

Epidemic simulation of a foot and mouth disease outbreak in Minnesota

S.B. Gale ⁽¹⁾, G.Y. Miller ^{(1, 2, 3)*}, C.E. Eshelman ⁽¹⁾ & S.J. Wells ⁽¹⁾

(1) Center for Animal Health and Food Safety, and Department of Veterinary Population Medicine, College of Veterinary Medicine, 1354 Eckles Ave., University of Minnesota, St. Paul, MN 55108, United States of America

(2) Department of Pathobiology, Division of Preventive Medicine and Epidemiology, College of Veterinary Medicine, 2001 S. Lincoln Ave, University of Illinois, Urbana, IL 61802, United States of America

(3) Department of Agricultural and Consumer Economics, College of Agriculture, Consumer and Environmental Sciences, 1301 W. Gregory Ave. University of Illinois, Urbana, IL 61802, United States of America

*Corresponding author: gymiller@illinois.edu

Summary

Foot and mouth disease (FMD) is a primary transboundary livestock disease of international concern. Outbreaks of the disease have recently occurred in several countries that were previously FMD-free. For countries with limited direct experience of this disease, modelling is a useful tool for the study of a potential outbreak. The objectives of this study were to determine specific FMD risk parameters for Minnesota and the United States (USA) and to use these parameters to create a baseline FMD outbreak model for Minnesota. Of specific interest was to assess whether the type of herd in which the outbreak began (a dairy herd or a large-scale swine herd) influenced the basic model outcomes of outbreak size and duration, and to examine the effects of depopulation and movement controls. The mean values for disease duration, outbreak duration and number of farms and animals infected were larger in the scenario with a dairy index herd. The results of these two outbreak models demonstrated the entire spectrum of FMD outbreak types; that is, from limited, focal outbreaks to widespread, uncontrolled outbreaks. The findings from this study provide details of a baseline model that emergency preparedness planners can use to evaluate response strategies for a potential incursion of FMD into the USA. These findings are also of value for all countries as veterinary authorities develop or adjust their FMD emergency response plans.

Keywords

Epidemiology – Foot and mouth disease – Minnesota – Modelling – Outbreak – Simulation.

Introduction

Foot and mouth disease (FMD) is a primary transboundary livestock disease of international concern, with a major impact on international trade and local economies. An FMD outbreak presents the greatest economic threat to developed FMD-free nations with large-scale livestock production agriculture, such as the United States (USA) (1). In the global market of today, 'FMD remains the single most important constraint to trade in live animals and animal products' (2).

The FMD virus is a non-enveloped, single-stranded RNA virus and the only virus in the genus *Aphthovirus*, which belongs to the *Picornaviridae* family. The virus has seven distinct serotypes: A, C, O and Asia 1, together with the

South African territories (SAT) serotypes SAT 1, SAT 2 and SAT 3. Importantly, natural exposure to or vaccination with one serotype generally does not induce cross-protection to the other serotypes. Many animal species are susceptible to FMD, including cattle, sheep, goats, pigs, bison and deer. Clinical signs include: drooling; fever; vesicles and erosions of the oral and nasal mucosa, coronary band, inter-digital area and teats; lameness; sloughing of claws; reluctance to move; anorexia; mastitis; decreased milk production; and abortion or weak newborns (3). The disease is highly contagious and can be spread by contact with infected animals, virus-contaminated objects, people or aerosol. The incubation period ranges from 2 to 14 days depending on the species, dose of virus and route of infection. Recent outbreaks have shown that FMD can readily spread from farm to farm through regular movement of animals, personnel and vehicles (4).

The disease is currently endemic in many regions and outbreaks have recently occurred in several countries that were previously FMD-free. Over the past 16 years, acute outbreaks have occurred in countries previously recognised by the World Organisation for Animal Health (OIE) as FMD-free: Chinese Taipei, the United Kingdom, the Netherlands, Uruguay, Argentina, Japan and South Korea (5, 6, 7, 8, 9). The substantial economic losses associated with these epidemics were due to the cost of control measures, loss of revenue in the trade of animals and animal products, and the negative impact on related industries (10).

