level is a driver for cattle movement.
This work provides a description of mobility patterns in West Africa and identifies some of the driving factors of the mobility network for small ruminants and cattle in the region. Such analysis gives insights to guide and improve surveillance and control measures in the region.

External validation of spatial qualitative risk analysis

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Spatial Qualitative Risk Analysis (SQRA) is a collaborative method and tool developed by Cirad and partners for sharing the knowledge of a college of academic and field experts in veterinary epidemiology and animal health about the relative risks of introduction and dissemination of an animal or zoonotic infectious disease within a territory. SQRA is of particular interest when historical records about the disease in question are scarce or inexistent (exotic, or new emerging disease). It is also very useful to target high-risk areas and / or time periods, and to prioritize disease surveillance and control activities. Although the collegial procedure might help reducing subjective biases, the accuracy of the outcome is necessarily limited by the quality and amount of information available to the experts and to the analyst. Therefore, a validation step is proposed to assess the predictive performance of the SQRA maps, based on either observed disease outbreaks or planned surveillance data such as a serological survey on a representative sample of the target population. Rather than adopting a binary mindset of either accepting or rejecting an SQRA map, this analysis should be regarded as an assessment of prior knowledge embodied in the map. It provides an opportunity to identify gaps in the epidemiological knowledge to update the collective perception of disease risk in a progressive process of learning by accumulating evidence.

Digital transformations of the analog hunting grounds maps

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Introduction

The aim (focus) of this poster is to consider digital transformations of Analog Geography Hunting Grounds Maps (AGHGMs) (image 1) as well opportunities of introduce digital hunting grounds maps (DHGMs) in veterinary surveillance, monitoring, control programme for wildlife populations. Geographical Information System (GIS) as a computer based analyzing system displaying digital data with spatial sets. Spatial veterinary epidemiology (SVE) enabled the spatial/location of TADs and FAST diseases to aim identify the susceptible populations (domestic and wildlife) and epidemiological risk factors. Epidemiologic surveys calculate the disease incidence to facilitate the disease investigation and to frame preventive measures.

Materials

1) 2 (AGHGMs) - scale 1:250000 (1 for big game and 1 for small game).
2) 256 (AGHGMs) - scale 1:25000 (114 for big game and 142 for small game).

Method

(AGHGMs) converted to digital raster format, and then to digital vector format. Digital maps (DM) processing includes 5 stages:
[1] Scanning the cartographic source (used scanner, PC and software package)
[2] Preparing the raster form for digital processing. Covers a series of procedures that are essential before starting the digitalization process as:

• Clear the scanned image: improve contrast and brightness, remove shadows that were created during

the scan.
• Geocoding or georeferencing procedure: the cartographic raster image of the (HGs) is transformed into a real coordinate system, according to the applied cartographic projection.

At least 4 edge points are always selected.
[3] Digitalization process: where each Hunting grounds (HG) was drawn according to the borders and treated as closed areas (polygons). This process involves the digital recording of coordinates in a real coordinate system.
[4] Vector data attribution: (HG) that already have a spatial location are described in more detail. Attribute data: textual, numeric, tabular etc.
[5] dDta storage: in order to ensure stability, consistency and reliability and to maintain the data in a way that will provide the greatest flexibility in the handling, analysis and modeling of (HG) data.

Results

DHGMs (spatial data) GIS display as subject layers that can be displayed à one by one or together (Images 2).
These are stored in a spatial linked database. Each data could be analyzed and retrieved as and when needed (outbreaks of TADs and FAST disease, zooning- enable easy to prepare of zones (Images 3). infected -protected zone, surveillance zone, buffer zone, to determine measures for prohibition of hunting – to determine (Images 3), present distribution and density of population etc.).

Discussion

(DHGM) could upgrade the veterinary information system (VIS). All data (species of wild life populations, found dead animals for passive surveillance, all results from active surveillance) for each (HG) should be collected in special designated module in VIS. Multidisciplinary approach and collaboration with other institutions-organizations should be continued and upgrade. Prerequisite is necessary in process of introductions of DHGM in VIS with power hardware and software. In next steps of categorizations of (HG), DMs are essentials.

Conclusions

Introduction a (DHGMs) in SVE for wild life populations in consideration of TADs and FAST diseases is essentially. Veterinary epidemiologist with (DHGMs) obtains power tool for implementation measures and activities related to wild life populations.

Abbreviations: Geographical Information System-GIS, Transboundary Animal Diseases -TADs; Foot-and-mouth disease And Similar Transboundary animal diseases – FAST; Digital maps -DMs; Hunting grounds – HG; Analog Geography Hunting Grounds Maps – AGHGM; Digital Hunting Ground Maps – DHGM; Veterinary information systems -VIS; Spatial Veterinary Epidemiology- SVE; African swine fever – ASF.

Keywords: digital hunting ground maps, analog hunting ground maps, digital transformations, wild life populations, spatial veterinary epidemiology

Modelling the persistence and control of Rift Valley fever virus in the Comoros archipelago

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Introduction

Rift Valley fever (RVF) is a major emerging, zoonotic and arboviral haemorrhagic fever that greatly affects public and animal health, primarily in Africa. The ability of RVF virus to persist within distinct environments has raised questions over its potential to spread and persist within currently disease-free settings. Viral persistence requires suitable meteorological factors for vector competence and breeding alongside sufficiently susceptible local host communities. Prior to our work, no study had formally estimated the importance of these persistence mechanisms from field data, preventing any formal assessment of disease control strategies in a real-world setting.

Materials and methods

We developed and fitted a mathematical model to disease data, to estimate the importance of climate, animal movements and livestock susceptibility on viral persistence in a heterogeneous environment. Our mathematical model (i) accounted for climate, animal movements and livestock susceptibility, (ii) considered spatial heterogeneity of these factors, and (iii) was fitted in a Bayesian framework to the largest (2004–15) published RVF serological dataset from the Comoros archipelago–a network of islands, repeatedly affected by RVF, located in the South-Western Indian Ocean. We then used our model to assess the potential impacts of different control strategies to reduce disease incidence.

Results

We estimated the importance of island-specific environmental factors and inter-island animal movements on RVF virus persistence in the archipelago, suggesting that two islands–Grande Comore and Mohéli–were most suitable for RVF virus transmission. We demonstrated that the archipelago network was able to sustain viral transmission over 10 years in the absence of explicit disease introduction events after early 2007. We further found that within-island control measures (e.g., vaccination or vector controls) were more effective inter-island movement restrictions at reducing overall disease incidence.

Discussion

Our interdisciplinary approach not only advances knowledge on RVF transmission dynamics and disease control in spatially heterogeneous landscapes, but also illustrates how long-term surveillance data can be used to rigorously evaluate the effectiveness of different control measures against major emerging zoonotic infections.

Assessment of impacts of "Time to detection" of a FMD outbreak using a multi-country EuFMDiS model

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Introduction

The early detection of foot-and-mouth disease (FMD) incursion in an FMD-free country is of critical importance for timely control and eradication. The objective of this study was to assess the epidemiological and economic impacts of different 'times to detection (TTD)' of a potential FMD outbreak using a multi-country version of the EuFMDiS model.

Materials and Methods

FMD outbreaks were simulated in the susceptible livestock population (n=316,444 herds) of four Central European countries (Austria, Croatia, Hungary, and Slovenia) using the EuFMDiS model. The impacts of four TTD parameter values (Day 7, Day 14, Day 21, and Day 28) were assessed separately. In addition, three different control measures (stamping out only (SO), stamping out plus ring culling (SO_RC), and stamping out plus suppressive vaccination within a 3km radius of each infected herd (SO_SV)) were combined with each of the TTD values to understand how early or delayed detection of an incursion of FMD in the region may impact the effectiveness of these control measures. Outbreak scenarios were initiated in a dairy cattle herd and a large commercial breeding pig herd separately for each of the control strategies. Altogether 24 scenarios were simulated; each simulation comprised 500 iterations and was run with a daily time-step.

