

Improving US animal disease preparedness: Animal disease traceability and biosecurity with an
emphasis on Foot-and-Mouth Disease

by

MaRyka Renae Smith

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AN ABSTRACT OF A DISSERTATION

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Abstract

Foot-and-Mouth Disease (FMD) is a highly contagious, transmissible, viral disease of cloven-hooved livestock. The clinical signs in animals infected with FMD are vesicular lesions around the hooves, teats, and mouth that develop 2 to 14 days after infection. Animals may be infectious to others in as few as 2-3 days after infection, during the preclinical phase. Infected animals often experience production losses due to the pain associated with the clinical signs. Outbreaks of FMD cause economic losses for the country or region affected due to depopulation, trade losses, outbreak control costs, and disruption to business continuity. The United State (US) has not had an outbreak of FMD since 1929, but the ongoing global movement of humans, animals, and animal products, means that the threat of FMD remains constant. The virus's rapid spread and the potential for economic devastation highlight the need for research into FMD response planning.

The current US FMD response is described in the Foot-and-Mouth Disease Response Plan (“The Red Book”). The Red Book is designed to swiftly control and eradicate an outbreak in order to return the US to FMD freedom as quickly as possible. A potential cost of strict disease control measures is loss of business continuity on farms that are not infected. To balance this need for disease control and business continuity, the “Secure Food Supply” plans have been developed to assist producers with biosecurity and contingency planning. Both the Red Book and Secure Food Supply plans recommend best practices for disease control. However, there is a gap in empirical data supporting the efficacy of many field biosecurity practices.

Effective disease traceability can also aid outbreak control and business continuity by identifying dangerous contacts and enabling the accurate implementation of surveillance and quarantine. Currently, the US does not have complete digital traceability of susceptible livestock.

Producers are not legally required to apply electronic identification (EID) to all animals and not all animal movements are required to be reported. This can lead to delays or failure in identifying all diseased and at-risk animals in a disease investigation, which could ultimately allow the continued transmission of disease. There have been recent advances in the use of electronic identification (EID) and digital movement reporting, but quantitative data on the impacts of improving digital traceability are limited.

To address the biosecurity knowledge gap, a scoping review was conducted on the implementation of a biosecurity measures for FMD mitigation at the farm level. A systematic search of 4 databases identified 3,153 unique records. The inclusion criteria for further review required reports to be original, peer-reviewed research, published in English, to describe or evaluate a biosecurity measure applied at the farm level to mitigate FMD risk, and to include at least one of the US domestic, FMD-susceptible livestock species. After abstract and full-text evaluation, 22 reports were included in the review. The reports included 2 experimental studies and 20 field reports. The experimental studies showed that hand washing, showering, and changing outerwear were more effective than no interventions. The field studies reported many measures, but none were consistently reported as effective for FMD mitigation across multiple reports. This scoping review highlighted the insufficiency of the published literature on FMD field biosecurity measures and the difficulty of acquiring biosecurity data in the field setting. The findings of this review can be used to shape future research questions in biosecurity field studies and to improve the reporting of biosecurity measure literature. Improving biosecurity knowledge can help producers and animal health officials develop FMD response plans that are effective for risk mitigation, economically responsible, and feasible to implement.

To address gaps in animal disease traceability, we assessed the impacts of EID and digital tracing using simulated FMD outbreaks in the US. The program InterSpread Plus (ISP) was used to simulate FMD outbreaks from feedlot, cow-calf, and dairy farms across multiple locations in the US. The outbreaks were defined by their starting location and farm type, the level of tracing, and the day the first farm was detected. The tracing levels represented the current tracing speed and accuracy, a partial implementation of EID (approx. 70% success), and an ideal implementation of EID tracing (99% success). Each scenario was tested with 100 simulated outbreaks. The primary outcome of interest in simulated outbreaks was the size of the outbreak, measured as the number of infected premises (IPs). The day the outbreak was detected was highly influential in determining outbreak size. Outbreaks detected on days 8 and 14 were smaller in size than those detected on day 21. Outbreaks detected on day 21 had the largest reduction in the number of IPs from the current tracing to the improved tracing scenarios. Improved tracing suggested a decreased likelihood for the largest and most devastating outbreaks across all introduction locations. These results support the need for improved traceability to aid in controlling an FMD outbreak.

The simulation of FMD outbreaks and the improvement in traceability focused on the speed and accuracy of completing a trace, but did not address the proportion of farms that must use the tracing technology to achieve those metrics. The final project in this dissertation addressed this gap by applying tagging and digital reporting to simulated movement networks. The ISP FMD outbreak model was reconfigured to remove outbreak controls to generate a movement network of cattle. Cattle move between farms, markets, feedlots, processors, and other cattle premises. The farms in the simulated network were then randomly assigned as tagging and reporting farms at varying rates. The traceability scenarios were developed to

represent the current status of EID and digital reporting, and were progressively improved toward a hypothesized ideal EID utilization. If the source farm of a movement originated tagged and the destination farm reported it was deemed “traceable.” The traceable movement networks were then subjected to contact tracing to assess whether contacts from randomly selected farms could be located. The simulation of the current level of EID and digital tracing had near-zero success for contact tracing. The number of traceable contacts did not exceed 50% for cow-calf farms until 75% of all farms tagged and reported movements. In the highest-traceability scenario, 75% of farms were tagged, and 90% reported, resulting in traceability of 60% of cow-calf contacts and over 80% of market contacts. Additional analysis showed that the increase in tagging without an increase in digital reporting did not improve traceability. These results highlight the need for substantial improvements in EID tag utilization and in digital reporting database infrastructure.

The combination of these projects adds to the body of literature that animal health officials, livestock producers, and veterinarians can use when preparing for and responding to a potential introduction of FMD. These results could be extrapolated to control many other livestock diseases and used to develop novel research topics for disease preparation.

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Approved by:

Major Professor
Michael W. Sanderson

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Abstract

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To address gaps in animal disease traceability, we assessed the impacts of EID and digital tracing using simulated FMD outbreaks in the US. The program InterSpread Plus (ISP) was used to simulate FMD outbreaks from feedlot, cow-calf, and dairy farms across multiple locations in the US. The outbreaks were defined by their starting location and farm type, the level of tracing, and the day the first farm was detected. The tracing levels represented the current tracing speed and accuracy, a partial implementation of EID (approx. 70% success), and an ideal implementation of EID tracing (99% success). Each scenario was tested with 100 simulated outbreaks. The primary outcome of interest in simulated outbreaks was the size of the outbreak, measured as the number of infected premises (IPs). The day the outbreak was detected was highly influential in determining outbreak size. Outbreaks detected on days 8 and 14 were smaller in size than those detected on day 21. Outbreaks detected on day 21 had the largest reduction in the number of IPs from the current tracing to the improved tracing scenarios. Improved tracing suggested a decreased likelihood for the largest and most devastating outbreaks across all introduction locations. These results support the need for improved traceability to aid in controlling an FMD outbreak.

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Table of Contents

List of Figures	xvii
List of Tables	xviii
Acknowledgements	xxi
Dedication	xxii
Chapter 1 - Foot-and-Mouth Disease Considerations for the United States mixed-animal veterinary practitioner.....	
Abstract	1
Introduction.....	3
Foot and Mouth Disease Virus	4
Identification	5
Global Distribution and Outbreaks	6
United States Response Plan.....	10
Biosecurity and Personnel Considerations	12
Conclusion	13
References	14
Figures	21
Tables.....	22
Chapter 2 - A condensed review of Foot-and-Mouth Disease research for the United States mixed-animal veterinary practitioner.	
Abstract	23
Introduction.....	25
Research Considerations and US Facilities	26
Introduction Risks and Pathways.....	28
Transmission and Pathogenesis	30
Biosecurity, Disinfection, and Virus Survival	32
Vaccinology	34
Computer Modeling.....	35
Observational and Review Research	38
Conclusion	39

References.....	41
Tables.....	49
Chapter 3 - A scoping review of farm-level biosecurity measure effectiveness against Foot-and-	
Mouth Disease to inform planning and preparedness efforts in the United States.....	51
Abstract.....	51
Introduction.....	53
Methods	55
Information Sources and Search Strategy.....	55
Screening Process	56
Eligibility Criteria	58
Data charting and synthesis	58
Results.....	59
Selection of Sources of Evidence.....	59
Characteristics of Reports	60
Biosecurity Measures Demonstrated to be Efficacious	61
Other Implemented Biosecurity Measures.....	62
Biosecurity Measures for Livestock and Their Products.....	62
Biosecurity Measures for Personnel and Visitors	65
Biosecurity for Vehicles and Fomites.....	67
Disinfection.....	69
Discussion.....	71
Conclusion	78
Funding	80
Acknowledgments	80
References.....	80
Figures	87
Tables.....	88
Chapter 4 - Animal Disease Traceability: Evaluation of Simulated Foot-and-Mouth Disease	
Outbreak Metrics with Implementation of Improved Contact Tracing of Cattle	95
Abstract.....	95
Introduction.....	97

Materials and Methods.....	101
Modelling Program	101
Basic Parameters and Population.....	101
Initiation of Outbreaks	103
Scenario Specific Parameters.....	104
Tracing Parameters	104
Zones.....	105
Analysis.....	105
Results.....	107
Convergence	107
General Results	107
Level of Tracing.....	108
Infected Premises (IPs)	108
Duration of Outbreaks.....	109
Number of farms under surveillance.....	110
Reduction of Control Areas and Surveillance Zone Size	112
Discussion.....	113
Conclusions.....	118
Funding	118
Acknowledgements.....	119
References.....	120
Figures	125
Tables.....	133
Chapter 5 - Assessment of Electronic Identification of Cattle and Digital Movement Reporting in Simulated United States Cattle Movement Networks	134
Abstract.....	134
Introduction.....	136
Materials and Methods.....	138
Objective 1: Network Simulation	138
Initialization of Model	138
Post Processing of Movement Simulation Data.....	140

Market Movements	140
Model error messages: Failed movements and correction.....	141
Network description.....	141
Objective 2: Utilization of Electronic Identification.....	142
Application of Tagging and Digital Reporting	142
Scenario Development	143
Traceable Network Analysis.....	144
Tracing Individual Farms of Interest (FOIs).....	145
Cow-calf and feedlot FOIs.....	145
Market FOIs	147
Analysis of FOI Tracing Outcomes	147
Results.....	148
Description of the Full Network	148
Number of Contacts Found for each FOI in the Full Network	148
Number of Movements in the Traceable Network per Scenario	149
Untraceable Individual Farms.....	149
Percent of Contacts Traceable.....	150
Cow Calf FOIs	151
Feedlot FOIs.....	151
Market FOIs	152
1 Phone Call Tracing	152
Discussion.....	153
Conclusion	159
Funding	160
Acknowledgements.....	160
References.....	161
Figures	164
Tables.....	170
Chapter 6 - Dissertation Conclusions	182
Appendices and Supplementary Materials.....	184
Appendix A - Chapter 3 Supplementary Materials.....	185

Appendix B - Chapter 4 Supplementary Materials	197
Supplement 1	197
Supplement 2	221
Supplement 3	221
Supplement 4	223
Supplement 5	224
Supplement 6	237
Appendix C - Chapter 5 Supplementary Materials	273
Supplement 1	273
Supplement 2	279
Supplement 3	294
Supplement 4	298
Supplement 5	309