North American countries are currently FMD-free and have been so for decades. The disease was last reported in North America in 1929 (USA), 1952 (Canada) and 1954 (Mexico). Nevertheless, FMD can be introduced in a number of ways, as other FMD-free countries have learned in recent outbreaks. The probability of introduction of the disease through importation of live animals has been estimated as less than one introduction into the USA in approximately 240 years (11). Additional routes of introduction include infected product, virus carried on the contaminated clothing or footwear of exposed international travellers returning to the USA, and any number of other means (3). Although the probabilities of introduction from these various sources are not generally known, the risk of an FMD outbreak in the USA is real. Understanding the important elements influencing the spread of the disease, should it be introduced, is critical to subsequent choices for managing the outbreak. In addition, modelling the outbreak to understand the probable size and speed of spread is critically important for emergency preparedness.

Thus, the objectives of this study were to determine specific FMD risk parameters for Minnesota (MN) and the USA and to use these parameters to create a baseline FMD outbreak model for MN. Of specific interest was to assess whether the type of herd in which the outbreak began (a dairy herd or a large-scale swine herd) influenced the basic model outcomes of outbreak size and duration, and to examine the effects of depopulation and movement controls. The study provides information on a detailed baseline model that emergency preparedness planners can use to evaluate response strategies for a potential incursion of FMD into the USA. Output data analysed included the mean number of infected herds and animals, mean duration of active FMD disease and mean duration of the outbreak.

Materials and methods

Description of the model

The North American Animal Disease Spread Model (NAADSM), version 3.2.18, was used to simulate an FMD outbreak in MN (the NAADSM User's Guide is accessible

at www.naadsm.org). The NAADSM is a stochastic, spatial, state-transition simulation model for the spread of highly contagious diseases of animals. It was developed with broad international support to assist in policy development and decision-making in disease incursions (12).

In the model, investigator input parameters determine disease progression and can be categorised as model population, disease state, and disease transmission and control measures. Wherever possible, parameter values were obtained from the scientific literature. However, literature review identified very few specifically stated model parameter values that could be used. Parameters that were not documented in the literature were developed using the Delphi method in consultation with subject-matter experts (SMEs) (13, 14). Meetings were held with MN SMEs in July and August 2011 to discuss and determine these parameters, which are described in more detail below.

Model population

The population framework on which the model was run requires precise farm locations, designation of production type and numbers of animals at each farm. The MN Board of Animal Health provided data on farm locations and type of livestock at each location. Individual identifying data such as the name and address of the farmer were not included in the location data set. Categories of production type were designated as 'beef', 'dairy', 'small ruminant' (goats and sheep), 'large swine' and 'small swine'. Review of data from the National Agricultural Statistics Services (NASS) MN survey 2007, together with SME opinion, demonstrated that most dairy, beef and small ruminant operations were of similar size in terms of numbers of animals per premises (Table I); no stratification on the basis of size was deemed necessary in these production types. However, for swine operations there was a distinct division based on size and production practices, such that stratification into two separate production types was deemed necessary: 'large swine' for operations with 1,000 animals or more, and 'small swine' for operations with fewer than 1,000 animals. The number of animals per herd was not consistently available. Population data from NASS were used to provide estimated proxies of numbers of animals on each farm, and the total animal numbers per county for each production type were randomly distributed to the appropriate farm locations within each county.

Disease state-transition parameters

There are four disease state-transition designations in the model: susceptible, latent, infectious and recovered/destroyed. Unless otherwise stated, values for disease state-transition by production type were based on data from the technical document, 'Vaccination against foot and mouth disease: resource requirements for initiation of a vaccination campaign', produced by the Animal and Plant Health

Inspection Service (APHIS) of the United States Department of Agriculture (USDA) in 2011 (15).

To provide a starting point for the model iterations, a single herd was designated as latently infected on day 0 and referred to as the index herd. However, this first herd infected may not be the first herd detected in the model; this differs from the common epidemiological use of 'index herd' as being the first herd detected and from which contact tracing begins.

Two different types of index herd were selected for this study: dairy and large-scale swine production. Choosing more than one species as an index herd allowed examination of particular species-specific parameters for disease spread, particularly early on in an FMD outbreak when initial spread may be more likely within a production type. This was done for three reasons. First, the species differences in susceptibility and transmission of FMD are important factors in the model. Second, the concentration of dairy versus large-scale swine operations differs spatially within MN. Large-scale swine operations are mainly clustered along the southern border with Iowa, whereas dairy operations are mainly concentrated in central and south-eastern MN (Figs 1 & 2). Thus, the swine index herd was located near the area of high density of such herds, and the

dairy index herd was located near the central area of high dairy-herd density. Third, consultation with SMEs suggested that existing differences in biosecurity and management practices in these production types could affect the spread of FMD. The two production types were run separately; that is, the outbreak began in either a dairy or a large swine herd.