Results

The TTD had a large impact on the magnitude of the epidemic and associated costs. As the time to detection was increased from Day 7 to Day 28, the number of infected herds, epidemic duration, the number of culled animals, countries impacted, and total costs increased. The median (25th, 75th percentile) number of infected herds were 6 (3, 9), 28 (15, 37), 84 (47, 120), and 204 (141, 285) on Day 7, Day 14, Day 21, and Day 28 for SO (dairy cattle), respectively. The median (25th, 75th percentile) number of infected herds was 13 (9, 18), 35 (27, 44), 83 (63, 112), and 179 (132, 238) for Day 7, Day 14, Day 21, and Day 28 for SO_SV (breeding pig), respectively. Overall, the impacts of control measures were comparable for Day 7 and Day 14, however, SO_SV was more efficient and cost-effective on Day 21 or Day 28. For any TTDs, SO_RC did not offer additional benefits over SO. Outbreaks initiated from a breeding pig herd led to a larger and longer epidemic. The median numbers of impacted countries varied from 1 (Day 7 & Day 14) to 4 (Day 28). The median (25th, 75th percentile) total cost (in million Euro) was 41 (35, 47) (lowest) for TTD of Day 7 (SO, dairy cattle) and 461 (110, 627) (highest) for the TTD of day 28 (SO_SV, breeding pig).

Discussion

This study confirms that the time to detection is a major determinant of the magnitude of an outbreak and related economic losses. Targeted surveillance and real-time training on FMD outbreak investigations for veterinarians could be crucial in the early detection and reporting of FMD. The study also confirms previous simulation studies that emergency vaccination is unlikely to offer any benefits in smaller, rapidly detected outbreaks but might be useful as a control measure in larger outbreaks.

A scoping review of FMD risk, based on spatial and spatio-temporal analysis of outbreaks in endemic settings

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Introduction

Foot-and-mouth disease (FMD) is one of the most important transboundary animal diseases affecting livestock and wildlife species worldwide. Spatial and spatio-temporal analysis using outbreak data have been increasingly used to study the burden of the FMD in endemic settings with the purpose of identifying high-risk areas or factors facilitating viral introduction and transmission. However, an in-depth analysis that consolidates their results has not been conducted. The objective of this scoping review was to systematically retrieve spatial and spatial-temporal studies that use FMD outbreak data as a source of information, summarize key aspects of their methodological approach and identify the epidemiological factors associated with FMD risk in endemic contexts.

Materials and methods

Electronic searches were conducted in Embase, CAB Abstracts, Medline and Google Scholar. Studies eligible for inclusion reported FMD outbreak patterns or modelled FMD risk in livestock species using geographically or/and temporally linked data collected in endemic countries. The analytical focus of the study was identified (e.g., description, pattern recognition, statistical modelling) and information on the methods used and their results were extracted. Epidemiological factors used for the purpose of risk analysis or prediction were identified and classified.

Results

Forty-seven studies were included. A high proportion of papers described and visualized the outbreaks (70.2%) and several approaches to study spatio-temporal aggregation of outbreaks (48.9%) were reported. Evidence of spatial autocorrelation and identification of outbreak clusters was frequent. Modelling approaches were often guided by variations in the spatial and temporal granularity of available data and presumed causal pathways affecting FMD risk at the local level. While the format and type of epidemiological factors used for modelling FMD risk varied across studies, it was possible to broadly classify them into 5 themes representing risk pathways relevant for FMDv introduction and spread (Figure 1). The epidemiological factors assessed in the models fell more frequently under the categories of animal demographics and livestock-wildlife interactions (n = 10 studies), trade (n = 10), accessibility (n = 9) and, environment (n = 8) and less frequently, socioeconomics (n=2).

Discussion

Common aspects were identified when analysing the epidemiological factors linked to the risk of FMD outbreaks in endemic settings. The consistency observed across studies highlights different pathways in which the virus is sustained in endemic areas, with the potential to exploit them to design tailored evidence based-control strategies for the local needs. There was limited data linking the socioeconomics of communities and modelled FMD risk, leaving a gap in the current knowledge. Despite its limitations, we highlight the value of using spatial epidemiology tools on outbreak data to enhance the understanding of FMD and map its risk in data-scarce endemic environments. A thorough analysis of the risk of FMD outbreaks requires a systemic view as multiple epidemiological factors can contribute to better understand viral circulation and may improve the accuracy of disease mapping. Future studies should explore the links between epidemiological factors (e.g., socio-economic, environmental aspects) and FMD outbreak risk as a foundation to improve the outcomes of FMD control initiatives implemented at a larger scale in endemic contexts.

Session VI. Surveillance and control

How are information and communication technologies improving data collection and reporting and guiding informed and timely decisions on surveillance and control?.

How systems and knowledge developed for surveillance of COVID-19 can be used and adapted for FAST diseases?.

What are novel approaches in evaluating surveillance systems and overall surveillance system sensitivity?

How can combined surveillance and control for different FAST diseases increase resource efficiency in countries?.

What is the future of molecular techniques like whole genome sequencing and metagenomics in FMD and similar TADs surveillance?.

How can in-field technologies and Artificial Intelligence be used for improving surveillance and data collection?.

How do socioeconomic approaches and public-private partnerships contribute to improved FAST surveillance and control?.

Aim

To share innovative experiences, ideas and approaches for the development, implementation, monitoring and evaluation of FAST surveillance and control programmes.

Session VI. Oral presentations

Lessons learned from SARS-Cov-2 surveillance and control and implications for FMD/FAST surveillance and risk reduction

K. Sumption

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Sustainable market-driven early disease detection approaches

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Introduction

Effective early detection surveillance requires that every incursion of an exotic disease, or emergence of a novel disease is detected early enough to be affordably and rapidly controlled and eradicated. To achieve this, the entire animal population must be under constant surveillance, and significant or unusual disease events promptly and effectively investigated. Even in high-income, but especially in low- and middle-income countries, government animal health services alone are not able to meet these stringent demands. Private sector participation in disease surveillance is required, but currently levels of active participation and collaboration with government surveillance efforts vary greatly between production sectors.

This presentation is based on some of the work of the 5-year USAID-funded TRANSFORM project being undertaken in Vietnam and Indonesia, which aims to develop sustainable market-driven risk mitigation approaches for transboundary animal diseases, including through improved early detection capacity.

Materials and methods

The approach adopted is based on identifying alignment of interests (disease mitigation, commercial and other interests) between stakeholders, and the use of data to transfer value between stakeholder groups to overcome surveillance weaknesses and support sustainability. Some core tenets include: the target of early detection surveillance is to identify every disease event (considered to be of importance to the animal owners), everywhere, immediately; animal owners are generating this information constantly – the challenge is to capture it for analysis; the effective collection, management, analysis and reporting of surveillance data is expensive and sustainable operation requires a reliable funding stream; and improved access to industry-wide information on disease risks and early warning can generate benefit and increase income to certain commercial stakeholder groups.

A needs and capabilities study of poultry production stakeholders was conducted in Vietnam and Indonesia to determine how disease and related information could be captured and used to improve production. The results were used to develop a prototype cross-sector market-drive information system for disease risk management.