List of Figures

Figure 1.1: World Organisation for Animal Health Members’ official FMD status map.	21
Figure 3.1: Flow diagram of the number of records and reports identified, screened for eligibility, and retained for inclusion in the review from an original and an update search.	87
Figure 4.1: Number of infected premises for outbreaks that began in feedlots.	125
Figure 4.2: Number of infected premises for outbreaks that began in dairies.	126
Figure 4.3: Number of infected premises for outbreaks that began in small outbreak scenarios.	127
Figure 4.4: Shift function plots for duration of outbreaks in days.	128
Figure 4.5 Shift function plots for number of farms in surveillance zones.	129
Figure 4.6 Change in number of IPs and farms in surveillance zones in outbreaks that began in feedlots and used reduced control area and surveillance zone radii.	130
Figure 4.7 Change in number of IPs and farms in surveillance zones in outbreaks that began in dairies and used reduced control area and surveillance zone radii.	131
Figure 4.8 Change in number of IPs and farms in surveillance zones in small outbreak scenarios that used reduced control area and surveillance zone radii.	132
Figure 5.1: Distribution of contacts in the full network for cow-calf farm FOIs	164
Figure 5.2: Distribution of contacts in the full network for feedlot FOIs.	165
Figure 5.3: Distribution of contacts in the full network for market FOIs.	166
Figure 5.4: The percent of contacts from Cow-Calf FOIs that were traceable in each scenario	167
Figure 5.5: The percent of contacts from feedlot FOIs that were traceable in each scenario.	168
Figure 5.6: The percent of contacts from market FOIs that were traceable in each scenario.	169

List of Tables

Table 1.1: Summary of selected global outbreaks.....	22
Table 2.1: Disease Modeling Terminology	49
Table 3.1 Search strategies by database and number of records returned by date.....	88
Table 3.2: Key data items.	89
Table 3.3: Report characteristics.....	90
Table 3.4: Number of reports where unique biosecurity measures for livestock and livestock products were implemented by their reported effectiveness.....	91
Table 3.5: Number of reports where unique biosecurity measures for personal protective equipment and individual management were implemented by their reported effectiveness.	92
Table 3.6: Number of reports where unique biosecurity measures for fomite management were implemented by their reported effectiveness.	93
Table 3.7: Number of reports where unique disinfection biosecurity measures were implemented by their reported effectiveness.	94
Table 4.1 Details for Index Case Selection.....	133
Table 5.1: Farm types included in the simulated movement network and number of farms represented of each type. Represented farms are farms that had at least one contact in the full network.	170
Table 5.2: The tagging and reporting rates for each farm type in the baseline scenario.	171
Table 5.3: The tagging and reporting rates for each farm type in the cow-calf focused scenarios.	172
Table 5.4: The tagging and reporting rates for each farm type in the market focused scenarios.	173
Table 5.5: The tagging and reporting rates for each farm type in the scenarios developed to assess industry-wide improvement	174
Table 5.6: The tagging and reporting rates for each farm type in the scenarios developed to assess tagging and reporting separately.	175
Table 5.7: Full and Traceable Network Metrics	176
Table 5.8: The total number of FOIs that had zero traceable contacts in each scenario	177

Table 5.9: The mean and percentiles of percent of contacts traceable by scenario for cow-calf FOIs.....	178
Table 5.10: The mean and percentiles of percent of contacts traceable by scenario for Feedlot FOIs.....	179
Table 5.11: The mean and percentiles of percent of contacts traceable by scenario for market FOIs.....	180
Table 5.12: Results of “1 phone call” tracing method.....	181
Appendix A.1 Table 1: Livestock and product management: description and effect of biosecurity measures for managing livestock, and livestock products at the report level.....	185
Appendix A.2 Table 2: Personal protective equipment and individual management: description and effect of biosecurity measures for managing farm personnel and visitors at the report level.....	188
Appendix A.3 Table 3: Fomite management: description and effect of biosecurity measures for managing fomites at the report level.....	190
Appendix A.4 Table 4: Disinfection: description of on-farm disinfection measures and their effectiveness to control FMD introduction or spread at the report level	192
Appendix B 1: Population File	221
Appendix B 2: Direct Farm to Farm Movements	221
Appendix B 3: Farm to Market Movements	222
Appendix B 4: Current Tracing Speed Parameters.....	223
Appendix B 5: Current Tracing Accuracy	223
Appendix B 6: Partial Tracing Speed Parameters.....	223
Appendix B 7: Partial Tracing Accuracy Parameter.....	223
Appendix B 8: Ideal Tracing Parameters for all beef and dairy	223
Appendix B 9: Overflow tables from Chapter 4.....	224
Appendix B 10 Tables for Outbreaks Detected on Day 8	237
Appendix B 11 Tables for Day 14 Outbreaks.....	254
Appendix C 1: Sample Movement Parameters.....	273

Appendix C 2: Post Processing of Movement Network R Code	279
Appendix C 3: Example Creation of Traceable Network: Ideal 75/90	294
Appendix C 4: Example Tracing Protocol: 100 Cow Calf FOI in All 75/90 Scenario	298
Appendix C 5: Additional Network Metrics	309

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Dedication

I dedicate this work to my dog, Hazy. She was born in my final semester of undergraduate work and has been a constant companion, reading buddy, and my motivation to get outside and get some sun when the work was tough. She deserves to be called Dogtor Hazy after being with me every step of my combined DVM/PhD program.

Chapter 1 - Foot-and-Mouth Disease Considerations for the United States mixed-animal veterinary practitioner.

MaRyka R. Smith¹, Christy J. Hanthorn¹, Sara McReynolds², Michael W. Sanderson¹

¹Center for Outcomes Research and Epidemiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506, United States of America

²Kansas Department of Agriculture, Manhattan, Kansas 66506, United States of America

Abstract

Foot-and-Mouth Disease (FMD) is a highly contagious disease of cloven-hooved animals that has not been identified in the United States (US) since 1929. The potential introduction of FMD to the US remains a constant threat given its global distribution and outbreak activity. Detection of FMD in the US would result in the closure of many export markets for animal products, causing severe economic losses. As the first line of defense in detecting FMD, the US mixed-animal practitioner should be aware of the virus, its clinical presentation, and the current US biosecurity and response plans.

The clinical signs of FMD are clinically indistinguishable from other endemic vesicular diseases in the US. Veterinarians must be able to recognize and report suspicious clinical signs of all vesicular diseases to the correct authorities to ensure swift detection and disease control. Delays in detection could result in significant increases in outbreak size and cost.

Producers may bring questions about FMD to their veterinarian and seek guidance on developing their own preparation plans. Knowledge of the producer's operation, current federal guidance on disease control, and industry specific plans will allow practitioners to provide their clients with sound guidance.

The objective of this condensed review is to summarize key FMD information for food animal or mixed animal practitioners, including the identification and diagnosis of FMD, its global distribution and recent outbreaks, the US response plans, and factors that may impact practitioners during an outbreak.

Introduction

Foot-and-Mouth Disease (FMD) has not been identified in the United States (US) since 1929. Because of this, most veterinarians have not personally seen a case, yet, having been taught the potential severity of the disease, no veterinarian wants to be the one that fails to recognize the first case of an FMD outbreak. The clinical signs of FMD are clinically indistinguishable from diseases that are endemic to the US, such as Vesicular Stomatitis Virus which further complicates the identification process. Veterinary practitioners are a first line of defense to recognize signs of a potential foreign animal disease and report suspicions to state and federal authorities [1]. The report can trigger a chain reaction of early recognition which is crucial to rapid outbreak control [1].

Potential foreign animal disease reports occur regularly and are investigated by veterinarians from the state animal health office and United States Department of Agriculture Animal and Plant Health Inspection Service Veterinary Services (USDA-APHIS-VS). From 2019 to 2023, USDA-APHIS- VS conducted an average of over 2,800 foreign animal disease investigations annually [2]. Foreign animal disease investigations are common and essential to assure early detection of any incursion.

The identification of FMD in a free country, such as the US, would have immediate and potentially devastating impacts on international trade of susceptible meat and animal products [3]. Upon the detection of FMD, many export markets would cease to accept US meat and animal products. The current estimated value of export products are \$67 per head of pork slaughtered and \$423 per head of beef [4]. The loss of this market, coupled with the already narrow profit margins on animal products, could quickly become devastating to the livestock and allied industries and potentially spill over to the general US economy. Pendell, et al, estimated in

2015 that the potential costs of an accidental FMD Virus release from National Bio and Agro Defense Facility in Manhattan, Kansas, USA could range from \$16 to 140 billion [5]. Other estimates of the cost of FMD outbreak scenarios in the US are similar in magnitude [6, 7]. There are many costs associated with the control of and recovery from an FMD outbreak including but not limited to: personnel labor, vaccinations, animal indemnity, laboratory testing, sample transportation, depopulation, decontamination, and carcass disposal. The larger and more widespread an outbreak becomes; the more additional costs may accrue.

Many livestock producers rely on their veterinarians for expertise about foreign animal diseases, including FMD, and for guidance regarding preparedness plans like those recommended by the Secure Food Supply plans [8-10]. The current US Foreign Animal Disease surveillance systems also depend heavily on astute observations and timely reporting from practitioners to begin disease investigations. However, due to the lack of first-hand experiences with these diseases, practitioners may feel less confident in making these diagnoses and reports. The aim of article is to provide practical information that will prepare both food-animal exclusive and mixed-animal practitioners with knowledge about the FMD virus, identification and diagnostic process, the status of global outbreaks, and the current response plans.

Foot and Mouth Disease Virus

FMD is a non-enveloped single stranded RNA *apthovirus* in the family *Picornaviridae* [11] [12]. There are 7 immunologically distinct serotypes of FMD: O, A, C, Asia-1, South African Territory (SAT) 1, SAT 2 and SAT 3. Within each serotype there may be multiple antigenically distinct subtypes which makes the development of broadly protective vaccines difficult [13]. Currently available vaccines offer limited cross-protection between FMD strains and serotypes.

The FMD virus does not infect humans and is distinctly separate from Human Hand-Foot-and-Mouth Disease (HFMD)[14]. However, FMD and HFMD can be confused by media and the public resulting in fear of human infections during FMD outbreaks. While both viruses belong to the *Picornaviridae* family, HFMD is caused by a human-specific coxsackievirus in the genus enterovirus and typically only infects infants and children.

Identification

The primary species infected by FMD are those with cloven-hooves [15]. This includes domestic cattle, pigs, sheep, goats and bison in the US. FMD has also been shown to infect many wildlife species including feral hogs, deer, and elk [16]. Species exotic to the US, including giraffes and camels, are potentially susceptible as well [16]. Susceptibility to the virus varies based on the route of transmission, specific serotype and strain of the virus, and the species exposed [17-19]. For example, swine typically excrete a higher volume of infective virus that can spread readily via aerosol transmission, but they tend to be less susceptible to infection via virus inhalation [20]. Comparatively, sheep and cattle tend to be more susceptible to infection via aerosol transmission [20]

Clinical signs in animals infected with FMD include blister-like vesicular lesions around the coronary bands, on the tongue and oral mucosa, and on the mammary teats. The lesions are clinically indistinguishable from other vesicular diseases such as Vesicular Stomatitis, Bluetongue virus, Seneca Valley Virus, and Vesicular Exanthema of Swine. Vesicular Stomatitis has the unique characteristic of infecting horses while the other vesicular diseases are limited to cloven-hooved animals or only swine. All of these diseases are legally required to be reported in most states and should always be treated with the same degree of caution as FMD [21]. All

potential foreign animal diseases will be investigated using the USDA-APHIS foreign animal disease reporting process [1].

Infected cattle and swine often have a short febrile reaction prior to developing vesicles [19]. Cattle may be noticeably off-feed, salivating excessively, and lame. Swine may experience foot lesions so severe that the hoof capsule sloughs off entirely. Both species are likely to show inappetence and reluctance to move or rise as early signs of pain in the mouth and feet. Severity of signs for each species can vary with the infecting strain so any vesicles should be reported and investigated.