Disease transmission parameters

Contact between farms that may result in disease transmission was modelled with regard to three possibilities: direct contact, indirect contact and local contact. Direct contact occurs when an animal from farm A is moved to farm B; indirect contact occurs when people and/or equipment move from farm A to farm B; local contact includes airborne contact and other unexplained contact between farms. The components of an effective contact include rates of contact, probability of infection given the contact rates, and the probable distance from infected farm to contacted farm.

Contact rates describe how often each type of contact may occur between production types. For example, a direct contact rate (Table II) of 1.0 between a dairy operation and a beef operation means at least one calf or cow moves from each dairy operation to a beef operation each day. Values greater than one represent more than one such animal

Table I
Population profile of Minnesota livestock

Production type	No. of farms	No. of animals	Average herd size
Beef	21,899	1,300,000	60
Dairy	6,667	1,100,000	165
Small ruminants (goats, sheep)	6,445	180,000	28
Swine (small-scale production)	7,059	996,000	141
Swine (large-scale production)	4,580	7,652,000	1,211
Totals	46,650	11,228,000	321

Table II
Direct contact rates: numbers of live animal movements per day

From farm	To farm				
	Beef	Dairy	Small ruminants	Swine (small) ^(a)	Swine (large) ^(b)
Beef	0.03	0.0	0.0	0.0	0.0
Dairy	0.07	0.0025	0.0025	0.0	0.0
Small ruminants	0.0	0.0	0.005	0.0025	0.0
Swine (small) ^(a)	0.03	0.0	0.0	0.03	0.0
Swine (large) ^(b)	0.0	0.0	0.0	0.003	0.05