Results

The prototype system, FlockWorks, is being implemented in the Vietnamese and Indonesian poultry industries, targeting all production sectors from vertically integrated high-biosecurity companies to low biosecurity independent farms and smallholder non-commercial poultry production. An example business model for the transfer of value, made possible by this system, is the mix of village-level surveillance and commercial benefit to vertically integrated farms. Improved access to surveillance data on the threats present in local village production systems can allow appropriate timely preventive measures to be taken (e.g., adjusting vaccination and biosecurity), resulting in fewer losses, higher efficiency, and greater profitability. Investment in this data provides funds to improve surveillance in the non-commercial sector, by, for example, subsidising laboratory testing which would otherwise be uneconomical.

Discussion

The TRANSFORM project is researching novel approaches to sustainability in disease risk mitigation by moving away from international donor and government-funded time-limited projects and developing market-driven alternatives where the interests of improved production and disease risk management align. Powerful information technology, effective business models and strong data governance are pre-requisites for successful implementation of such approaches.

Longitudinal animal and environmental sampling for FMDV in Northern Nigeria

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Introduction

Environmental sampling, in particular taking swabs of any surfaces likely to have been contaminated by infected animals, presents an opportunity for non-invasive sample collection, enabling cost-effective FMD surveillance beyond regular investigation of clinical cases. Linking the results of environmental sampling with those of other surveillance methods (e.g. oral swabs or serum samples) allows a comparison of the methods and shows how the results of different sampling methods are correlated.

Materials and methods

Animal and environmental samples were collected once a month for seven months (March-July 2021 and September-October 2021) in two areas of Plateau State in northern Nigeria (Bassa and Jos South) at one livestock market, one transhumance location and five households in each area. At each visit, blood samples and oral swabs were taken from up to 15 cattle, sheep and goats, along with up to 10 environmental swabs in each location. All samples were tested for the presence of FMDV RNA using a pan-serotype real-time RT-PCR. Nine positive samples were selected for sequencing using a probe enrichment technique.

Results

For environmental samples collected between March and July 0.5% (2/372) were positive for FMDV RNA. One sample was taken at a household in Bassa and the other from a transhumance site in Jos South. Over the same period 1.4% (8/567) of serum samples were positive, all taken at different locations and times in both areas. None of the 331 oral swabs collected was positive. Furthermore, no outbreaks were reported during the sampling period. By contrast, 18.6% (16/86) of environmental samples collected in September and October were positive for FMDV RNA. Positive samples were collected from four households and a livestock market in Jos South. The proportion of positive environmental samples for a site ranged from 33% (1/3) to 100% (5/5). In addition, 1.5% (2/132) of serum samples and 8.8% (12/136) of oral swabs were positive. The proportion of positive oral swabs from a site ranged from 8.3% (1/12) to 50% (2/4). Outbreaks were reported during the sampling period. The sequencing results will be presented, but were not available at the time of writing.

Discussion

FMDV RNA can be detected sporadically in animal and environmental samples at times when no outbreaks are reported. However, higher numbers of positive samples in environmental and oral swabs are obtained at times when outbreaks are reported. This suggests that environmental sampling could give a representative picture of levels of infection or disease at a location. More frequent sampling would be needed though to determine if environmental sampling could be used as a means of early detection of an affected location (i.e. prior to clinical onset).

The PCP-FMD progress in Georgia and how it advances FAST control

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Available upon request

Is FMDV serotype C extinct: What can the data tell us?

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Introduction

Seven serotypes of foot-and-mouth disease virus (FMDV) (O, A, C, SAT (1, 2, 3), and Asia 1) occur across seven regional virus pools. In each pool, the specific serotypes that circulate in the susceptible populations varies. Since 2004 there has been a noticeable absence of serotype C from recorded outbreak data. This serotype historically occurred across European countries, however the most recent cases (2004) occurred in pool 4 (Eastern Africa) and pool 7 (South America). Detailed reports from these outbreaks suggest the outbreak in pool 4 resulted from vaccine escape, while in pool 7 the outbreak resulted from natural infection in an isolated cattle population. Following these outbreaks, response measures were taken to address the vaccine quality and coverage in isolated populations. Now, with continued lack of serotype C detection, we are evaluating whether the available data and knowledge about FMD epidemiology can substantiate a claim of serotype C extinction.

Material and methods

Using surveillance data from the FAO World Reference Laboratory (1942-2021) at Pirbright and the WOAH/FAO FMD Reference Laboratories Network (2012-2020) for regional pools 1-6, we have built a framework to analyze the data grouped by pool at three levels of data summary, (a) by year and country, (b) combined over years for each country, and (c) combined over years and countries within a pool. Using these datasets, the surveillance effort was analyzed by estimating the probability of detection at specified prevalence thresholds (0.01, 0.02, 0.05) and calculating the detection capability at a 95% detection probability standard. These measures provide meaningful quantitative comparisons of sampling efforts for each country through time. Additionally, we provide distributions of the posterior density function of prevalence for circulating serotypes to assess the epidemiological beliefs about the detection capability of FMD surveillance and the expectation for serotype C. Population data from the FAO Hand-in-Hand database for each country was used to evaluate the distribution of livestock, adding contextual details about surveillance efforts relative to connectivity, outbreak occurrence, and reporting.

Results

This analysis framework supports claims of freedom from FMD serotype C at different scales with varying degrees of certainty by combining data with explicit epidemiological assumptions. For example, at the finest scale of surveillance data available, only one country in pool 2 is likely to detect <1% prevalence of serotype C for 5 of the 9 years. When data is combined temporally, while only one country has a surveillance detection capacity of <1%, all reporting countries have a 95% probability of detection at a 5% prevalence threshold.

Discussion

Assumptions, such as negligible risk for serotype C reintroduction over time and homogeneous mixing in regional pools, provide the basis for combining data temporally and spatially and using it to assess whether there is sufficient evidence to support claims of serotype C extinction. Through expert solicitation, we will clarify appropriate assumptions for each pool, which will improve the analysis framework, results, and help identify gaps in the data or FMD epidemiology needed to increase confidence that serotype C is extinct. Furthermore, additional data from Members in virus stores and last reported outbreaks are critical in the ultimate assessment of serotype C extinction and reemergence.

Investigating gaps for novel animal health surveillance data within Scotland

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Introduction

Sensors have become ubiquitous in our current world and the livestock farming sector offers multiple research avenues for the application of sensor technology, from early disease detection to virtual fencing. Animal health surveillance in Scotland currently relies on post-mortem examinations of animals and on data derived from laboratory submitted samples. Sensor-derived syndromic surveillance of livestock has been identified as a gap in Scotland's current animal health surveillance capabilities. Real-time data from on-farm herds has the potential to underpin improved production and endemic disease detection and the earlier identification and investigation of potential outbreaks. Using the data journeys approach, the aim of this project is to elucidate the conceptual journey of thermal imagery and drone-derived data from farm to policy. This approach aims to situate data across interconnected sites of practice, highlighting the movement of data in and between sites and exposing areas of potential 'data friction'. The term 'data friction' is used to describe the complex factors (political, ethical, legal, social and economic) that come together to slow down and restrict data generation, movement and use.

Materials and methods

To investigate potential barriers to taking sensor-derived data from the farm and utilizing this data to develop actionable animal health policy at the state level, a preliminary 'data journeys' exercise was undertaken to map stakeholders and sites of practice through which data is collected, transformed, stored, managed and used. From this map, stakeholders were identified and engaged to participate in qualitative interviews to gauge concerns and attitudes towards precision and smart farming uptake, data sharing, data protection regulations, perceptions of data sharing and of algorithms in animal health decision making.

Results

Qualitative interviews were undertaken with stakeholders from commercial, academic, policy, legal, farming and animal health technology sectors to gather information concerning five main areas: (i) background and general understanding of sensor-derived data and precision livestock farming; (ii) position on data use and access; (iii) position on data usage; (vi) data storage and privacy implications; and (v) other considerations. A thematic analysis was carried out to build a hypothesis/picture around what data is currently in use and where sensor-derived data could fit in the scheme of veterinary surveillance data in Scotland and further afield. The project identifies a realistic pathway for novel data within the Scottish and UK animal health surveillance landscape, ensuring its utility for multiple stakeholders.