FMD infection in sheep and goats may have less obvious clinical signs than those observed in cattle or swine [22]. Sheep are often considered “silent spreaders” of FMD, showing relatively mild lameness that is easily mistaken for endemic diseases, such as foot rot, resulting in delayed diagnosis. This silent spreader nature was influential in the early days of the 2001 UK outbreak resulting in delayed diagnosis and implementation of controls [23]. Additionally, vesicles may rupture very quickly in the interdigital cleft of sheep and may be hidden by wool or hair on the legs [22]. Goats present similarly with mild signs, but milking goats may have more noticeable lesions on the teats or a noticeable decrease in milk production [22].

Global Distribution and Outbreaks

The FMD endemic regions tend to experience specific FMD serotype outbreaks. Asia experiences outbreaks of serotypes O, A, SAT, and Asia-1. While Africa routinely sees outbreaks of all serotypes. No serotype C infections have been reported globally since 2004, and this serotype is presumed to be extinct. The most recent detections of FMD in North America were 1952 in Canada and Mexico in 1954 [24]. South America has historically seen outbreaks of serotypes O and A. Currently in South America, Venezuela does not report FMD status, but

many other South American countries are currently free from FMD. Specifically, Peru, Brazil, Argentina, and Bolivia have not had an FMD outbreak since 2004, 2005, 2006, and 2007 respectively [25]. Figure 1.1 shows the current global distribution of official FMD status by the World Organization of Animal Health (WOAH).

WOAH (formerly Office International des Epizooties) began FMD-Free status recognition in 1996. The recognition can be applied to the entire country or, within a country, there may be regionalization that allows one country to have multiple FMD designations. An example of this is in Argentina, which is free with vaccination in the northern region and free without vaccination in the southern. Both regions of Argentina are free from FMD but the northern region may still have trade restrictions due to concerns of surveillance limitations, suppressed clinical signs, and FMD asymptomatic carrier status in vaccinated animals.

Since the WOAH designations of freedom began in 1996, there have been incursions of FMD into free countries. Cabezas, et. al, (2022) reviewed the WOAH database and found 21 events between 1996 and 2020, where a country that was FMD free without vaccination had a suspension and recovery of that status [3]. For six countries that are free from FMD but do practice vaccination there was 1 suspension and recovery of that status. This article will review a few notable outbreaks and summarize them in Table 1.1.

Many veterinarians are likely aware that there was a large outbreak of FMD in the United Kingdom (UK) in 2001. The outbreak was detected in February of 2001, when symptomatic pigs were found in an abattoir [26]. The virus was a Pan-Asian Type O virus. The outbreak origin was traced back to a swine farm that had been feeding untreated food waste. The virus, which caused relatively few clinical signs in sheep, had been spreading locally to sheep that were then dispersed through the auction market system [27]. At the time of detection, FMD had been

spread to a wide geographic area [27]. Across the entirety of the outbreak, cattle and sheep were the predominant species infected and depopulated. It is estimated that over 6 million animals were depopulated from over 2000 farms' herds and flocks at an estimated cost of £5 billion (approx. 6.8 billion USD) [28]. The last case was detected on September 30, 2001. Other incursions from the UK outbreak occurred in France, Ireland, and the Netherlands [29]. The Netherlands adopted a vaccination strategy to control disease spread, but still depopulated approximately 260,000 animals [29].

On April 24, 2001, FMD serotype A was confirmed in Uruguay, near the Argentinian border [30]. The virus found in Uruguay was genetically very similar to the virus that was detected in Argentina (A/Arg/01) [31]. A genetically similar virus was also detected in Brazil in 2001. The initial response in Uruguay was to control the disease through the use of biosecurity, limitation of animal and fomite (people) movements, and culling animals that were clinically infected and those in contact. Ring vaccination was also utilized within a 10km radius of infected premises starting on April 26th. Just days later, on April 30th, vaccination efforts were expanded to build a wider buffer zone of vaccinated animals. On May 5, 2001, vaccination efforts were extended to include the entire national cattle population. A second vaccine was administered to all cattle between June 15th and 22nd 2001. Approximately 2.9 million animals were affected during the outbreak [30]. The last case in the outbreak was reported on August 21, 2001 and freedom with vaccination was restored in 2003 [30, 32]. The World Bank contributed 24 million USD to the FMD Emergency Recovery Project for control effort support no other estimates of cost were found by the authors [33].

On January 10, 2025, Germany confirmed detection of serotype O in a water buffalo herd; its first outbreak of FMD since 1988 [34]. Within the herd, 3 animals died and the

remaining 11 were swiftly depopulated to control the disease. Neighboring susceptible livestock were culled in a 1km radius around the index site, including 170 pigs, 55 sheep and goats, and 3 cattle [35]. No further cases were detected and Germany returned to freedom without vaccination in April, 2025. Current estimates report that the cost to the German economy was near 1 billion euros (~1.2 billion USD) [36].

On March 3, 2025, a 1,400-cow dairy farm in Hungary, near the Slovakia border, detected clinical signs of FMD with laboratory confirmation on March 6, 2025 [37, 38]. Subsequently, cases of FMD were detected in dairies in Slovakia beginning on March 20, 2025 [39]. This was the first occurrence of FMD in Hungary and Slovakia since 1973. Over the course of March and April, at least 10 more outbreak farms were detected with the last case detected in Slovakia on April 4th and Hungary's last case on April 17th. In Hungary, 3,928 domestic cattle were affected, with 44 case mortalities. In total 8,422 cattle were culled and disposed of as a result of control efforts [37]. In Slovakia, 7,490 animals were culled and disposed of to control the outbreak. The control efforts in Hungary and Slovakia prioritized disinfection, suppressive vaccination, movement control, and depopulation of affected livestock.

The Hungarian animal movement restrictions were lifted on June 6, 2025. WOAHP restored Hungary's FMD-free status on September 10, 2025 and Slovakia's on October 31, 2025 [40]. The outbreak virus was determined to be serotype O, but genetically different from the German outbreak strain. This virus in Hungary-Slovakia shared 98-99% similarity to a virus from an outbreak in Pakistan in 2017/2018 [41]. Estimated cost analyses are ongoing.

Outbreaks are currently ongoing in Greece and Cyprus. Prior to the introductions in February and March of 2026 both countries were recognized as FMD free. The outbreaks have

primarily infected sheep and cattle [42]. Culling and disinfection have been implemented thus far.

There have been other large outbreaks of FMD in countries that do not maintain official recognition of FMD freedom. This includes, but is not limited to, The Republic of Korea, China, and many countries in Africa. The Republic of Korea specifically, has had multiple incursions of FMD that have proven to be very costly in control and export market losses. In one example, the Republic of Korea saw three outbreaks in 2010 and 2011 that were estimated to have cost 26.2 billion (approx. 18 million USD), 101.5 billion (approx. 67 million USD), and 2,044.5 billion Korean Won (1.4 billion USD) respectively [43].

Despite the physical distance of the US to the current and past outbreaks, the global movement of animals, humans, and animal products make the introduction of virus to the US possible at any time. The virus is capable of surviving on a wide variety of surfaces and substrates including feed and imported meats, legal or illegal for extended periods of time [44, 45].

United States Response Plan

The US and other FMD-free countries such as Australia and Canada have similar response plan documents [46, 47]. Implementation specifics vary across plans, but they all include goals of enhancing biosecurity and culling animals quickly to control the outbreak.

The USDA's "play-book" for FMD response is referred to as "The Red Book." The Red Book is formally named the Foot-and-Mouth Disease Response Plan and has been developed by the USDA-APHIS-VS as part of the Foreign Animal Disease Preparedness and Response Plan (FAD-PRP). Within this plan, the USDA will be the coordinating agency, but many other state, tribal, and federal agencies will be needed to complete FMD response tasks [48].

When a potential case of FMD is suspected by a practitioner in the field, the state animal health official office should be called to activate a foreign animal disease investigation. They will most likely dispatch a certified Foreign Animal Disease Diagnostician (FADD) to collect and begin a chain of custody for the official samples. The FADD will collect duplicate samples and submit one sample set to the nearest laboratory approved for FMD preliminary testing. The second sample set will be sent to the Foreign Animal Disease Diagnostic Laboratory (FADDL) on Plum Island or in Manhattan, KS for confirmation and, if positive, virus typing.

If a presumptive positive diagnosis is made in the US, there will likely be several events that occur in the first 72 hours. First, the state animal health official has the ability to place the suspect premises under quarantine and hold orders based on their level of suspicion for FMD [48]. For high priority/high suspicion investigations, the officials may begin tracing all the movements on and off of the site in the last 28 days, they will also begin appraisal of the animals on the infected site, and depopulation planning [48]. These events may occur simultaneously with the samples being shipped and tested.

Upon the receipt of a confirmed positive test, herd depopulation will begin and the entire US should be prepared for movement standstill of 24 to 72 hours duration. During the movement standstill, traces and further investigation will continue and, at the end of the 72 hours the USDA expects to have a more complete understanding of the scope of the outbreak to guide the specific response plan. The specific plan may include further culling of animals and other control measures. As soon as the virus is typed, a matching strain will be selected from the National Animal Vaccine and Veterinary Countermeasures Bank to begin vaccine production so that stocks of vaccine are ready as soon as possible if a decision is made to vaccinate. For more details on specific response actions, readers are directed to the Red Book [52], the FMD

Response Ready Reference Guide – Understanding Response Strategies [49], and the Classification of Phases and Types of an FMD Outbreak [50].

Biosecurity and Personnel Considerations

FMD is highly contagious, requiring relatively few virus particles to infect a naïve animal. The virus can spread through direct contacts, short and long-distance airborne spread, and via fomites including humans, trucks and equipment, rodents, and birds [15, 20]. The potential for fomite spread is a critical consideration for veterinarians that may be called to examine sick animals. In the 1967-69 outbreak in Great Britain, 6 of 51 new cases were attributed to contaminated Veterinary Surgeons and 4 linked to other persons [51]. The use of personal protective equipment and proper decontamination between farm visits should always be utilized, but especially when a potential case of FMD has been seen [52].

Biosecurity recommendations are detailed in the “Secure Food Supply” plans that have been developed by collaborating veterinarians, industry representatives, and state and federal regulators to assist producers, veterinarians, and animal care takers in planning for disease events and protecting business continuity during a foreign animal disease outbreak [53]. Specific plans have been developed for each commodity group including the Secure Beef Supply (SBS) plan [10], Secure Milk Supply (SMS) plan [54], Secure Sheep and Wool Supply plan, [55] and Secure Pork Supply (SPS) plan [56]. These plans have resources tailored to each classification of animal production and have unique recommendations to fit the various subtypes within each production type. All of the plans have specific recommendations for implementing enhanced biosecurity to prevent FMD from entering farms, active monitoring of animals for early disease detection, and animal or product movement permitting guidance. The elements of these plans can also be readily extrapolated to help control and prevent other endemic or foreign animal diseases.

In the event of an outbreak, the demand for veterinarian labor will increase dramatically. Private veterinarians may be called to assist the control efforts if federal, state, and tribal resources are exhausted. Veterinarians will need to balance maintaining farm biosecurity with also ensuring animals continue to receive veterinary care as needed. The use of personal protective equipment (PPE) paired with personal hygiene, including showering and handwashing, has been demonstrated to be efficacious in preventing disease transmission [57-59]. It will be important that personnel not travel between known infected and unknown or non-infected farms. If travel between infected premises and unknown or non-infected premises is required, the current Red Book recommends, in addition to the use of extensive biosecurity and personal hygiene, that personnel wait a period of time (typically 24 to 72 hours, specific guidance will be given based on the outbreak behavior) [48]. Ultimately, veterinarians and responders must adhere to the guidance given by officials during the outbreak.