a) small-scale production

b) large-scale production

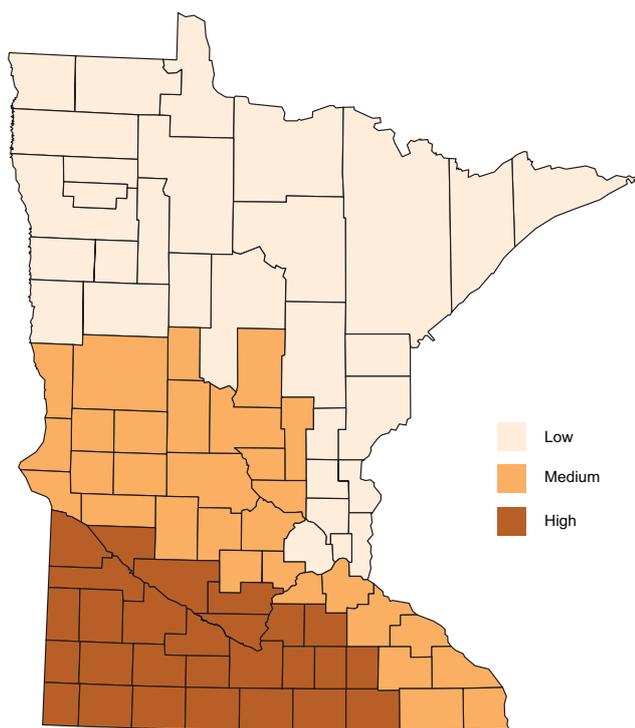


Fig. 1
Density of swine farms in Minnesota

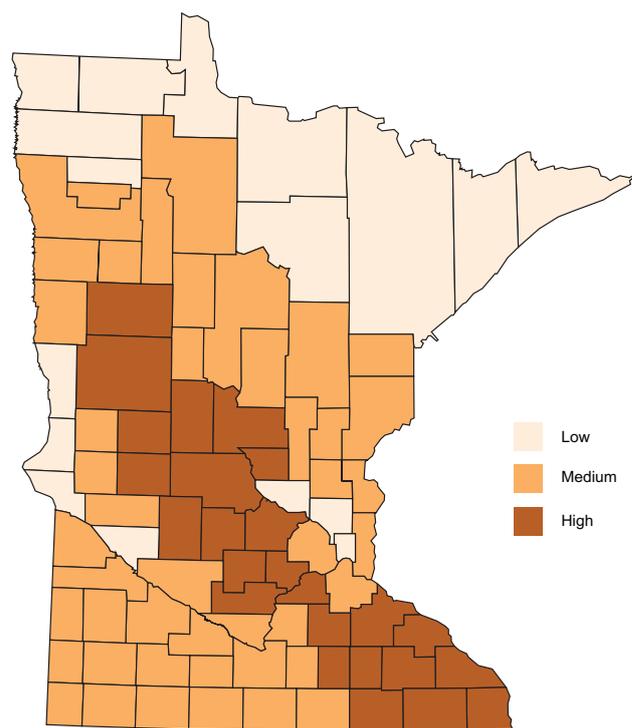


Fig. 2
Density of dairy farms in Minnesota

movement per day and values less than one represent less frequent contact. Thus, 0.5 (1/2) equals one contact every other day, 0.14 (1/7) equals one contact per week, and so on. The same applies to indirect contact rates (Table III).

Each direct and indirect contact has an associated probability density function (pdf) for distance from the source farm and a value for probability of infection transmission. The pdf for direct contact distance from the source farm to other farms was BetaPERT with a minimum, mode and maximum of 1.6 km, 32.2 km and 80 km, respectively. The exception was direct contact from dairy to dairy, where the respective values were 1.6 km, 65 km and 125 km. The probability of infection transmission from direct contact was 0.99 for all production types. The pdf for indirect contact distance from the source farm was BetaPERT with a minimum, mode and maximum of 1.6 km, 32.2 km and 80 km respectively. The exception was indirect contact from dairy to dairy, where the respective values were 1.6 km, 8.0 km and 32.2 km. The probability of infection transmission through indirect contact (Table IV) varied according to the production types of source and recipient.

The parameter for local contact was set as a 1-km ring around each infected farm. The local contact rate was 0.08 and this decreased linearly as distance from the farm increased.

Control measure parameters

Once a herd becomes infected, the model progresses the herd through four disease state-transitions: susceptible, latent, infectious and recovered/destroyed. Detection of an infected herd depends on whether the product of the probability of observation of clinical signs and the probability of reporting those signs is greater than a number between zero and one randomly chosen by the model (15). Detection of an infected herd also causes control measures to be implemented within the model.

Control measures applied to this model included movement restrictions and depopulation of detected herds. On the basis of SME input, movement restrictions were assumed to be 95% effective for cattle and small ruminants for both direct and indirect contact rates; for swine, movement restrictions were assumed to be 75% effective for direct contact rates and 50% effective for indirect contact rates. These values for effectiveness of movement restriction indicate how much the contact rate was diminished after the first infected herd was detected. For example, in the model for indirect rates for dairy cattle, a contact rate of 1.0 would become 0.05 once movement restrictions were implemented. Movement controls were assumed to be in effect within 24 h of the first herd detected.

Table III
Indirect contact rates: movement of people and equipment between farms per day

From farm	To farm				
	Beef	Dairy	Small ruminants	Swine (small) ^(a)	Swine (large) ^(b)
Beef	0.17	0.028	0.0025	0.02	0.0025
Dairy	0.88	2.99	0.033	0.33	0.0025
Small ruminants	0.005	0.005	0.01	0.005	0.0
Swine (small) ^(a)	0.12	0.12	0.0	0.37	0.001
Swine (large) ^(b)	0.12	0.05	0.0	0.08	0.08

a) small-scale production

b) large-scale production

Table IV
Probability of infection from indirect contact

From farm	To farm				
	Beef	Dairy	Small ruminants	Swine (small) ^(a)	Swine (large) ^(b)
Beef	0.1263	0.2795	0.4286	0.5937	0.5937
Dairy	0.1263	0.2795	0.4286	0.5937	0.5937
Small ruminants	0.1263	0.2795	0.2143	0.5937	0.5937
Swine (small) ^(a)	0.1083	0.2396	0.4286	0.3299	0.3299
Swine (large) ^(b)	0.1083	0.2396	0.4286	0.3299	0.3299

a) small-scale production

b) large-scale production

The depopulation rate of detected infected herds was set at 20 herds per day, in accordance with the advice of the MN emergency response SMEs. However, depopulation did not begin until 48 h after the first infected herd was detected, to allow time to dispatch the response teams. In order to evaluate the effect of limited depopulation, pre-emptive depopulation of contiguous farms or farms traced through contact with infected farms was not included in this model; incident management SMEs were consulted to estimate these parameters.