Discussion

Previous research has explored potential future scenarios with regards to trade policy, data collection and sharing, and resourcing for surveillance in order to better prepare a resilient surveillance model for Scotland post-Brexit. As we have now entered the post-Brexit era, it is of the utmost importance to not only research new technologies in the agricultural sector, but to ensure that these technologies are developed with future use and application in mind from the outset, fostering resilience at both the farm level and the surveillance level.

The potential use of drones in surveillance of FAST diseases

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Introduction

Following an important outbreak of Lumpy Skin Disease in Israel, a question raised concerning the possible use of drones for the disease surveillance. The idea of using drones to assist in finding affected herds in the field and surveil affected herds seemed logical and useful. A pilot study has been done to evaluate the pros and cons to this thought.

Material and Methods

The Veterinary Services owns a drone classified as multi rotor under 4 kg - DJI Inspire 2.
During the outbreak of Lumpy Skin Disease, the team reached the field and applied the use of the drone in order to find symptomatic animals in known affected herds and to watch the possibility of finding new infected free ranging herds in the field.

Results

The use of drones seemed to be useful, mostly in remote or hidden herds in open fields that can be difficult to reach. A large scale of advantages have been revealed, such as the possibility to scan large areas in a short time, which leads to a reduction of working time searching animals in the field. Obstacles as water ponds or difficult terrain or dense and high vegetation were overcome easily. The advantage of the drone has been emphasized especially when searching animals in dangerous areas such as mine fields, frequent in the north of the country. The use of drone can also bypass other safety issues to the staff such as hot/cold weather, rain, snow, dust and air pollution, animal's aggressions, snakes, arthropods etc.

High quality photos and videos taken during the activity presented the easiness of counting animals in the field, a tool that can assist in censuses that have to be conducted during surveillance, assuring that no animals "escaped" the quarantine. Use of drone has been found useful also in herds with reduced owner's cooperation.

No disturbance stress and fear was observed among animals while the drone approached them. Symptomatic animals could be easily found within the herd and the zoom of the camera could approach the lesions (Figure 1) such as it was possible to identify the age of the lesions and even the species of insects on the animal. Identification of animals was easily effectuated by reading the ear tag or tattoos.

Discussion

Many advantages have been noticed in the use of drones in animal diseases identification and surveillance. Additional advantage that was elaborated is the biological safety that drones can provide in infectious diseases such as FMD, PPR etc. In these cases, the entrance of additional persons into the herd is avoided, minimizing the danger of spreading the disease. Some disadvantages as the need of license and permits, short time battery etc, have also been dealt.

OpenFMD: A data sharing and analytical portal to enhance genomic and epidemiological surveillance of FMD

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Introduction

Analytical dashboards and visualization tools support pathogen surveillance and stimulate the real-time exchange of data between laboratories and animal health officers involved in disease control initiatives. The speed, nature and extent of foot-and-mouth (FMD) data sharing is inconsistent and global surveillance is further limited by opportunistic sampling of cases and the paucity of epidemiological information from several regions. Therefore, both genomic and epidemiological data need to be made more publicly available and disseminated openly in order to enhance knowledge of FMD virus (FMDV) lineages circulating globally. During the last few years, substantial efforts have been made by the OIE/FAO Reference Laboratory Network for FMD towards the harmonisation of data collection, to promote data sharing and easily accessible epidemiological analysis. We present an open-access web resource developed to explore and retrieve FMD genomic and epidemiological data, interactively query and visualise historical and recent FMD trends at both country level and across each FMD endemic pool, and to further generate customised epidemiological and genotyping reports.

Material and Methods

openFMD is an online portal that consists of several analytical modules coded in R Shiny and complemented by HTML, CSS and JavaScript. Each module provides unique and easy to use functionalities for analysis of FMD surveillance, genomics and vaccination data, stored in centralised databases created using MySQL. *FMDbase* provides a unique repository of FMDV sequence data, currently hosting 17,146 FMDV sequences and their associated metadata, of which 2,062 are complete or near-complete genome. The full system is hosted and maintained by the FAO World Reference Laboratory for FMD (WRLFMD) at The Pirbright Institute, UK.

Results

Modules currently available in *openFMD* are: i) *FMDbase* dashboard where users can search, filter and retrieve FMDV sequences; ii) *FMDtype* an interactive dashboard that provides users the ability to query their own FMDV sequence data against *FMDbase* and generate customised FMDV genotyping reports; iii) PRAGMATIST an evidence-based decision support tool for FMD vaccine strain selection. A further module that will allow users to search and visualise epidemiological and surveillance data on historical and recent FMD trends is currently under development and will be made available to external users in the future.

Discussion

We expect that the *openFMD* initiative will not only promote the vital role of the OIE/FAO Reference Laboratory Network for FMD as leading the global surveillance of FMD, but it will further improve timely analysis and communication of FMD data, identification of surveillance gaps and emerging disease trends in order to support evidence-based decision-making processes for FMD control. The ultimate goal is to help and assist regional GF-TADs roadmaps, governments and public health officials in planning and prioritising support activities, thus contributing to reduce the risk of FMD introduction in disease-free areas.

Digitalization of FMD datasets using visualization tool on SEACFMD portal

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Introduction

Dataset visualization has now become the most popular and user-friendly tool for enabling audiences to capture data easily in a visual context. There are varied tools available for data intelligence and analytics which use an interactive environment to explore datasets. Digitalization of animal disease outbreak data using interactive visualization tools allows end-users to gain insights into vast amounts of data by clear display of disease patterns, including spatial and temporal trends, and provides direction for interventions needed to enhance disease prevention and control. This paper focuses on the interactive presentation of FMD datasets collected from SEACFMD Members and visualized using Microsoft Power Business Intelligence (BI). FMD outbreak data were mined from various available resources, then analyzed by location, the species affected, FMDV subtypes detected during 2019-2021, and visualized using figures such as graphs and maps in an interactive tool.

Material and methods

An FMD dataset covering 2019–2021 was compiled in a Microsoft Excel worksheet. The dataset was based on information submitted by The South East Asia, China and Mongolia Foot and Mouth Disease (SEACFMD) members, via the ASEAN Animal Health information system (ARAHIS), the World Animal Health Information system (WAHIS) of the World Organization for Animal Health (WOAH, founded as OIE), reports from WOAH World Reference Laboratory for FMD in Pirbright (UK), the FMD Diagnostic Laboratory in Pakchong (Thailand), and country reports presented at the SEACFMD Governance meetings.
The dataset structure was designed on the basis of the ARAHIS report, screened for missing or outlier data, and followed up with member countries for validation. Power BI Desktop Version was used to process the data with selected maps, graphs, and other visualization. The maps were generated from Mapbox with the WOAH access token and basemap links. The final SEACFMD dashboard was published as a report to the Power BI web service after checking for errors and with an embedded link for sharing purposes.

Results

The FMD situation dashboard created in Power BI will be shared with Member countries. The dashboard contains FMD outbreak information illustrated by spatial and temporal distribution, FMD cumulative heatmaps, FMDV subtypes circulating in the region, FMD-affected species, and PCP stages of the member countries.

Discussion

The visualization allows users to observe any spatial or temporal trends of FMD and circulating FMD virus strains which will enhance early warning and response. This interactive, user-friendly visualisation tool allows users to filter information by country, reporting year, month, location, animal type affected, FMDV topotype etc. The FMD situation dashboard presented in the Power BI can be extended annually for long-term data storage, and it is customizable depending on users' feedback and needs. Such dynamic data visualization and analysis tools have become an important end-user friendly asset in every business organization, and their further development is recommended.