Conclusion

Practitioner vigilance is critical for timely detection of disease outbreaks in the US. The rapid identification of suspicious clinical signs and reporting to the state animal health officials along with a plan of action for veterinarians, staff, and clients will be critical in minimizing the impacts of an FMD outbreak. The guidance provided by The Red Book and within the Secure Food Supply plans is publicly available to producers and practitioners and should be utilized in making disease management plans. Veterinarians are a critical source of preparedness information for livestock producers.

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Figures

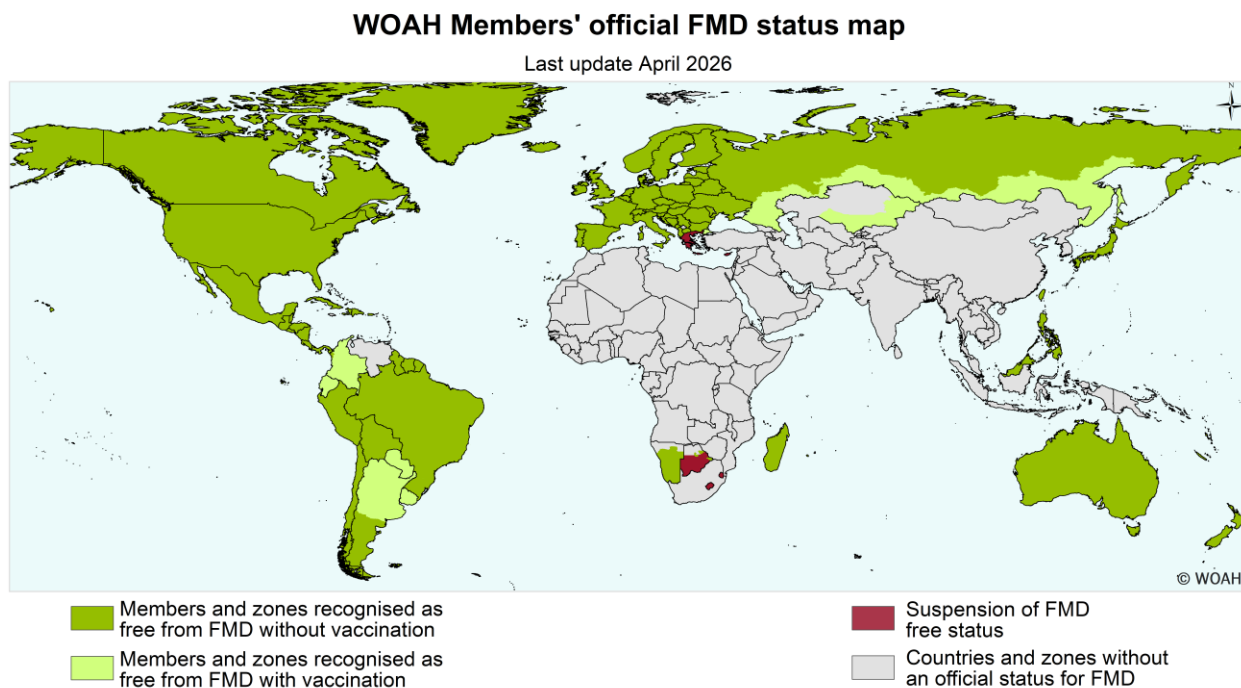


Figure 1.1: World Organisation for Animal Health Members' official FMD status map.

Source: [World Organisation for Animal Health (WOAH)] (2026). – [Foot and mouth disease <https://www.woah.org/en/disease/foot-and-mouth-disease/#ui-id-2>]. Reproduced with permission.

Tables

Outbreak Country	Start of Outbreak	Return to FMD Freedom	Primary Species	Number of animals impacted	Cost	Control Measures
United Kingdom	2001 (Feb)	2001 (Sept)	Cattle, sheep	6 million animals depopulated	6.8 billion USD	Stamping out, movement control
Uruguay	2001	2003	Cattle	2.9 million animals on case farms	FMD Emergency Recovery Project bank loan of 24 million USD	Stamping out, vaccination
Germany	2025 (Jan)	2025 (Apr)	Water buffalo	14 water buffalo 170 pigs	1.2 billion USD	Stamping out
Hungary and Slovakia	2025 (Mar)	2025 (Sept/Oct)	Cattle	Hungary: 8,400 animals culled Slovakia: 7,450 animals culled	Ongoing	Disinfection, vaccination, culling, movement control
Greece and Cyprus	2026 (Mar)	Ongoing	Sheep and cattle	Ongoing	Ongoing	Culling and disinfection

Table 1.1: Summary of selected global outbreaks.

Not an inclusive list of all FMD outbreaks in free countries.

Chapter 2 - A condensed review of Foot-and-Mouth Disease research for the United States mixed-animal veterinary practitioner.

MaRyka R. Smith¹, Christy J. Hanthorn¹, Sara McReynolds², Michael W. Sanderson¹

¹Center for Outcomes Research and Epidemiology, College of Veterinary Medicine, Kansas
State University, Manhattan, Kansas 66506, United States of America

²Kansas Department of Agriculture, Manhattan, Kansas 66506, United States of America

Abstract

The introduction of Foot-and-Mouth Disease (FMD) to the United States (US) would potentially devastate the susceptible livestock population and the economy. FMD is a highly contagious disease of cloven-hooved animals that can spread rapidly between animals and farms. In the US, veterinarians are a common source of information for producers on animal health topics. Thus, veterinarians should have a baseline knowledge of FMD and its characteristics. This knowledge includes the basics of where FMD research is conducted, the research methods, and the research results. In the US, live-FMD virus research is legally restricted to a single, high-containment laboratory, approved by the USDA Secretary. Researchers in high-containment are investigating FMD transmission, pathogenesis, biosecurity, vaccination and more. Field-based research in endemic countries can also improve our knowledge of FMD transmission dynamics and mitigation strategies. Computer-based mathematical models are developed from laboratory and field research findings. The models are then used to simulate FMD behavior under various conditions, including outbreak control and response. The results of these research efforts shape FMD control policies that affect veterinarians and their clients in the event of an outbreak. The objective of this article is to update veterinarians on the recent developments in FMD research in a way that is meaningful to food-animal or mixed-animal practitioners. The research topics

covered include FMD transmission and pathogenesis, biosecurity, disinfection, vaccinology, computer simulation models, and observational studies.

Introduction

The United States (US) is currently free without vaccination from Foot and Mouth Disease (FMD). FMD is a highly contagious disease of cloven-hooved animals that can spread very rapidly from animal to animal and farm to farm. Animals infected with FMD may be infectious to others within 2 to 3 days [1]. Infected animals may even be infectious before the development of clinical signs [1]. FMD introduction into the US remains a constant threat, as international travel and trade could bring the virus from endemic areas of the world.

If federal, state, and tribal resources are exhausted, food-animal and mixed-animal practitioners may be recruited to perform a crucial role in outbreak control and response by aiding in animal health procedures. Prior to an outbreak, veterinarians are often the first line of defense in disease detection and serve as advisors to their clients in disease control and risk mitigation [2, 3]. Thus, veterinarians must maintain a baseline knowledge of current FMD research as it pertains to clinical settings.

The designation of FMD freedom without vaccination comes from the World Organisation for Animal Health (WOAH) and is critical for maintaining US export markets of FMD-susceptible animals and their products. The World Trade Organization (WTO) uses the WOAH disease designation standards for fair trade requirements. If FMD detection occurs in a free country, the country will immediately lose the WOAH designation of freedom and will likely lose export opportunities with free countries. This could lead to massive economic losses.

To return to freedom, the infected country must document sufficient surveillance testing to meet WOAH standards as defined in the Terrestrial Animal Health Code Chapter 8.8 [4]. Upon redesignation as FMD-free, the recovery of trade with other countries will likely take time to be re-established. The ability to quickly respond to and control the introduction of FMD in the

US will be critical to minimize the economic effects and facilitate rapid recovery from trade losses. The current US plans for response and return to freedom are the result of decades of FMD research in the US and globally.

The purpose of this article is to describe the recent developments in FMD research relevant to mixed-animal practitioners, including research findings regarding FMD transmission and pathogenesis, biosecurity, disinfection, vaccinology, computer simulation models, and observational studies.

Research Considerations and US Facilities

Given the US FMD-free status and the highly infectious nature of the disease, field research on FMD cannot be conducted in the US. To support the need for domestic FMD research, in 1948 the US Congress passed Law 496, authorizing the creation of the Plum Island Animal Disease Center (PIADC) [5]. The law also designated PIADC as the only site allowed to conduct FMD research, specifying that no research or transportation of FMD was to occur on the US mainland [5]. This remained the law until the United States Department of Agriculture (USDA) began construction on a new research facility, the National Bio and Agro Defense Facility (NBAF) in Manhattan, Kansas. To allow NBAF to become a functional laboratory for FMD research, a 2008 congressional amendment required the USDA Secretary to provide one research permit to the Department of Homeland Security for one facility to succeed PIADC in conducting FMD research on the mainland US [5]. The transition will occur when the NBAF is fully operational and all safety inspections have been completed. The legal requirement to conduct all live FMD virus work in containment and at one location limits the potential risk for virus release and exposure, but also limits the number of researchers who can investigate FMD.

The PIADC and NBAF have FMD research missions that are similar to high-containment laboratories in other developed countries. Many of the laboratories are connected through the WOAHP reference laboratory network, which serves to assist scientific, technical, and diagnostic demands for global animal diseases [6]. The Pirbright Institute in England, the Australian Centre for Disease Preparedness, and the National Centre for Foreign Animal Disease in Canada all conduct FMD research and are located on the mainland of their respective countries. These facilities, and the US labs, apply biosafety level 3 (BSL-3) safety and containment measures to contain FMD and prevent release. These measures include highly filtered exhaust air, effluent waste treatment and decontamination, and controlled destruction of organic waste via digester or incinerator. In comparison to biosafety level 2 (BSL-2) measures utilized in most state diagnostic laboratories, BSL-3 research is much more expensive.

Efforts to prepare the US for an FMD outbreak have been strengthened in a step-wise fashion over the years. In 1982, the US joined Canada and Mexico to develop the North American Foot and Mouth Disease Vaccine Bank (NAFMDVB) which supports vaccine needs for the three member countries [7]. To support the speed and efficacy of domestic response efforts, in 2004, Homeland Security Presidential Directive 9 established the National Veterinary Stockpile (NVS) that can deploy countermeasures for many animal diseases, including FMD [8]. The stockpile contains personal protective equipment (PPE) for responders, testing supplies, and other equipment. In 2018, Congress directed APHIS to improve domestic FMD vaccine preparation and established a National Animal Vaccine and Veterinary Countermeasures Bank to house a stockpile of FMD vaccine for the US [7]. This bank is in addition to the shared NAFMDVB as the US remains an active participant in the NAFMDVB. To support domestic novel vaccine development, NBAF was designed with a Biologics Development Module that can

aid the transition of research findings to the production of vaccines and diagnostics to contribute to the US stockpile [9]. There are additional vaccine banks for FMD and other diseases around the world that belong to various countries and organizations.

Introduction Risks and Pathways

There is a myriad of potential pathways through which FMD could be introduced and released within the US. Potential introduction could come from the importation of infected animals, humans or vehicles contaminated with the virus, contaminated animal feeds, or many other potential sources [10]. The mechanism of introduction could be from accidental carriage of virus from an endemic area or active outbreak, but the risk of FMD introduction as a bioterror act cannot readily be predicted, nor ignored.