Model scenario output

One thousand iterations were run for each dairy index herd and large swine index herd scenario. The model automatically records many basic measures reflecting the extent of the simulated outbreaks. The output variables collected for this study were as follows: number of farms infected, number of animals infected, length of disease duration (days) and length of outbreak duration (days). Disease duration

refers to the active spread of FMD; when there were no longer any infectious herds (no herd in latent, subclinical or clinical disease phase), disease spread was considered ended. Outbreak duration refers to the completion of all disease control measures; depending on outbreak size, depopulation may continue after active spread of disease has ceased. A fixed end point was set at 1,095 days (three years) to enable the running of 1,000 iterations of each type of index herd within a reasonable amount of time.

Statistical differences between means were evaluated using SAS (9.2). Multivariate analysis of variance was used to assess mean differences between the testing scenarios, using observations associated with both testing groups. With the index herds as the main explanatory variable, data associated with outbreak duration, number of farms infected, number of animals infected and disease duration were used as the outcome variables. A *p* value of 0.05 was considered to be statistically significant.

Results

The details of direct contact parameters from live animal movements (Table II), indirect contact parameters (Table III) and probability of infection given indirect contacts (Table IV) are important and influence the outcomes from the model. These parameters reflect the views of SMEs and emergency responders in MN in relation to movements of animals, people and equipment, and so on, that influence the transmission risk of FMD.

Differences between the large swine index herd scenarios and the dairy index herd scenarios were found in the outcomes evaluated (Table V). Thus, the mean values for disease duration, outbreak duration and number of farms and animals infected were larger in the dairy index herd scenario, where mean disease duration was 54 days, mean outbreak duration was 56 days, mean number of farms infected was 282 and mean number of animals infected was 62,000. For the swine index herd scenario, mean disease duration was 27 days, mean outbreak duration was 27 days, mean number of farms infected was 29 days and the mean number of animals infected was 8,000 (Table V). These mean differences were statistically significant ($p < 0.0001$). The largest outbreak modelled that began in a swine index herd resulted in 3% of animals (2% of herds) infected, whereas the largest outbreak that began in a dairy index herd resulted in 75% of animals (60% of herds) infected.

A longer and larger MN outbreak should be anticipated if the index herd is at a dairy farm. Results might also suggest that a longer and larger outbreak should be anticipated if the outbreak begins in an area with a high density of dairy herds, in comparison with an area of high-density swine herds (Figs 1 & 2).

The USDA FMD Response Plans (16) describe six types of outbreak which are categorised according to the number of affected premises. The categories range from focal (smallest) to catastrophic (largest). Comparison of the distribution of outbreak sizes between a dairy index herd and a swine index

herd (Table VI) demonstrates the full range of outbreak types as described by USDA (16):

- Type 1: focal outbreak
- Type 2: moderate regional outbreak
- Type 3: large regional outbreak
- Type 4: widespread FMD outbreak
- Type 5: catastrophic USA outbreak
- Type 6: catastrophic North American outbreak.

In this study, for example, 50.2% of swine index herd iterations infected ≤ 5 herds, whereas only 1% of dairy index herd iterations were as limited in size (Table VI). Conversely, approximately 50% of dairy index herd iterations resulted in > 100 farms infected, but this magnitude of outbreak was reached by only about 7% of swine index herd iterations.

In addition, in dairy index herd scenarios there was a large gap between the largest five modelled outbreaks (basically uncontrolled outbreaks) and the sixth largest outbreak. These uncontrolled outbreaks were characterised by disease and outbreak duration of more than 600 days, with tens of thousands of farms and more than eight million animals infected. Outcomes associated with the sixth (at the 99.5th percentile) and fifth largest dairy index herd iterations were, respectively, 270 and 639 days for disease/outbreak duration, 1,378 and 27,447 farms infected, and 204,421 and 8,290,000 animals infected. Outbreaks of this size and duration would be categorised as widespread and catastrophic (Table VI). Uncontrolled outbreaks did not occur in the swine index herd scenarios.