Identifying and addressing the barriers to effective FMD vaccination in Nakuru county Kenya

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Introduction

Foot-and-mouth disease (FMD) is endemic in Kenya, with frequent outbreaks. Understanding socioeconomic drivers affecting disease control within Kenya's livestock systems, and the cost-effectiveness of control options, are important components of designing an FMD control programme. This study aimed to integrate quantitative economic analysis with qualitative data to provide recommendations for disease control.

Materials and methods

A cross-sectional questionnaire survey of 159 small-scale dairy households was conducted in Nakuru County Kenya, in areas known to have experienced FMD outbreaks in the previous 12 months. Data on husbandry systems, production losses and expenditure associated with FMD were collected. Household profiles were identified using data reduction techniques. In addition, 69 key informant interviews were conducted over a 24-month period exploring their experience of FMD and its control in Kenya, interactions with other stakeholders, and the FMD control system's strengths and weaknesses. Quantitative and qualitative data were used in an FMD vaccine chain analysis and partial budget analysis for effective disease control through a hypothetical "ideal" vaccination campaign, assuming a perfectly-effective vaccine and vaccination every six months.

Results

Three household profiles were identified. Households in profile one had 3-8 cattle, utilizing zero or private grazing; only 14% earn over half their household income from livestock enterprises. Households in profile two had 3-9 cattle, and were commercially-focused often utilizing semi-zero or private grazing. Households in profile three had 25-87 cattle in low-input semi-extensive grazing systems. The costs and revenue forgone associated with an outbreak of FMD in small-scale farms were very variable, with an interquartile range of $28 to $208 across profiles. Many expenditures were only experienced by a low proportion of farms. Using partial budget analysis, the median benefit of vaccination was calculated as $93/cow/year (IQR $27–$242) for profile one, $68/cow/year (IQR $28–$148) for profile two and $38/cow/year ($10–$113) for profile three.

An unclear process for FMD control was found with different animal health providers reporting different processes for prescription and sale of FMD vaccine, and government-imposed restrictions experienced in different ways by stakeholders. County-level demand for vaccination is not coordinated on a national basis, and it can fluctuate as outbreaks occur, applying unpredictable production pressure on vaccine production and impacting disease coordination between neighboring counties.

Privatization of animal healthcare has resulted in an increase in animal healthcare providers, with different veterinary professional (veterinarians, paravets) often not easily distinguished from each other by farmers. Government services are therefore seen as a trusted source of disease control compared to private providers and remain responsible for the majority of vaccinations. However, this can mean that vaccination is delayed when government campaigns are under-resourced, resulting in low vaccination coverage.

Discussion

These results demonstrate that although vaccination may provide economic benefits to small-scale dairy farmers by reducing costs associated with FMD, additional barriers exist. These include uncertainty in costs associated with an FMD outbreak, challenges in disease control coordination and unclear relationships between farmers and animal healthcare services. Cross-cutting policy and behavioral changes designed in tandem to address these challenges are required.

Session VI. Poster presentations

First isolation, molecular detection and phylogenetic analysis of FMDV A/AFRICA/G1 in the Sultanate of Oman

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Introduction

Foot-and-mouth disease (FMD) is a transboundary and contagious viral animal disease. It is endemic in several parts of the world. FMD is considered the most economically important and significant endemic viral disease of livestock. Given the genetic diversity of FMD virus (FMDV) and the lack of cross-protection among various viral strains, identification and characterisation of circulating FMDV strain is crucial for effective disease control. So far, the strains of FMDV responsible for outbreaks in Sultanate of Oman remain poorly characterized. In this study, we report for the first time the isolation and molecular characterization of FMDV serotype A topotype G-I circulating in the country between 2018 and 2021.

Materials and Methods

Following FMD outbreaks and notifications by the veterinary authority, a total of 13 oral epithelial tissues samples were collected from cattle from Dhofar, Ad Dhakhyilia, Ash Sharqiyah North and Al Batinah North governorates. The viral RNA was extracted from the samples and screened by real-time reverse-transcription polymerase chain reaction (rtRT-PCR). FMDV was isolated on IB-RS-2 cells and the serotype of the virus isolates was identified by using an antigen capture ELISA. Molecular characterization of the virus isolates was conducted by conventional RT-PCR amplification of VP1 coding region, sequencing and phylogenetic analyses.

Results
The FMDV RNA was detected from the 13 samples and isolated after first or second passages on cells. All isolates were found positive for the serotype A by antigen ELISA. Phylogenetic analysis of VP1 sequence revealed one group of A isolates belonging to the AFRICA topotype, G-I genotype. The isolates were genetically related to viruses circulating in Kenya in 2017 by 93.4% to 99.1% and in Bahrain in 2021 by 93.5% to 99.5%.

Discussion

This study provides information about the epidemiological situation of FMDV serotype A in Oman and the implication of transboundary transmission of FMD from East Africa. Improved monitoring and

surveillance are essential for implementing effective control measures.

Potential public-private partnerships applied to control FMD and Similar Transboundary animal diseases in Sudan

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Introduction

Public-private partnerships (PPPs) in the veterinary domain are "a joint approach in which the public and private sectors agree on responsibilities and share resources and risks to achieve common objectives" (OIE, 2019a). FAO and WOAH's Global Framework for the Progressive Control of Transboundary Animal Diseases (GF-TADs) promote such partnerships to rationalize national veterinary responsibilities and enhance the development and sustainability of the animal health sectors. The European Commission for the Control of Foot-and-Mouth Disease (EuFMD) provides technical and organizational assistance to neighboring countries by promoting new or enhancing existing public-private partnerships (PPP) to control foot-and-mouth disease (FMD) and other transboundary animal diseases (referred to as FAST diseases). In 2019 and 2020, the EuFMD delivered a virtual-learning course to European neighborhood Veterinary Services to develop and implement FMD control strategies within the PCP-FMD. This course taught participants how to analyze opportunities for PPPs related to FAST diseases control, develop and evaluate a business case, and share experiences to develop an enabling environment for PPPs in FAST control.
As a follow-up to the aforementioned course, the EuFMD has identified several countries in the European neighborhood where assistance can be provided to promote Public-private partnerships (PPPs) in the veterinary domain, including Sudan.

Materials and methods

Under the current letter of intent between the EuFMD and the Arab Organization for Agricultural Development (AOAD), a consultation virtual meeting was held with the key persons from the public and private sectors in Sudan to identify the potential partners from both parties, followed by six hybrid workshops held by the EuFMD, hosted and facilitated by AOAD, in which the areas of applying potential PPPs in Sudan were identified and discussed in depth with the relevant participants.

Results and discussion

Five main areas of developing PPPs were identified as PPPs applied to pastoralist systems: vaccine security; export of live animals and animal products; camel and horse health and export issues; risk analysis and surveillance for HPAI in the poultry sector. It was decided to focus on the first three areas. Subsequently, a plan of action to form a PPP working group comprised of public and private sector representatives to collaborate on the development of a pilot project is agreed upon. The pilot project will focus on the application of public-private partnerships to the export of live animals and animal products from Sudan, with an emphasis on strengthening FAST disease surveillance in Kordofan, which is one of the most important supplier states of livestock animals for export in Sudan, and improving the capacity of quarantine stations along the same line of export from Kurdfan to importer countries.