The introduction via unprocessed, contaminated food products is of great concern, as travelers may not realize the risk posed by smuggling contraband or personal foods. The US maintains a list of countries and regions affected by FMD and heavily restricts importation of animal products [11]. However, complete identification of smuggled products cannot be guaranteed, and risks remain. One study that assessed introduction risk via imported cheeses used a quantitative risk analysis to evaluate the risk associated with importing cheese from countries with FMD, taking into account the viral reduction through pasteurization, pH changes during maturation, and aging processes. [12]. The results suggested that susceptible animals would need to consume several thousand kilograms of the imported cheese before an infectious dose was ingested [12]. The risk of infectious virus introduction to free countries by other foods, such as meat products, has limited empirical data, but one study found that the risk of live-virus introduction via bone-in-beef from countries that are FMD-free with vaccination is likely negligible [13].

The risk of importation of FMD via contaminated feeds is also an area of concern. In a recent study, the potential for FMDV introduction to the US via importation of animal feed was tested using Senecavirus A (SVA) as a surrogate for FMD [14]. SVA is in the same family as FMDV but does not have the same high-containment requirements for research [15]. The researchers inoculated 11 animal feed ingredients and products with SVA, then placed the ingredients in a chamber that simulated the environmental conditions of Trans-Pacific Travel. The environmental chamber simulated 7 days holding in Shanghai, 17 days on a cargo ship, 7 days in US customs in San Francisco, California 2 days of US highway travel to Des Moines, Iowa, and a final 3 more days in holding in Iowa. During the simulated 37 days of transport, the temperature and relative humidity in the environmental chamber was varied to represent the calculated conditions at each stage of transportation. The feeds inoculated with SVA maintained infectivity as shown by virus isolation assays and inoculation into naïve piglets. This study was limited by the use of a surrogate virus in place of FMD. A similar study was conducted with two strains of FMD virus, Type A (A24 Cruzeiro) and Type O (O/SKR/2010) inoculated onto pelleted pig feed and soybean meal and held at 4 or 20 degrees Celsius for 37 days [16]. After 37 days both strains were stable and recoverable in soybean meal held at 4 degrees Celsius but much less stable in the pelleted feed or at 20 degrees Celsius. In addition to the risk of introduction, the consumption of contaminated feed has also been assessed. One study estimated the potential minimum infectious dose required for FMD infection in pigs consuming contaminated feed [16]. Researchers inoculated pelleted pig feed with various infectious doses of FMD Type A (A24 Cruzeiro) or Type O (O/SKR/2010) then offered the feed to fasted naïve pigs approximately 2 hours later. The feeding was offered in 3 100-gram samples over a 2 hour time period. When the infectious dose reached 10⁷ TCID₅₀ for the Type A virus or 10⁵ TCID₅₀

for the Type O virus, pigs developed FMD. These studies support that feed ingredients or feeds contaminated with FMD in an endemic country could pose and FMD risk after transportation and importation to the US.

Transmission and Pathogenesis

Live animal studies in controlled laboratory settings are critical for understanding targeted aspects of viral pathogenesis and animal response. They involve an artificial environment, are limited in the number of animals included in studies and as such may be limited in application to the field. They are however a key foundation of research and understanding of FMD.

Research into the pathogenesis of FMD virus has shown that the primary site of FMD viral infection occurs in the epithelial cells that line the mucosa of the oropharynx or the nasopharynx [17]. Cattle tend to be more susceptible via inhalation as compared to swine that are more susceptible via oral inoculation. As the virus replicates and animals begin to shed virus they may experience an acute febrile period [18]. The animals may then develop clinical signs and lesions that shed virus for approximately 7 to 14 days. Most animals will then clear FMD from all tissues within approximately 4 weeks of the initial infection [17]. Some animals however, may remain persistently infected with FMD virus for several months to years after the initial infection [19]. It is estimated that up to 50% of animals that survive the disease may remain as carriers, but in laboratory studies, they have not been shown to be a source of virus transmission to others [19]. There is also not a clear consensus in the literature on the risk factors that result in carrier status of animals. The carrier status remains a controversial component of return to FMD freedom after an outbreak.

PIADC conducts studies on the transmission and disease progression in sheep, cattle, and pigs. A current focus of research at PIADC centers on determining the ability of cattle and pigs to shed infectious virus prior to developing clinical signs [1, 20]. In these experiments, inoculated animals are exposed to new naïve animals at specific time points post-inoculation to ascertain when the inoculated animals become infectious to others. In one study, inoculated, but preclinical, cattle were housed with naïve animals from 24 to 48 and 48 to 72 hours after inoculation. The inoculated cattle did not show clinical signs of FMD until 96 hours after inoculation. The contact exposed naïve animals had detectable FMD RNA (nasal swab or serum) within 24 hours of exposure to the preclinical cattle, and 3 of 4 exposed animals later developed clinical signs 96 to 120 hours after exposure. This indicated that the inoculated, pre-clinical cattle were able to spread the virus. This finding supports the need for rapid detection of infected and at-risk cattle to interrupt the transmission of FMD.

Another research topic of concern centers on FMD virus genetics and the ability of the virus to mutate or combine genetic materials from multiple strains of the virus. FMD uses RNA to encode its genetic material and does not have a strong mechanism for “proofreading” during replication, which results in high mutation rates [21]. In the study, researchers first inoculated cattle with either a FMD type A or type O virus then 21 days later inoculated the same animals with the alternate virus type. [22]. The genome of the viruses recovered at the end of the study possessed changes that were unique from the original viruses. This indicated that the viruses were able to exchange genetic material during the co-infection period. The researchers also observed clinical signs in the inoculated cattle at both the initial virus inoculation and following the second virus inoculation for both FMD strains, indicating that the animals did not develop cross protective immunity following the 1st virus type inoculation. The potential for FMD

genetic changes highlights the difficulty in matching the virus with the vaccine being deployed for outbreak control. Periodic genetic re-evaluation of the outbreak strains may be needed to facilitate continued vaccine efficacy.

Biosecurity, Disinfection, and Virus Survival

Biosecurity is widely considered an important aspect of FMD prevention and control [23-25]. Biosecurity has been defined as “the implementation of a segregation, hygiene, or management procedure (excluding medically effective feed additives and preventive/curative treatment of animals) that specifically aims at reducing the probability of the introduction, establishment, survival, or spread of any potential pathogen to, within, or from a farm, operation or geographical area” [26].

Humans, including veterinarians, may be a source of viral spread between farms and as such should be a focus of biosecurity efforts. In the 1967-69 United Kingdom (UK) outbreak there were documented cases of disease spread by veterinarians [27]. Similarly, in the 2002 Korean outbreak, the only epidemiological link between two infected farms was a worker who participated in depopulation at one site and then traveled to a site that was subsequently detected as positive presumably due to the contamination on his clothes or vehicle [28].

Two studies conducted at PIADC have focused on biosecurity interventions for research workers [29, 30]. In these two studies, the researchers handled infected animals then implemented an intervention: hand washing and changing outerwear or complete shower and new clothing prior to entering a room with susceptible animals. Compared to a “direct exposure” group where no biosecurity measures were implemented the handwashing and new outwear group resulted in fewer animals developing disease but 3 out of 5 sheep still became clinically

infected. In the complete shower and new clothing group, no animals became infected. These results highlight the potential value of properly implemented biosecurity measures.

FMD is highly unstable at pH extremes, both acidic and basic. This characteristic can be exploited in the development of disinfection protocols. Disinfection aims to decrease pathogen loads below infectious levels. Research by Hong, et al. in 2015 applied this characteristic in assessing disinfectants for FMD in cold temperatures. They assessed citric acid and sodium carbonate as disinfectants combined with de-icing solutions to aid the deployment of disinfectants during winter [31]. Citric acid diluted in ethyl alcohol was found to be an effective disinfectant for FMD virus in liquid solution that resisted freezing at negative 20 degrees Celsius while sodium carbonate was less reliable at below-freezing temperatures.

The USDA has published a list of disinfectants that are approved for use against FMD [32]. The list includes common, commercially-available products such as Virkon S® and INTERVENTION Farm Animal Care Disinfectant Cleaner & Deodorizer®. The list of approved disinfectants also allows for exemptions to use sodium hypochlorite (bleach) and acetic acid (vinegar) preparations in the event of commercial product shortage. [31].

The survival of FMD virus on porous surfaces and in organic material is also a potential source of virus transmission. Surfaces such as dirt pen floors and bedding cannot be disinfected using the commercial chemical preparations. A recent study assessed virus survival in various US soil samples and found that temperature is a strong predictor of virus survival with the exact composition of the soil being less impactful [33]. Their results suggested that areas that maintain temperatures at or below 25 degrees Celsius should be closely monitored after depopulation efforts [33]. Others have reviewed the survival of FMD in various environments and surfaces and have found that virus could survive for weeks on straw and hay [34].

Vaccinology

There are 7 immunologically distinct serotypes of FMD: O, A, C, Asia-1, South African Territory (SAT) 1, SAT 2 and SAT 3. These serotypes are further divided into over 60 subtypes with little to no cross protection among the subtypes. In order for a deployed vaccine to be protective it must stimulate a strong immune response and be an antigenic match to the field virus [35]. Effective use of preventive vaccines prior to an outbreak requires knowledge of the virus type circulating or that is going to be introduced in order to provide protection. As such, preventive vaccination is not practiced unless the subtype circulating is known in endemic countries or the subtype likely introduced can be confidently predicted.

An antigen-matched vaccine deployed in the face of an outbreak can decrease the likelihood of infection in exposed animals [36]. In modelling studies, the benefits of deploying an antigen-matched vaccine in the face of an outbreak can vary based on the speed of application and the outbreak behavior [37, 38]. Vaccine deployment does potentially come at a cost at the conclusion of the outbreak as vaccinated animals that remain in a naïve population may become infected and shed live-virus without development of clinical signs potentially propagating the disease without detection [17]. Thus, the desire for countries to achieve FMD freedom without vaccination.

Vaccines should be formulated to allow for the differentiation of vaccinated animals from those that were naturally infected. Vaccines that induce an immune response that is different from natural immunity are called DIVA vaccines (Differentiating Infected from Vaccinated Animals). Most commonly, DIVA vaccines consist of inactivated virus solutions that are purified to remove the FMD non-structural proteins (NSP) so that the resulting antibody response does not include NSP antibodies allowing differentiation from natural infection [39].

The ability to differentiate vaccinated from naturally infected animals is an important characteristic to aid in surveillance and eradication efforts and re-establishment of disease freedom following a vaccination effort.

Vaccine research is ongoing to develop more effective vaccines including using vectored platforms including adenovirus vectors, vesicular stomatitis vectors, and salmonella bacteria vectors [40]. These vaccines incorporate a specific FMD antigenic component to the vector's genome and maintain the DIVA compatibility of the vaccine

Computer Modeling

One of the most pressing issues for countries that are free from FMD is to identify effective ways to manage an outbreak, should one occur. While important data can be gathered from studies in infected countries or controlled lab settings, neither is directly applicable to the production system of an FMD-free country. Mathematical models of disease transmission within herds or between herds are the only way to research and estimate the impact of an outbreak in a population and explore multiple control methods.

There are many different types of models that are used to estimate the behavior FMD outbreaks in different countries and production systems. Models may be focused on either transmission between animals within a herd, or transmission between herds in a state or country. Table 2.1 contains examples of different model types and definitions.