Discussion

Types of index herd

The model used dairy herds and large swine herds as the designated latently infected index herds because they

Table V
Results of Minnesota foot and mouth disease simulation model

Scenario start	Disease duration (days)	Outbreak duration (days)	No. of farms infected	No. of animals infected
Swine (large)*, means	27 ^(a)	27 ^(a)	29 ^(a)	8,000 ^(a)
Range	6–276	6–276	1–854	859–390,873
Dairy, means	54 ^(b)	56 ^(b)	282 ^(b)	62,000 ^(b)
Range	9–887	9–1,095	2–27,760	138–8,472,730

*large-scale production; numbers with lettered superscripts are statistically different ($p \leq 0.05$)

Table VI
Distribution of outbreak size: percentage of iterations resulting in each outbreak type

Cumulative percentages of iterations

Outbreak types are those defined in the Foreign Animal Disease Preparedness and Response Strategy on the basis of the number of farms infected (16)

Outbreak type	Percentage of iterations	
	Dairy index scenarios	Swine (large)* index scenarios
Focal ≤ 5 farms	1.0	50.2
Moderate regional ≤ 25 farms	10.5	80.8
Large regional ≤ 100 farms	50.1	92.9
Widespread ≤ 250 farms	84.1	97.4
Catastrophic** ≤ 1,500 farms	99.5	100.0

* Large-scale production

** Catastrophic USA outbreak or catastrophic North American outbreak

represent two major MN livestock agriculture industries that would suffer serious consequences in the event of an FMD outbreak. They were also chosen because of differences in species FMD susceptibility and transmissibility, which were reflected in the probabilities of effective contact and disease state-transition parameters that the authors determined by working with MN SMEs. Differences in management and biosecurity measures were evident in the direct and indirect contact rates (Tables II and III). Swine herds had very low direct and indirect contact rates with other herds, whereas dairy operations had higher rates of indirect contact and this appears to be a major factor in large FMD outbreaks, as demonstrated here. Outbreaks that began in a dairy index herd had significantly higher mean values for disease duration, outbreak duration, numbers of farms infected and numbers of animals infected when compared with outbreaks with swine index herds (Table V).

The results on differences between swine and dairy index herds are supported by other modelling studies (17). Traulsen *et al.* found that FMD epidemics were long-lasting with a high number of infected farms when the index case was a dairy farm.

The probabilities of observing and reporting clinical signs of FMD were set higher (based on SME input) for large-scale swine productions than for dairy herds. This was because the SMEs considered that clinical signs were more likely/more severe in swine and were more likely to be more

rapidly reported by owners/managers of large-scale swine operations. This may help to explain why swine index herd scenarios had more limited spread.

Biosecurity measures in large-scale swine herds were better than in dairy herds; direct and indirect contact rates were lower both from and into the swine herds than for dairies (Tables II and III). Thus, it is not surprising to find differences in outbreak size between these two types of production.

Uncontrolled outbreaks and the limitations of depopulation

Noteworthy outcomes from this study were the uncontrolled outbreaks in the dairy index herd scenarios. In a literature review, no mention of this phenomenon could be found in other outbreak models. However, the findings of McLaws and Ribble (10) show a general pattern not dissimilar to the findings of the present study, even though those authors were reporting findings from actual outbreaks that occurred in many countries covering several continents. Of 24 outbreaks studied in non-endemic areas around the world, most involved fewer than 150 infected premises, whereas four large outbreaks each involved more than 2,000 infected premises. Those uncontrolled outbreaks, although less common perhaps, are important because they demonstrate what might happen when the spread of the outbreak outpaces the depopulation efforts, as seen in Chinese Taipei in 1997 (5), Japan in 2010 (7) and South Korea in 2010 (8).

Several factors in disease spread can be responsible for an outbreak that overwhelms the control measures. First, the outbreak could get a head start on the response before the first herd is detected. Second, the depopulation resources required may be underestimated. Third, there may be a prolonged infectious period before clinical signs are apparent. This was seen in the present study, where the median number of infected herds in swine index herd scenarios was five, although the number of days to reach five infected herds varied from 9 to 37 days. Infected herds that remain undetected for a period of time can cause further disease spread if movement controls are not adequate. Garner *et al.* (18) demonstrated that the resources required in response to a large FMD outbreak are substantial. They estimated that, in a scenario in which staff resources were unlimited, the number of people involved in bringing a modelled outbreak under control would be 2,724 (18). In the situation of an uncontrolled outbreak in MN, the required number of response personnel would easily exceed this estimate.