The first detection of a serotype O FMDV in Namibia

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Introduction

This report describes the molecular characterization of a serotype O foot-and-mouth disease virus (FMDV) recovered from a field outbreak in the Zambezi region, Namibia during July 2021. New genetically related FMDV sequences for samples collected in Zambia since 2018 are also included in this analysis to help understand the epidemiological connectivity in the region. These cases represent new threats with a potential for onward spread of this lineage to neigh- bouring countries where serotype O is not present.

Materials and methods

New FMD viral sequence data for samples collected from Namibia (2021) and Zambia (2018–21) are reported here. FMD cases in Namibia were detected in Zambezi Region of Namibia during June–July 2021. The diagnosis of FMDV was carried out as previously described (Teye et al., 2019). An in-house sandwich ELISA using serotype-specific rabbit and guinea pig antisera for FMDV serotypes O, A, SAT 1, SAT 2 and SAT 3 (Pirbright Institute, UK; Ferris & Dawson, 1988) was used to detect FMDV anti- gens and to define the serotype of the CPE positive samples. FMDV sequences encoding VP1 were generated for serotype O positive samples using a published RT-PCR amplification and sequencing method (Knowles et al., 2016).

Results

Sequence analysis demonstrates that this FMDV belongs to the O/EA-2 topotype sharing closest nucleotide identity (99.5%) to FMD viruses collected since 2018 in Zambia.

Discussion

This is the first detection of serotype O in Namibia, and together with the cases that have been recently detected in southern Zambia, represent the first time that this serotype has been detected in the Southern African FMD endemic pool since 2000, when a virus of Asian origin (O/ME-SA/PanAsia) caused an outbreak in South Africa. This incursion poses a new threat for the region and the potential onward spread of O/EA-2 will now need to be closely monitored since serotype O vaccines are not widely used in Namibia, nor in neighbouring countries.

Serological survey for the detection of FMD in livestock, Lebanon, winter 2020-2021

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Abstract

Background: Since the last detected FMD outbreak in Lebanon in 2010, no additional outbreaks have been notified. During winter of 2020-2021, a sero-survey was conducted with the primary objective to

detect the presence of antibodies against Non-Structural Proteins (NSP) of FMD virus as evidence of virus circulation in absence of notification of clinical cases.

Methods

Six different geographical areas were identified, with three of them considered to be at higher risk of FMD incursions. Within each area an average of 20 villages (10-30 villages) were expected to be randomly selected and from each village a total of 16-20 serum samples collected from large and small ruminants equally distributed in three age-groups: from 0 to 12, from 13 to 24 and > than 24 months of age. Based on the observed increasing proportion of NSP positives among the three age-groups considered, age specific monthly incidence rates (force of infection) in each age-group were estimated.

Results

A total of 510 serum samples were collected from Large Ruminants (LR) and 1,425 from Small Ruminants (SR). The unweighted overall seroprevalence of NSP positives was 19% and 18% in LR and SR respectively ranging from 5% in Nabatieh Governorate to 51% in Beqaa Governorate. Age-specific seroprevalence for age group ≤12, 13-24 and >24 months was 6.9%, 11.4%, and 35.1% for LR and 8.7%, 22.8% and 25.3% for SR, respectively. The estimated force of infection for each of the ≤12, 13-24 and >24 months old age-groups, was 7.8, 5.2 and 8.9 cases in LR and 8.6, 20.5 and 1.0 cases in SR (for every 1,000 animals at risk for one month).

Conclusions

This study indicates that FMD virus may be endemically present in Lebanon despite absence of clinical disease notifications since 2010. The results obtained will lead to design and implement various activities among which a top priority is to increase awareness among livestock keepers in order to strengthen passive surveillance and facilitate reports of suspected cases.

Keywords: Foot-and-mouth disease, Ruminants, cross sectional study, Seroprevalence, Lebanon

Environmental sampling as a surveillance tool for TADs in endemic settings

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Introduction

Many viruses are shed into the environment via the secretions and excretions of infected animals, providing the opportunity for non-invasive, low-cost sample collection methods which can be implemented to supplement diagnostic and surveillance efforts. Here we explored the use of environmental sampling as a means of detecting FAST diseases (foot-and-mouth disease and similar transboundary animal diseases) in endemic settings. Specifically, we considered detection of peste des petits ruminants virus (PPRV) in Nepal, and PPRV, sheeppox virus (SPPV), goatpox virus (GTPV) and lumpy skin disease virus (LSDV) in Nigeria.

Materials and methods

In Nepal electrostatic dust cloths were used to collect swabs from the environment (e.g. food troughs, hard floor surfaces and ropes in pens) at a live goat market in Kathmandu, Nepal. Four visits were made to the goat market between November 2016 and April 2018. Samples were collected, stored in lysis buffer and transported to The Pirbright Institute, where they were tested for the presence of PPRV RNA by rRT-PCR.
In Nigeria environmental swabs were collected (using the same sampling methods as in Nepal) from livestock markets, households and transhumance sites. Swabs were collected monthly between March and October 2021 from four local government areas (Bassa, Jos South, Wase and Kanke) in Plateau State, Nigeria. Samples were collected, stored in lysis buffer and transported to The Pirbright Institute for analysis. In this case, samples were tested for the presence of PPRV, LSDV, SPPV and GTPV using real-time PCR.

Results

A total of 217 samples were collected at the live goat market in Kathmandu, Nepal, of which 132 (60.8%) were positive for PPRV RNA. Viral RNA was detected in samples collected during all four visits to the market and in almost all (17/18) pens sampled. The proportion of positive samples per pen ranged from 13.3% to 100%.
In Nigeria a total of 458 environmental samples were collected. From these PPRV RNA was detected in 2.4% (11/458) of samples, with 9 of the positive samples being collected at livestock markets in Bassa and Jos South. Six samples were positive for capripox virus (CaPV) DNA, four of which were collected at the livestock markets. A CaPV differentiation assay showed that two samples were positive for each of CaPV (LSDV, SPPV and GTPV). Furthermore, the two samples positive for SPPV DNA were also positive for PPRV RNA, both collected at the livestock market in Bassa in May.

Discussion

Previously, we have demonstrated that environmental sampling is a useful tool for the surveillance of foot-and-mouth disease. Here we have shown that it also has the potential to be useful for other FAST diseases, specifically PPRV, SPPV, GPPV and LSDV. To develop the use of environmental sampling, future work should optimise methods of detection and sample types for each of the viruses and relate detection in the environment to the presence of infection or disease in animals.

Phylogenetic analysis of FMDV circulating in Bangladesh, 2021

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Introduction

FMD is highly endemic in Bangladesh, where serotype O is most prevalent among four reported FMDV serotypes (O, A, Asia1, and C). A review of different research articles showed that serotype O accounts for about 31%–85% of the outbreaks followed by types A (7%–47%) and Asia-1 (5%) at different times and in different regions of Bangladesh. The purpose of this study is to identify the genotype of the foot-and-mouth disease virus circulating in Bangladesh in 2021.

Materials and methods

A total of 30 clinical samples were collected from cattle in the FMD outbreak regions (9 provinces) in

Bangladesh. Viruses were isolated using LFBKavb6 cells, RNA was extracted from the isolated virus, and the VP1 region was amplified for sequencing. Following sequencing, the VP1 coding sequences were aligned using BioEdit 7.2.5. Phylogenetic trees were constructed using MEGAX software with the maximum likelihood method based on the generalized time-reversible model and bootstrap values were calculated on 1000 replicates.

Results

Sequencing and phylogenetic analysis of the VP1 sequences of the isolated viruses showed that they were classified into the O/ME-SA/Ind-2001e. The O/ME-SA/Ind-2001e viruses were divided into two clusters, and the nucleotide homology between the two clusters was 95.2-95.5%.