Models being used for FMD outbreak research are generally stochastic and spatially explicit. The parameters that define the system are optimized for the research question being asked and then a specific parameter in disease control is modulated and outbreak outcomes compared. The economic impacts of an outbreak can then be assessed by assigning costs to the control measures (e.g., surveillance, tracing, depopulation, and vaccination) as well as the lost

trade or loss of animals. The ultimate goal for disease modelling is to predict a control policy that provides robust disease control, acceptable business continuity for producers and with minimal costs, both direct control costs and impact on the livestock industry.

Models were used extensively during the 2001 UK outbreak to test potential control strategies based on the historical behavior of the outbreak [41, 42]. They were parameterized quickly with the limited data but informed decisions during the outbreak. The model outcomes were used to direct changes in culling and other FMD control policies by comparing the potential progression of the outbreak. The models did not specifically predict the next infected farm but rather the wider impacts of control policy implementation.

Following the outbreak, researchers used the complete outbreak data sets to assess models for accuracy [43]. For example, researchers evaluating the model accuracy found that the models represented the overall outbreak well but did not predict the risk of infection for individual farms [43]. As such, the models are likely a good representation of the range of outbreaks possible and the potential impact of control measures. The models have since been used to test other control measures retrospectively and compare outbreak results [44, 45].

Various models of FMD outbreaks in the US have been developed as well. The models range from single state or regional use to those that incorporate the entire nation and can address many aspects of disease control including culling, vaccination, and animal tracing. These models are parameterized using laboratory data on virus behavior and USDA data on the national livestock population, livestock movements, and the livestock production system.

Many of the models focus on between-herd disease spread to capture the regional or national outcomes of the outbreak. A model parameterized for the US state of Pennsylvania supported that movement restriction and depopulation of infected premises and dangerous

contacts could be sufficient to control a geographically small outbreak [46]. Other researchers have utilized California as the site of simulated FMD introduction and found that early detection [47], vaccination, and slaughter [48] decreased the predicted outbreak size. Models that focused on simulating improved animal disease traceability systems have suggested that improving the speed and accuracy of contact tracing could decrease outbreak impacts at regional and national scales [49-51]. Vaccination has also been found to be beneficial with dependence on what farm types are targeted for vaccination and how the vaccine is allocated between states [37, 52]. The results of these highlighted studies and many other modeling studies can be incorporated into the disease planning protocols or consulting during a disease outbreak to make predictions for the development of the outbreak.

There have also been models developed for within-herd spread that can be applied to the US production system [53]. Researchers that have focused on within-herd spread models have looked at methods to control the spread of FMD in large herds such as feedlots [53-55]. The researchers in both studies found that control efforts in feedlots were often ineffective and not practical to implement. The feasibility of depopulation of a feedlot coupled with the likelihood for negative public perception also makes the practice unlikely to be employed [56]. These large herds represent unique challenges for disease control as the logistical challenges for vaccination and depopulation can be greater than those for smaller herds or small ruminants.

FMD can spread from herd to herd under appropriate meteorological conditions. The weather risk across the US has been estimated and the most favorable conditions for FMD airborne spread were in the Midwest during the winter season [57]. Computer models have also been used to predict the likelihood windborne FMD spread from US beef feedlots in Kansas and Iowa under various environmental conditions [58]. The risk of infection increased with

appropriate weather conditions, increased proximity to the feedlot and with the size of the feedlot due to the potential for an increased number of shedding cattle. Under worst-case conditions the risk of infection could extend beyond the 10 km zones that the USDA currently plans to utilize for outbreak control [58]. Estimates of aerosol transmission risk based on real-time meteorological conditions could be utilized in an outbreak to target surveillance to the farms at highest risk.

While mathematical models can never fully represent every intricate detail of real-world systems, they can be useful for testing “what if” scenarios and developing a starting point for disease control in an outbreak.

Observational and Review Research

Observational research in FMD endemic regions or areas of an active FMD outbreak are an important source of data on FMD behavior. The strength of observational research is that the data comes from real-world situations where the infection risk and prevention efforts can interact in real-time. However, the collection of data during an outbreak is very difficult. Ascertaining the true exposure status of a farm as compared to the efficacy of a mitigation strategy cannot be fully known. In other words, if a farm does not become infected, is it due to the success of prevention strategies or in a lack of virus exposure? If a farm does become infected, it is also difficult to determine if it was due to overwhelming exposure, prevention failure, or failure to implement the prevention correctly. These limitations in data reliability can contribute to possible confounding variables and bias in the results.

The results of data collected in production systems that are substantially different than the US also make the outcomes difficult to apply. A robust way to summarize and interpret the findings of a wide-range research reports is to conduct a systematic review of the literature [59].

Systematic review research can be helpful in identifying consensus and knowledge gaps in the scientific literature around a topic but may also be prone to potential biases based on the quality of the review process and the reporting literatures.

Recent scoping reviews on the use of biosecurity measures in farms and auction markets in the face of an FMD outbreak are available [60, 61]. Smith, et. al (2026) found 20 reports that contained FMD biosecurity at the farm level [60]. Hanthorn and Sanderson (2026) found 8 reports that described FMD risks and mitigation efforts at auction markets [61]. In both reviews, most of the reports were vague in their descriptions of biosecurity measures and mitigation efforts implemented and none of the reported measures had clear consensus on actionable FMD mitigation.

Another review evaluated biosecurity measures more broadly for human fomite transmission of any animal disease and found that the most important recommendation for preventing transmission of disease was personal hygiene such as handwashing, and changing clothes and boots [62].

Other reviews can be unstructured and have value in identifying the current knowledge gaps. An example of such a review is Stenfeldt, et. al, who focused on pathogenesis of FMD Virus and other molecular study advancements [63]. They reported vast improvements in our understanding of how the virus moves through an animal in the initial phases of infection primarily in cattle and pigs but there is a dearth of knowledge in the virus behavior in other species, especially wildlife [63].

Conclusion

An introduction of FMD to the US would be devastating to the US livestock industry and food-animal and mixed-animal practitioners are integral as the first line of defense in ensuring

early detection and support of control efforts. Additionally, being familiar with the current best-practices for biosecurity, disease prevention, and disease control will aid practitioners in assisting producers with outbreak preparation efforts [64]. Lastly, awareness of the latest FMD research can be helpful in answering questions regarding how to prevent disease and respond if an outbreak occurs.

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Tables

Table 2.1: Disease Modeling Terminology

Table 1: Disease Modelling Terminology		
Model Terminology	Definition	Example Use
Mathematical Model	A representation of a real-world system using computer processes and parameters to understand or predict the behavior of the system.	A model that simulates FMD spread. In contrast to a statistical model that evaluates real-world data for patterns of significance.
Parameters	The range of values that describe a specific component of the model. The parameters that define the behavior of the disease include the time for incubation, infectious periods and infectivity level, and numerous other components. The parameters that define the production system includes but is not limited to; movement rates, tracing speed and accuracy, and the efficacy of biosecurity measures.	For example, a parameter may define the probability that a farm makes a contact with another farm.
Stochastic Model	A model that incorporates randomness into the outcomes. A random number generator selects the specific value from the parameter range used for each model component. These models are run for multiple iterations to estimate the range of behavior of the system.	A model has probabilities that a farm will contact another farm and that the contact will result in disease. Each contact will have an independent outcome in each model iteration.
Deterministic model	A model that uses fixed values for the parameters to generate the expected outcome. No randomness is incorporated.	A model that estimates a single expected value, behavior, or equilibria of a disease outbreak given the fixed inputs.

Spatially-explicit model	Within the model, each farm has a specific geolocation on a map and the distance between farms are considered in model outcomes	A model that captures the probability of airborne spread from one farm to another based on their physical distance or farm contacts based on physical distance.
State-Transition Model	A model that describes the specific transition from one disease phase to another.	It is explicitly modelled when a farm moves from susceptible to infected to infectious to recovered or depopulated
Within herd model	A model that simulates the spread of disease from animal to animal in one herd or group	A model that simulates how FMD might move through a large feedlot.

Chapter 3 - A scoping review of farm-level biosecurity measure effectiveness against Foot-and-Mouth Disease to inform planning and preparedness efforts in the United States

MaRyka R. Smith¹, Christy J. Hanthorn¹, Michael W. Sanderson¹

¹Center for Outcomes Research and Epidemiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506, United States of America

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Abstract

Introduction: Foot-and-Mouth Disease (FMD) is a global threat to cloven-hooved livestock and wildlife species. The causative agent, Foot-and-Mouth Disease Virus (FMDV) can be transmitted via aerosols, droplets, and fomites including humans. This makes the need for biosecurity measures that interrupt FMDV transmission during an outbreak critical. However, quantitative data supporting the effectiveness of many recommended biosecurity measures is limited. The purpose of this scoping review was to identify peer-reviewed literature that described or evaluated biosecurity practices to mitigate FMD risk at the farm level in order to inform planning and preparedness efforts in the United States.

Methods: A systematic search of four databases identified 3,153 unique records. Included reports had to be original, peer-reviewed research, published in English, include information about a biosecurity measure applied at the farm level to mitigate FMD risk, and address at least one major domestic livestock species in the United States (cattle, sheep, goat, swine, American bison). Reports describing results generated entirely in-silico or with surrogate viruses were not included.

Results: Twenty-two reports were included in this review describing data from 16 (one unreported) unique countries published between 1998 and 2024. Two reports describing experimental studies evaluated handwashing, showering, and changing outerwear, which were found to have variable efficacy. The use of biosecurity measures applied to livestock and their products, personnel and visitors, vehicles and fomites, and disinfection were identified from 20 field reports and observational studies. No biosecurity measures that appeared in more than one report were identified as being consistently effective at mitigating disease risk in a field setting.

Discussion: The inconsistent and limited evidence to support the effectiveness of specific biosecurity measures in field settings identified through this review makes meta-analysis infeasible at this time and hampers the ability of animal health officials and animal caretakers to plan for and respond appropriately during an FMD outbreak. Improved reporting of biosecurity measure implementation would improve our ability to assess their effectiveness and develop evidence-based biosecurity recommendations for FMD preparedness and response plans.

Introduction

Foot-and-mouth disease (FMD) is a viral vesicular disease that impacts cloven-hooved livestock in many areas of the world [1]. The global annual costs of FMD have been estimated at \$6.5 to 21 billion in endemic regions and an additional \$1.5 billion or more in free countries and zones [2]. FMD is highly contagious and easily transmissible between farms and among animals. The virus is shed in all bodily excretions and secretions with many animals becoming infectious prior to the onset of clinical signs [3]. The virus can also be spread via aerosolized particles and on fomites such as humans and vehicles [4]. The ease of transmission, highly contagious nature, and global cost of FMD make effective biosecurity measures a critical, albeit difficult to implement, component in controlling an outbreak.

Biosecurity measures are, “the implementation of a segregation, hygiene, or management procedure (excluding medically effective feed additives and preventive/curative treatment of animals) that specifically aims at reducing the probability of the introduction, establishment, survival, or spread of any potential pathogen to, within, or from a farm, operation or geographical area” [5]. Globally, producers, animal health officials, and veterinarians utilize many different biosecurity measures collectively to control outbreaks of FMD; however, quantitative data on the effectiveness, or ineffectiveness, of individual biosecurity measures in the scientific literature is lacking. Limited opportunities exist to evaluate biosecurity measure effectiveness during FMD outbreaks, and conducting research on FMD in countries that are free from the disease is challenging. In many free countries, including the United States (U.S.), FMD research is limited to high-containment, national laboratory facilities. Thus, researchers must rely on original research from FMD endemic or outbreak countries and reviews of global data to gather field-tested information that can be used to inform FMD response plans in the U.S.