Depopulation at a rate of 20 herds per day was effective in controlling most of the modelled outbreaks in the present study. A total of 90% of swine index herd outbreaks were

stopped within 50 days, with 65 or fewer farms infected and depopulated. A total of 50% of dairy index herd outbreaks were stopped within 40 days and 100 or fewer farms were infected and depopulated. However, when the number of farms infected in the first few weeks of the outbreak outpaced initial depopulation capacity, uncontrolled outbreaks occurred. In a report on a model used in the United Kingdom (UK), Thornley and France (19) stated that 'early disease detection, combined with immediate rapid slaughtering at the index site and restriction of... movements are relatively effective strategies' of FMD control, given current UK farm practice. The model used by those authors is in agreement with this MN model, where depopulation and movement controls often resulted in eradication of the disease.

Indemnity expenses associated with depopulation can be substantial (20). Indeed, food production systems are at risk of bankruptcy with traditional massive depopulation (20). Spread of infection outpacing depopulation is an important factor when considering the value of depopulation capacity and outbreak response alternatives to stamping out. The most recent (2011) outbreak in Japan is an example of this situation: the rapid increase in the number of infected farms caused depopulation delays and at the peak of the epidemic more than 100 farms awaited depopulation (21).

In the present study, the number of herds depopulated per day was not related to herd size. This is in contrast to other studies (18), which specify the number of animals depopulated per day. It is quite possible that depopulation, of large swine herds in particular but also of large dairy herds, could take several days for just one herd. Also, the model immediately assumes no risk of transmission, even indirectly, from a depopulated herd. This is not true in actual practice and other modelling studies make other assumptions. Depopulation must be coupled with effective disposal and decontamination to remove the risk of transmission from infected premises (18). Completion of all of these control measures often takes several days and contributes to the differences in disease duration versus outbreak duration.

Strengths and weaknesses of the study

Use of the NAADSM is a strength of the present study, in part because this model is similar to those used in other countries, such as Australia, Canada and New Zealand (22). Indeed, differences between the NAADSM and other models were small and would have resulted in recommendation of the same or similar management decisions (22). The NAADSM has been thoroughly reviewed and is also used by other states in the USA and by other countries.

A second strength of the study is the detailed description of the model assumptions, including specific parameter values

for progression of the disease and between farm contacts. Parameter estimates (Tables II, III and IV) can serve as baselines for use in other modelling studies and would be particularly useful in comparisons of different control measures; for example, in initial models before parameters more specific to the modelled situation could be determined, and for initial estimates in US states or countries with mixed livestock population profiles, as in MN. This is in line with recommendations from other FMD-free countries and is part of what makes the USA 'well-positioned ... to make more informed decisions in times of crisis' (23).

The third strength of the study is that it has demonstrated the entire range of possible FMD outbreaks, from limited focal outbreaks controlled with depopulation to widespread, potentially catastrophic outbreaks where depopulation alone is insufficient. Additional outbreak control measures, such as vaccination, may be necessary (24).

The model parameters used in the study were specific both geographically and non-geographically. For this project, the MN Board of Animal Health provided geospatial locations of all beef, dairy, small ruminant and swine operations within the state. This allowed the model to be both geospatially and temporally specific. Livestock production practices in MN were described by SMEs to enable development of MN-specific parameters for direct and indirect contact rates between farms. For all parameters that did not require local input, a set of parameters developed by researchers at the Center for Epidemiology and Animal Health (CEAH) were used (15). Availability and use of these non-geographically specific input parameters in other studies would enable comparison with the results reported here. Such comparative studies would also allow examination of the differences, and the implications, resulting from the impact of geographically-specific parameters.

A limitation of the study is that sales barns, expositions and other sites of animal co-mingling were not included. A further limitation is the defined geographic boundaries of MN; the random sampling of distance distributions might have selected a location outside the state boundary. This factor was not considered, because of a lack of any location data outside of MN. The results of the study may thus underestimate the duration and spread of an FMD outbreak in MN.

Conclusions

Comparison of data between these modelled FMD outbreaks, in which the index herd differed in both species and production system, showed significantly longer and larger outbreaks in dairy index herd scenarios. Insufficient depopulation capacity was one contributing

factor associated with the uncontrolled outbreaks observed in this study. Uncontrolled events ended when there were insufficient numbers of susceptible premises to sustain the spread of the disease. More frequent indirect contact and lower biosecurity levels in dairy operations were associated with the differences in size and duration of outbreaks in this study. Findings from the study will help inform emergency preparation planners as they consider depopulation capacities and develop FMD educational programmes directed at different types of farms in the USA. The findings are also of value to veterinary authorities developing or adjusting their FMD emergency response plans as they consider biosecurity measures and the associated implied contact rates and disease transmission risks in different species and types of farms.