Discussion

We confirmed in a previous study that O/ME-SA/Ind-2001e and A/AISA/G-VII are circulating in Bangladesh in 2020. In 2021, only O/ME-SA/Ind-2001e was identified, and these viruses were divided into two groups. Group 1 included viruses recently isolated from Pakistan and India as well as Bangladesh, and group 2 included only viruses that occurred in Bangladesh in 2020-2021. The two groups of viruses are circulating and evolving in Bangladesh, respectively, and it is considered that it is necessary to prepare for antigenic mutations according to virus evolution through continuous monitoring in the future.

FMDV surveillance at markets and abattoirs in Cameroon using environmental sampling

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Introduction

Active monitoring and understanding the epidemiology of foot-and-mouth disease virus (FMDV) form the foundations of control programmes in endemic areas. In many endemic areas, however, veterinary resources are limited, resulting in a requirement for simple sampling techniques to increase and supplement surveillance efforts. In this project, environmental sampling was used at livestock markets and abattoirs across Cameroon to assess the opportunities for broad scale disease surveillance at such sites.

Materials and methods

Environmental sampling methods for the detection of FMDV were used at cattle markets and abattoirs from six locations across Cameroon. A total of 1994 samples were collected, stored in lysis buffer and transported to The Pirbright Institute (UK). The samples were tested for the presence of FMDV RNA using a panserotype FMDV specific rRT-PCR assay. A subset of samples (n=24) positive for FMDV were further analysed using a probe enrichment-based sequencing method.

Results

A total of 173 (out of 1994) samples were positive for FMDV RNA, with the majority of positive samples deriving from two sampling locations (Douala, n=86/332 and Bertoua, n=79/332). Sequence data was generated from the VP1-encoding region of the FMDV genome, enabling characterisation of serotypes present in the samples. Sequence data demonstrated that viruses from the lineages O/EA3, A/G-IV and SAT2/VII were present in the samples, with two samples containing sequences from multiple lineages. Phylogenetic analysis demonstrated that sequences fit within clades of viruses known to be circulating

in the region.

Discussion

Environmental sampling provides a simple, non-invasive method for the detection of FMDV that avoids handling of individual livestock, a process that requires considerable time and specialist knowledge. Sampling at markets and abattoirs that are hubs for livestock movements presents an opportunity for broad scale surveillance of livestock diseases, not only FMD but other transboundary diseases that are the subject of control and eradication programmes, such as peste des petits ruminants (PPR). The data presented here show that with advances in sequencing protocols, such as the incorporation of probe-based library enrichment steps, viruses found in environmental samples can be characterised at a finer level to provide valuable epidemiological data for surveillance and eradication programmes. Environmental samples often contain low levels of poor quality genetic material, therefore the success of the probe enrichment approach is a valuable development in generating sequence data.

A modelling assessment of the value of environmental surveillance for FMDV in a cattle herd

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Introduction

Due to the fast-spreading nature of foot-and-mouth disease (FMD), early detection is essential to be able to control an outbreak in a disease-free country. In past outbreaks, detection has primarily relied on the identification and reporting of animals showing clinical signs. However, recently developed non-invasive, low-cost environmental sampling methods have been shown to successfully detect foot-and-mouth disease virus (FMDV) under field conditions. This could remove some of the workload of veterinarians during an outbreak and has the potential to speed up detection of suspected cases. In addition, environmental sampling could potentially be used to monitor at-risk herds as an alternative to pre-emptive culling.

Materials and methods

Using mathematical modelling, we assess the potential for environmental sampling as a surveillance strategy. We utilise a within-herd model of FMDV with transmission occurring via direct contact and through environmental contamination. The accumulation of virus in the environment is explicitly modelled so that the probability of detecting FMDV through sampling can be calculated. Different surveillance strategies are then introduced to the model to determine the speed of detection and the reduction in infectiousness if control measures are subsequently applied.

Results

Environmental sampling can reduce the time from infection to detection compared with previous epidemics provided enough samples are taken at sufficiently frequently. This is shown in Figure 1, with sampling strategies that improve on 2001 being represented below the red dotted line. We also estimate the confidence of detecting an infected premises from sampling which can be used to prove freedom from infection. The number and frequency of samples required for a high degree of confidence depends on the likely time of infection (i.e., when contact with an infected premises occurred). For example, daily sampling of at least five samples per day will take between 4 and 7 days to gain 99% confidence that a herd is free from infection.

Discussion

Our modelling shows that environmental sampling can be a useful tool for detection of FMDV-infected herds in the event of an outbreak in an FMD-free county. With a sufficient sampling strategy, detection times can be reduced to less than those from previous epidemics. It is also a low-cost and easy to use sampling method that can reduce the demand on trained vets and reduce the need for pre-emptive culling of at-risk farms.

Serological surveillance of FMD immunity level in Republic of Korea, 2021

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Introduction

Since 2018, the Republic of Korea (ROK) has been vaccinating all susceptible livestock with one out of three approved vaccines which serotype O and A antigens according to the prime and boost vaccination schedule. We were carrying out continuously monitoring the vaccination status and immunity level through serological surveillance and if the standard antibody positive rate is below, a heavy fine will be imposed. In this regard, in this study, serological surveillance was performed using serum collected in 2021, and the collected data were analyzed immunity level.

Materials and Methods

Serum samples were collected from cattle, pig, and goat farms by local veterinary laboratories in ROK in 2021. In case of cattle and goat farms, 5 animals from a farm were randomly selected and for pig farms, 16 animals from a farm were subjected to sampling. In the case of cattle, they were classified according to herd size and age, and collected with at least 2 samples from cattle aged 6-12 months. These serum samples were test by the 46 regional veterinary laboratories in cities and provinces using three commercial type SP-O antibody ELISAs: PrioCHECK™ FMDV Type O Ab strip kit (Thermo Fisher Scientific), VDPro FMDV Type O Ab b-ELISA (Median Diagnostics, ROK), and BIONOTE FMD Type O Ab ELISA (BIONOTE Inc., ROK). The ELISA tests were performed according to the manufacturer's recommendation. And seropositive rate were analyzed according to breed, herd size, age, and region.

Results

A total of 625,280 serum samples collected from 59,663 farms: 206,406 cattle from 36,331 farms, 408,718 pig from 21,954 farm, and 10,156 goats from 1,378 farms. Cattle (98.2%) were the highest seropositive rate followed by pigs (93.5%) and goats (89.8%). In the case of cattle, the antibody positive rate was higher in dairy cattle than beef cattle, and by herd size, small and large-scale farms were similar at 98.0% and 98.1%, respectively. According to age was lower in 6 to 12 months (96.0%) than other ages (98.7%). The distribution of seropositive rate by region was the lowest in Chungcheongnam (96.9%) and followed by Jeju (97.0%), Gyeongsangbuk (97.2%), Gyeongsangnam (97.6%). In the case of pigs, breeding pigs (97.1%) were higher seropositive rate than fattening pigs (91.3%). The distribution of seropositive rate by region was the lowest in Gyeongsangbuk (88.3%) and followed by Gyeongsangnam (89.9%), Jeollanam (90.1%), Jeju (90.4%), Gangwon (91.3%).

Discussion

National serological surveillance results showed that targeted all livestock seropositive rate was consistently higher than 80% including less than 12 month group, breed and pigs. In the case of pigs, considering that the immune response to FMD vaccine is weak and easily weakened, the high seropositive rate confirmed in this study is significant. Therefore, these results suggest that the vaccination program currently used in pigs, which adopted priming at 8 weeks old and boosting in a

month, is effective. In conclusion, vaccination is being carried out well and although the vaccination program is slightly different depending on the vaccine manufacturer, the vaccination program currently applied in ROK is considered to be effective for herd immunity of all livestock.