The U.S. has been free from FMD since 1929, but the volume of global trade and livestock movement heighten the concern of a potential foreign animal disease re-introduction, as has been seen with recent FMD introductions to countries that had previously eradicated the disease [1, 6]. In the event of an FMD incursion, the current United States Department of Agriculture (USDA) plans include the likely use of controlled movement orders and standstills that would temporarily halt movement of susceptible livestock and fomites [7]. These orders will most likely originate from federal animal health officials and be implemented at various levels of jurisdiction (state, local) depending on the location, type, and phase of the outbreak [8]. The cessation of animal movement, even temporarily, could prevent further FMD spread but would also negatively impact the continuity of business for producers whose livestock are not infected with FMD. To address this negative impact, methods to allow permitted or low-risk movement of animals are under development [9]. The Secure Beef Supply (SBS) plan has been developed to aid in the continuity of business in the face of an outbreak through the use of enhanced biosecurity and animal monitoring. The current SBS plan recommends identifying a Biosecurity Manager, actively monitoring animals for clinical signs of disease, creating a line of separation with access points to the animal areas, and implementing enhanced biosecurity measures, such as cleaning and disinfection stations [10]. In other developed countries, including (but not limited to) Australia and Canada, the plans for response to and control of FMD outbreaks include similar elements of biosecurity measure implementation [11, 12]. The recommended biosecurity measures in these plans are best practices for decreasing the likelihood of FMD introduction and spread among farms, but data on the effectiveness of any specific procedure is sparse in peer-reviewed literature sources. To address this knowledge gap, a scoping review was chosen as the preferred method to gather and summarize the breadth of information on biosecurity measure

effectiveness in endemic or outbreak settings. To the authors' knowledge, this review is the first of its kind to comprehensively summarize data on individual biosecurity measure effectiveness in decreasing FMD risk.

The aim of this scoping review was to identify, from peer-reviewed literature, biosecurity measures that have been described and/or evaluated for effectiveness in preventing or controlling FMD introduction or spread at the farm or animal level in order to inform U.S. planning and preparedness efforts. Identifying and addressing the data scarcity regarding estimates of biosecurity measure effectiveness at the farm-level can help researchers plan targeted research and develop more accurate disease spread models, U.S. animal health officials improve plans and policies, and veterinarians and producers to make informed decisions to prevent and control FMD. Such information could also be utilized beyond the U.S. to aid FMD response plans globally. Further, the ability to estimate the potential economic value of the recommended biosecurity measures would be informed by data on their effectiveness.

Methods

This scoping review was conducted according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) [13]. The objective was developed by group discussion as part of a larger review project; therefore, the expanded scope is reflected in the search strategy. A formal protocol for this scoping review was not developed *a priori*.

Information Sources and Search Strategy

The search strategy was developed by the reviewers in collaboration with a librarian within Kansas State University's College of Veterinary Medicine. Inclusion of the phrase "foot and mouth", but not "hand foot and mouth," in the title or abstract was required as well as at

least one of the variations of topic keywords relevant to biosecurity or the wider search being conducted by the reviewers (e.g., surveillance, transmission). The search was completed in two steps with an initial search in 2021 and an update in 2024. Detailed search strategies and results are presented in Table 3.1. Both the initial and updated searches were limited to records available in English but were not limited by date.

For the initial search performed on September 29, 2021, authors utilized CAB Abstracts (via CAB Direct), Scopus, Web of Science, and PubMed databases. These databases were selected based on the findings in Grindlay, et al. (2012) and their availability to the reviewers via the Kansas State University library system [14]. For the search update conducted on June 5, 2024, authors utilized PubMed, Scopus, and Web of Science. The same search strings were used for each database for both the original and updated search; however, the search algorithm in CAB was no longer compatible with the original search string; therefore, an updated search in CAB was not included. The records identified with the 2024 search update were deduplicated against all records returned by the 2021 search. Hand searching of literature was not utilized for this review.

Screening Process

The records returned by the databases were exported as RIS files and imported to R statistical software [15]. The package RevTools was then used to identify and remove duplicate records based on the DOI number and title [16]. The remaining records were imported to Zotero which identified and consolidated further duplicate records [17]. Resultant records were exported to Microsoft Excel for screening [18]. Titles and abstracts were screened in duplicate with one reviewer (MRS) screening all titles and abstracts and two other reviewers (CH, MWS) each screening half of the total titles and abstracts. Any disagreements on a specific record were

discussed between the two assigned reviewers and if an agreement was not reached, the third reviewer was consulted to achieve consensus. Following title and abstract screening, full-texts of reports were sought. All retrieved reports were screened following the same process of reviewing in duplicate. Both screening processes utilized a screening tool developed by the reviewers. The tool was piloted on a subset of records and reports for quality and agreement with adjustments being made as needed. Questions included in the screening tool were:

- 1) Is the record or report available in English?
- 2) Does the record or report describe Foot and Mouth Disease?
- 3) Is the report original work published in a peer-reviewed journal?
- 4) Does the report describe whole animal studies (in vitro studies excluded)?
- 5) Does the report describe outcomes for topics other than vaccination strategies or development, virus diagnostics, viral genetics, or immune response?
- 6) Is the data reported from non-simulated studies? (computer simulations or estimations excluded)
- 7) Does the report describe or evaluate a biosecurity measure applied at the farm level?
- 8) Does the report include outcomes for at least one of the U.S. domestic livestock species of interest (cattle, goats, sheep, swine, American bison)?

Screening questions could receive a “yes” or “no” answer. If the record or report received two “no” responses to any single question from both reviewers it was immediately excluded. If the record or report received a “yes” to all questions from both reviewers it was included in the next review step. The search update utilized the same tools as the original search and screening process.

Eligibility Criteria

To be included in this review, reports had to fulfill the screening criteria described above. Reports that only addressed wildlife or livestock species not common to the U.S. (e.g., African buffalo) were excluded in order to align with the aim of the review to inform U.S. planning and preparedness efforts. In-vitro studies, immunology studies, pathology studies (including challenge models), studies which utilized surrogate viruses, surveillance reports, and reports that utilized vaccination as the sole means of FMD control were excluded. Reports that only contained data from mathematical or simulation models were excluded. Authors needed to evaluate or describe biosecurity measures intended to be implemented at the farm level rather than measures implemented nationally, regionally, or off-site for a report to be included. Generalized biosecurity recommendations for livestock industries (such as for exhibition) were excluded. Biosecurity measures not included in this review were the utilization of vaccination or culling as the sole means of disease control and national or regional animal movement controls. No date or geographic location restrictions were applied to reports.

Data charting and synthesis

For all reports included in the review, data were charted by a single reviewer (MRS) and verified by a second reviewer (CH). Key data items were charted at the report level and are summarized in Table 3.2. Citation information, country and year(s) of data collection, animal species and use, and biosecurity measure descriptions were charted as reported by the authors. If available, biosecurity measure effectiveness was charted as reported by report authors, or if sufficient information was available, was summarized by reviewers. Biosecurity measures which were both evaluated and demonstrated to be efficacious or effective are presented separately from biosecurity measures that did not have data to support their effectiveness. Biosecurity

measures that were only described as being implemented and those that lacked data to demonstrate effectiveness were categorized by reviewers into: 1.) biosecurity measures for livestock and livestock product movement, 2.) biosecurity measures for personnel and visitors, 3.) biosecurity measures for fomites, and 4.) disinfection measures. Biosecurity measures for livestock and their products included management policies for susceptible livestock species of interest (e.g., isolation and quarantine) and their products (e.g., carcass, manure, and milk disposal). Biosecurity measures for personnel and visitors included personal protective equipment use and management policies regarding workers and/or visitors (e.g., access to animal areas). Biosecurity measures for fomites included management policies for vehicles (e.g., designated parking areas), non-livestock species management, and management strategies for other routes of indirect viral transmission. Disinfection measures included disinfection strategies for clothing, vehicles, and facilities to limit viral spread as reported by authors. Data are presented in tabular or text format.

Results

Selection of Sources of Evidence

Results of the two searches and screening processes are summarized in Figure 3.1. The 2021 search of the four databases returned 5,763 records. After 3,475 duplicate records were removed, 2,291 records were eligible for title and abstract screening. Following title and abstract screening, 103 reports were sought for full-text retrieval and further screening. Four reports could not be retrieved. Of the 99 reports evaluated for eligibility, 83 were excluded based on the criteria detailed in Figure 1. Sixteen reports met the eligibility criteria for inclusion in this review.

The 2024 search of three databases returned 5,264 records. Following deduplication, 861 records were eligible for title and abstract screening where 792 were excluded. The remaining 69 reports were sought for retrieval and further screening. All 69 reports were retrieved, and 6 met the eligibility criteria for inclusion in this review. A total of 22 reports identified from the two searches were charted.

Characteristics of Reports

Report characteristics are summarized in Table 3.3, including susceptible species (and use), country and year of data collection, and reference. The 22 included reports described FMD data collection between 1952 and 2022 from 16 countries, with one report not specifying the country of data collection. No reports were identified that addressed FMD biosecurity measures for American bison, but all other species of interest were represented. Reports that addressed FMD biosecurity measures for cattle were most common (n=18), followed by swine (n=8), sheep (n=6), and goats (n=3). Of the 18 reports with cattle in the study population, dairy cattle alone were included in 6 reports, beef cattle alone were included in 2 reports, beef and dairy cattle were included in 2 reports, and 8 reports did not specify the type of cattle. Reports included in the review were published in 12 different journals. The journals most frequently represented were *Preventative Veterinary Medicine* and *Frontiers in Veterinary Science* each with 4 included reports, and *Veterinary Record* and *Transboundary and Emerging Diseases* each with 3 included reports. No reports were identified where biosecurity measures were described with data demonstrating effectiveness, but two included reports described biosecurity measures with accompanying data to demonstrate efficacy. The remaining 20 included reports either simply described biosecurity measures implemented or had data that did not support the biosecurity measure's effectiveness.

Biosecurity Measures Demonstrated to be Efficacious

Two included reports experimentally evaluated the efficacy of biosecurity measures for preventing FMD transmission [19, 20]. Both reports describe studies conducted at the Plum Island Animal Disease Center (PIADC) in the United States. Readers are directed to the original reports for full study design and sample collection information. Both studies utilized FMD inoculated pigs as the source of infection and assessed transmission to sheep and/or pigs via human contacts. The researchers handled the pigs two days after inoculation, collecting various samples, then they moved to a room with five naïve animals of each species after implementing one of three levels of biosecurity measures. The first experimental group received no biosecurity intervention. Researchers directly contacted naïve animals after handling the infected animals, deemed “direct human exposure” by the authors. For the second group, researchers washed their hands and changed outerwear between animal rooms. For the third group, researchers completely changed their clothing and showered between animal rooms.

Amass et al. (2003) used the strain FMDV (O/UK/35/2001) which is known to infect both sheep and pigs [19]. In the direct human exposure group, all animals (5 pigs, 5 sheep) developed gross lesions consistent with FMD infection, and three of the five sheep seroconverted. In the hand washing and new outerwear group, three out of five sheep developed gross lesions, and three out of five sheep seroconverted, but none of the pigs (0/5) showed signs of clinical disease or seroconverted by the end of the study. In the shower and new outerwear group, none of the animals (0/5 pigs, 0/5 sheep) developed gross lesions or seroconverted.

Amass et al. (2004) used the FMDV (O/TAW/97) strain, which is known to infect pigs but not sheep, therefore only pigs were used to evaluate the biosecurity measures implemented in this study [20]. In the direct human exposure group, all five of the pigs developed gross lesions

consistent with FMD infection, and one of the pigs developed IgM antibodies. None of the pigs in either the handwashing and clean outerwear group (0/5) or the shower and clean outerwear group (0/5) developed gross lesions or seroconverted.