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Simulation épidémique d'un foyer de fièvre aphteuse au Minnesota

S.B. Gale, G.Y. Miller, C.E. Eshelman & S.J. Wells

Résumé

La fièvre aphteuse est une maladie transfrontalière grave du bétail domestique, qui revêt une importance internationale. Récemment, des foyers de fièvre aphteuse sont apparus dans des pays précédemment indemnes. Le recours à des modèles est un outil intéressant grâce auquel les pays ayant une expérience directe limitée de la maladie peuvent étudier l'évolution d'un foyer potentiel. Les auteurs décrivent une étude visant à déterminer quels sont les paramètres spécifiques du risque de fièvre aphteuse au Minnesota et aux États-Unis afin de les utiliser pour créer un modèle de foyer primaire de fièvre aphteuse au Minnesota. L'un des objectifs attendus était de déterminer si le type d'élevage (laitier ou porcin industriel) dans lequel survenait le foyer initial influait sur les données élémentaires générées par le modèle concernant la taille et la durée du foyer et d'examiner les conséquences qu'entraînerait l'adoption de mesures de dépopulation ou le contrôle des mouvements d'animaux. Les valeurs moyennes correspondant à la durée de la maladie, à la durée du foyer et au nombre d'élevages et d'animaux infectés étaient plus élevées dans le scénario où le foyer se déclenche initialement dans un élevage laitier. Les deux modèles ont fait ressortir toutes les modalités possibles de survenue d'un foyer de fièvre aphteuse, depuis les petits foyers localisés et à faible rayonnement jusqu'aux foyers de

grande envergure et se propageant de manière incontrôlable. Les indications détaillées sur la modélisation d'un foyer initial qui ressortent des résultats de cette étude donneront aux responsables de la préparation aux urgences des orientations utiles pour évaluer les stratégies envisagées en cas d'incursion de la fièvre aphteuse aux États-Unis. Ces résultats peuvent intéresser tous les pays dont les autorités vétérinaires entreprennent d'élaborer ou de corriger les plans d'intervention d'urgence en cas de fièvre aphteuse.

Mots-clés

Épidémiologie – Fièvre aphteuse – Foyer – Minnesota – Modélisation – Simulation.



Simulación epidémica de un brote de fiebre aftosa en Minnesota

S.B. Gale, G.Y. Miller, C.E. Eshelman & S.J. Wells

Resumen

La fiebre aftosa es una de las principales enfermedades transfronterizas del ganado de importancia internacional. En fechas recientes se han producido brotes de la enfermedad en varios países que hasta entonces estaban libres de ella. Para los países que tienen escasa experiencia directa de lucha contra esta enfermedad, el uso de modelos es una herramienta útil para estudiar posibles brotes. Los autores describen un estudio encaminado a determinar los parámetros específicos del riesgo de fiebre aftosa en Minnesota y los Estados Unidos (EE.UU.) y a utilizar esos parámetros para generar un modelo inicial de referencia de brote de fiebre aftosa en Minnesota. Había además especial interés por determinar si el tipo de rebaño en el que daba comienzo el brote (rebaño lechero o piara porcina industrial) influía en los resultados básicos del modelo en cuanto a dimensiones y duración del brote y por estudiar los efectos del sacrificio sanitario y del control de los desplazamientos. Los valores promedio de duración de la enfermedad, duración del brote y número de explotaciones y ejemplares infectados eran superiores en la hipótesis que partía de un rebaño índice de carácter lechero. Los resultados de estos dos modelos de brote abarcaban todo el espectro de tipos de brotes de fiebre aftosa, esto es, desde pequeños episodios de alcance local hasta brotes muy extendidos y fuera de control. Las conclusiones de este estudio ofrecen indicaciones detalladas sobre un modelo inicial de referencia que los responsables de definir planes de emergencia pueden emplear para valorar estrategias de respuesta ante una eventual incursión de la fiebre aftosa en los EE.UU. Estas conclusiones también revisten utilidad para todos aquellos países cuyas autoridades veterinarias estén elaborando o adaptando sus planes de respuesta de emergencia a la fiebre aftosa.

Palabras clave

Brote – Epidemiología – Fiebre aftosa – Minnesota – Modelización – Simulación.



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