West Nile virus signals detected by Padi-web Google news reports to improve disease risk mapping in Europe

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Introduction
In this study, we used the Platform for Automated extraction of Disease Information from the web (PADI-Web) as an epidemic intelligence tool to detect West Nile virus (WNV) outbreak signals, and epidemiological information throughout Europe from 2006 to 2021 in online news reports. The purpose of this study is to characterise epidemiological information on an outbreak event (such as: location and date of the event, diseased host, implicated vector and covariate risk factors) found in media reports. This descriptive analysis will allow us to explore the role of media reports and how they can help map disease occurence and predictions in complement with traditional indicator based surveillance.

Materials and methods

Google news media articles were automatically collected through PADI-web, which uses structured data services, i.e., Really Simple Syndication feeds to screen the web. Collected relevant media articles were then manually verified to select only the articles that mentioned WNV outbreaks occurring in Europe from 2006 to 2021.
Epidemiological outbreak information was also automatically extracted from PADI-web and then manually verified. A curated dataset was then produced and was used to visualize outbreak regions per NUTS level 3 subdivisions throughout Europe, our dataset was also compared to official WNV outbreak reports to calculate PADI-web's sensitivity and positive predictive value (PPV).

Results

706 media articles were automatically classed as relevant for WNV outbreaks by PADI-web. These articles were then manually screened by title and abstract to verify that the outbreak occurred in the correct study zone and timeline. After screening, 242 media news articles were included in our study. Locations for each outbreak event from included articles were also automatically collected by PADI-web and were then manually screened to extract all Human WNV outbreaks in Europe from 2006 to 2021. A total of 708 outbreak locations were included in our study.
The included WNV outbreak locations dataset was visualized though QGIS version 3.24 and was compared to official WNV reports from the ECDC (Figure 1). PADI-web's sensitivity was analyzed and was equals to 50.2% compared to 86.8% for official reports.

Discussion

PADI-web detected 50.2% of WNV official cases per NUTS level 3 subdivisions. Although PADI- web did not detect all official WNV reports, it did however provide useful insight on WNV outbreak regions in 29 NUTS level 3 subdivisions that were not available through official reports. 19 NUTS level 3 subdivisions detected by PADI-web were identified false positives after manual verification, giving PADI-web a PPV of 90.5%. Collection of climate covariates and WNV vector information were also collected and can be used to improve WNV risk mapping as well as help text mining projects to improve automatic bio surveillance systems. PADI-web offers open access epidemiological information. In complement with official outbreak data, PADI-web can be used as a helpful tool for disease risk mapping.

Understanding the role of small ruminants in the spread and endemicity of FMD

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Introduction

Globally, small ruminants represent the largest population of FMD susceptible domestic livestock. However, their role in the epidemiology of FMD is generally neglected and often poorly understood, partly due to the often inapparent nature of clinical disease in these species. Nigeria is affected with continuous FMD outbreaks and has one of the largest small ruminant populations in Africa. The aim of this study was to get a better understanding of the role of small ruminants in the spread and endemicity of FMD.

Material and Methods

A longitudinal study was conducted between March and October 2021. Five households, one livestock market and one transhumance site were visited in two local-government-areas in Plateau State, Nigeria, previously identified as high risk for FMD (active surveillance component). Serum samples were collected from 9 animals (3 sheep, 3 goats and 3 cattle) and oral swabs were collected from a subset of animals at each premise. Serum samples and oral swabs were tested for the presence of FMDV RNA by rRT-PCR.
During the same months, outbreaks reported in the study and surrounding areas were investigated and tissue samples collected from animals with clinical signs (passive surveillance component). Serum samples were tested for FMDV non-structural proteins (NSP), oral swabs for FMDV RNA, and serotype was identified from tissue samples collected.

Results

As part of the active surveillance, serum samples were collected from 273 cattle, 101 sheep and 432 goats; oral swabs were also collected from 455 animals (all small ruminants). Ten animals (1.2%; 5 cattle, 4 sheep and 1 goat) tested positive in serum throughout the sampling period, suggesting a recent infection. Eight animals came from households and 2 from transhumance sites. Twelve animals (2.5%; 10 sheep and 2 goats) had positive oral swabs. There was no correlation between serum and oral swab results (p=0.12). Three cattle had FMD-like signs during routine visits, one each in March, September and October. Only one of the three cattle was positive by rRT-PCR in serum. Small ruminants from the same household did not show clinical signs, but two female sheep were positive in oral swabs and one was also positive in serum.
Outbreaks in five households were reported through passive surveillance, all of which had cattle with clinical signs (median attack rate 20%). Serum samples were collected from 40 animals (2 cattle, 36 sheep and 2 goats) across the households, and oral swabs from 6 sheep. Both cattle had lesions in their mouths, were identified as NSP positive and the tissue samples were characterised as serotype O. Twenty-six (72%) sheep were NSP positive and 5 out of 6 had oral swabs positive by rRT-PCR. Five sheep (all from the same household) presented lameness as a clinical sign, of which three were NSP positive and four were oral swab positive.

Discussion

Results suggest that small ruminants play an important role in the epidemiology of FMD in endemic settings. Testing oral swabs by rRT-PCR might be an effective tool for FMDV surveillance in small ruminants.

EuFMD's programme, tools and initiatives

FAST
Foot-and-mputh And
Similar Transbouday
animal diseases

Dt
eufmd digital
transformation

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vlearning
eufmd virtual learning
centre

microLearning
eufmd virtual learning

vlc EA
virtual learning centre
for East Africa

Tom
eufmd training
management system

SimExOn
simulation exercises
online

KnowBank
eufmd knowledge bank

GetPrepared
emergency preparedness toolbox

RiskComms
risk communications

SQRA
a method for spatial qualitative
risk analysis applied to fmd.

Pragmatist
prioritization of antigen management
with international surveillance tool

EuFMDiS
european foot-and-mouth disease
spread model

RMT-FAST
risk monitoring tool for foot-and-mouth
and similar transboundary animal diseases

Vademos
fmd vaccine demand
estimation model

GVS
global vaccine
security

PQv
vaccine
prequalification

PCP
progressive control
pathway

PSO
pcp practicioner
officers

VPP
veterinary
paraprofessionals

PPP
public private
partnership

Sustainable development goals, UN-SDGs. EuFMD's programme has a focus on

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EuFMD Committees

Executive Committee, Standing Technical Committee (STC), Special Committee for Surveillance and Applied Research (SCSAR), Special Committee on Biorisk Management (SCBRM), Tripartite Groups.

Hold-FAST tools

AESOP. Assured emergency supply options; EuFMDiS, FMD spread model; GET PREPARED toolbox. Emergency preparedness; GVS. Global Vaccine Security; Online Simulation Exercises; Outbreak Investigation application; Pragmatist. Prioritization of antigen management with international surveillance management tool; PCP-FMD. Progressive Control Pathway for foot-and-mouth disease; PCP-Support Officers; SAT. PCP Self-Assessment Tool; RTT. Real Time Training; SMS Disease reporting; SQRA toolkit. A method for spatial qualitative risk analysis applied to FMD; Telegram; TOM. EuFMD training management system; Global Monthly reports; VADEMOS. Vaccine Demand Estimation Model; VLC. Virtual Learning Center. Microlearning.

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Food and Agriculture Organization of the United Nations
Rome, Italy

United Nations Sustainable Development Goals (UN-SDGs)

EuFMD's programme has a main focus on

1 NO POVERTY	2 ZERO HUNGER	4 QUALITY EDUCATION
5 GENDER EQUALITY	9 INDUSTRY, INNOVATION AND INFRASTRUCTURE	12 RESPONSIBLE CONSUMPTION AND PRODUCTION
17 PARTNERSHIPS FOR THE GOALS		

Thinking of the environmental footprint

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