Other Implemented Biosecurity Measures

Twenty reports described biosecurity measures that were implemented on farms specifically for FMD prevention or control, but the authors either did not evaluate the biosecurity measure for effectiveness or provided data that indicated the biosecurity measure was not effective. Biosecurity measures for livestock and their products were most common in the literature appearing in 15 reports. Biosecurity measures for personnel and visitors were identified in seven reports. Biosecurity measures for vehicles and other fomites were identified in six reports. Disinfection measures were identified in 11 reports.

Biosecurity Measures for Livestock and Their Products

Reported biosecurity measures applied to livestock included isolating infected animals from the rest of the herd, physical separation and separate management of animal groups within a farm, isolating, quarantining, or inspecting livestock prior to herd introduction, and maintaining separation between herds. Biosecurity measures applied to livestock products included management strategies for transport and disposal of animal wastes (feces and carcasses) and products (milk). The number of reports where unique biosecurity measures for livestock and their products were implemented by their reported effectiveness is summarized in Table 3.4. Expanded descriptions for livestock and livestock product biosecurity measures and their effectiveness are reported in Supplemental Table 1 of Appendix A.

Isolating clinically ill animals was the most commonly described biosecurity measure for livestock, appearing in eight reports [21-28]. Two included reports described implementation of

isolation practices in such a way that it exacerbated disease spread. Byomi (2015) reported that the placement of isolation pens near a highway and without sufficient separation from other groups of livestock on the farm was a contributing factor for disease spread among cattle on a dairy in Egypt. Lyons et al. (2015) described a situation where the movement of infected cattle on a dairy in Kenya from their home paddock to an isolation paddock resulted in viral exposure of other groups of cattle on the farm, both from the movement of the infected cattle and from placing another group of cattle on the contaminated pasture. Ali et al. (2022) used a case-control study design to compare farms that did and did not isolate clinically ill animals. Isolation was significantly associated with being a case farm ($p < 0.2$) in a univariable model but was not retained in the final multivariable model. Isolating infected animals was only described and was not evaluated in the remaining five reports. Specific details on isolation practices were lacking in most of the reports included in this review. Miller, et al. (2018) reported that 31.7% ($n=20$) of the households that they surveyed in the Greater Mekong Subregion of Lao People's Democratic Republic responded that they isolate clinically affected livestock until clinical recovery. No other reports specified a duration for isolation. No other reports, aside from those above, specified locations for the isolated livestock.

Utilizing spatial separation as a management strategy for groups of livestock within herds was described in three reports [22, 29, 30]. Lyons et al. (2015) reported that small ruminants were kept on a separate pasture “a few kilometers” from the dairy cattle present on the farm, and Poulin and Christianson (2006) reported that apparently healthy piglets were transferred to a site 300 meters from their farm of origin following weaning. Both of these strategies appeared to be sufficient for preventing FMD transmission during the reported outbreaks. Hutber and Kitching (2000) described using pens of immune calves to separate clinical and healthy cattle on a dairy in

Saudi Arabia, which also appeared to be sufficient for preventing FMD transmission during that outbreak. Conversely, Hutber and Kitching (2000) reported that the use of physical and spatial boundaries slowed disease transmission between pens of cattle but were not sufficient for preventing transmission. Additionally, Poulin and Christianson (2006) reported that moving apparently healthy sows from an infected farm to a separate site was not sufficient to prevent infection.

Four reports described utilizing quarantine, isolation, and/or inspection procedures for incoming livestock [23, 28, 31, 32]. In their case-control study Ali et al. (2022) did not find a significant association between farms that utilized a quarantine measure for new herd introductions and disease risk. Details of the quarantine measures, including quarantine length and location were not reported. Young et al. (2016) reported that surveyed smallholder cattle farmers in Cambodia that experience epidemic waves of FMD responded that they always (26.3%), sometimes (25.8%), or never (47.9%) isolated incoming stock for 2 weeks; however, no estimate of preventive effectiveness was reported. Manyweathers, et al. surveyed Australian beef (2020) and sheep producers (2021) and found that the majority of survey respondents inspect or isolate incoming livestock, but these procedures were not evaluated for their effectiveness regarding disease prevention. Additionally, specific inspection and isolation protocols were not reported.

Two reports described efforts to maintain a closed herd, limiting contact with outside animals [28, 33] Seifu et al. (2023) reported that only a small percentage of surveyed dairy farmers in Ethiopia who were “aware of FMD” keep cattle within the farm compound (9.6%), prevent other cattle from entering their farms (6.3%), or do not bring new cattle to the farm (3.1%) to prevent FMD infection. Young et al. (2016) reported a that higher percentage of

surveyed smallholder cattle farmers in Cambodia reported preventing their cattle from having direct contact with other farmers' cattle (19.2%) or keeping their cattle in a fenced area (78.3%). However, neither author evaluated the effectiveness of these biosecurity measures.

In a multivariable model for their retrospective case-control study, Hayama et al. (2015) reported that the following measures were not significantly associated with increased FMD transmission risk to Japanese cattle and pig farms: utilizing burial sites within 500 meters of farms or the presence of transportation roads within 200 meters. These risk factors were evaluated in conjunction with using waterproof sheets to cover carcasses during transport, transporting carcasses in sealed containers to burial sites, and disinfecting vehicles and equipment to prevent disease transmission [34]. Kass et al. (2022) reported burning as a means of carcass disposal during an FMD outbreak in Soviet Estonia between 1982 and 1983. They also described the storage of manure and disposal of milk from infected animals during the outbreak but did not evaluate the effectiveness of these waste disposal methods on limiting disease spread [35].

Biosecurity Measures for Personnel and Visitors

Reported biosecurity measures applied to farm personnel and visitors included wearing personal protective equipment (PPE) such as disposable work suits, gloves, boot covers, or farm specific clothing and/or footwear. Additional biosecurity measures that impacted the management of personnel and visitors included restriction of visitor access, farm lockdowns, bathing, and specific assignment of animal caretakers to individual livestock groups. The number of reports where unique biosecurity measures for farm personnel and visitors were implemented by their reported effectiveness is summarized in Table 3.5. Expanded descriptions for farm

personnel and visitor biosecurity measures and their effectiveness are reported in Supplemental Table 2 of Appendix A.

Six instances of wearing PPE were described in three reports [35-37]. Wee et al. (2008) described a situation from the 2002 FMD outbreak in Korea during which a worker who was part of swine culling activities was issued a disposable work suit and boot covers for the duration of the cull, and which were destroyed afterward. However, in the subsequent outbreak investigation, it was determined that the jeans worn underneath the work suit were still likely contaminated during the culling event and served as a source of contamination for the worker's car and eventually another site during the outbreak. Kass et al. (2022) also reported the use of protective clothing by dairy farm workers during the 1982 FMD outbreak in Soviet Estonia. However, since the district where this biosecurity measure was implemented did not experience any FMD cases, it is not possible to determine the effectiveness of the practice. No detail was given regarding the material or specifics of the clothing that was used. Additionally, Kass et al. (2022) reported that workers on dairies that did have FMD cases during Soviet Estonia's 1982 FMD outbreak used rubber gloves when handling sick animals and when milking animals with sores on their udders. No indication of the effectiveness of this practice was reported. Ellis-Iverson et al. (2011) used a case-control study to investigate the association between providing clothing or footwear to farm staff and being a case farm during the 2007 FMD outbreak in Southern England. Neither practice was significantly associated with the farms' FMD infection status. Details regarding the specific clothing and footwear provided to workers on each farm were not given, but it was noted that the clothing provided could include overalls and coats.

The management of farm personnel or visitors was mentioned in six reports, but none of the reported biosecurity measures were evaluated for effectiveness [22, 31-33, 35, 36].

Restricting visitor access to farms was mentioned in three reports, all surveys of livestock producers, with only one survey being conducted in an FMD endemic location [31-33]. Seifu, et al. (2023) reported that restricting visitor access to the surveyed dairy farms in Central Ethiopia, an area where FMD is endemic, is not widely practiced as only 2.1% of the surveyed dairy farmers reported doing so. Manyweathers, et al. (2020) surveyed Australian beef producers to assess vulnerability in the event of an FMD outbreak and reported that only 25% of the surveyed farms always restricted visitor access and 23% never restricted access. They also reported that over 39% of the surveyed beef farms did not require visitors to undergo any biosecurity practices. Biosecurity practices that were imposed by the remaining farms were not reported. In a similar study, Manyweathers, et al. (2021) surveyed Australian sheep producers and found that 32% of producers reported regularly restricting visitor farm access but over half (53%) of the surveyed farms responded that they did not require visitors to follow biosecurity practices.

The use of farm lockdowns, bathing, and specific assignment of animal caretakers to individual livestock groups were mentioned in one report each. Kass et. al (2022) reported that strictly enforced, complete farm lockdowns for FMD positive herds were utilized during the 1952 and 1982 FMD outbreaks in Soviet Estonia. Wee et al. (2008), reported that public baths were used as part of a decontamination process for workers following the completion of culling events during the 2002 FMD outbreak in Korea. Lyons, et al. (2015) reported the assignment of stockmen to single animal groups on a large dairy in Kenya during an outbreak in an effort to minimize cross-contact among animal groups and reduce within-herd FMD spread

Biosecurity for Vehicles and Fomites

Biosecurity measures for fomites were identified in six reports and included control of non-livestock species, vehicle access control, and limiting shared equipment. The number of

reports where unique biosecurity measures for fomites were implemented by their reported effectiveness is summarized in Table 3.6. Expanded descriptions for fomite biosecurity measures and their effectiveness are reported in Supplemental Table 3 of Appendix A.

Three reports addressed the control of feral animals [29, 31, 32]. Poulin and Christianson (2006) reported that rodent control efforts were strengthened to prevent recontamination of cleaned areas during a successful FMD eradication process on a swine farm in Asia. Manyweathers, et al. (2020) found that approximately 20% of surveyed Australian beef producers never, rarely, or occasionally control feral animals on their farms, compared to their subsequent 2021 survey of sheep producers, where the percentage of producers who did have control plans for feral animals was slightly less than 30%.

In their case-control study of the 2007 U.K. FMD outbreak, Ellis-Iverson et al. (2011) investigated risk factors associated with FMD infection on secondary case farms (i.e., farms that became infected due to disease spread from primary case farms which were infected from the direct viral source). They reported, based on univariable p-values, that control farms were more likely than case farms to have biosecurity measures in place to control vehicle movement on their farms, including having a car parking location away from animal areas and having physical barriers to the animal areas. They also reported that control farms were more likely to allow dogs to accompany staff into livestock areas than case farms.

In their case-control study of cattle farms in Pakistan Ali et al. (2022) did not identify an association between FMD risk and equipment sharing based on a univariable p-value. However, Seifu et al. (2023) reported that 4.2% of surveyed Ethiopian dairy farmers who were “aware of FMD” did not share equipment as a means of preventing FMD spread.

Disinfection

Eleven reports discussed disinfection measures for FMD at the farm level, including those targeting clothes and footwear, vehicles, barns, premises, and various other targets. Four reports mentioned disinfection strategies targeting clothing and footwear which included descriptions and the effectiveness of disinfecting worker clothing or utilizing boot dipping stations. Eight reports mentioned disinfection strategies targeting vehicles including descriptions of general vehicle disinfection, disinfection of wheels and tires specifically, and a description of utilizing vehicle disinfection equipment. Two reports described disinfectant strategies targeting barns specifically. One report described general site disinfection strategies, and three reports described disinfection strategies for other targets (e.g., staff, equipment, and supplies). The disinfectant product used was often not specified within the reports, but when reported, disinfectants included Virkon S [38], lime and ash water [35], slaked lime, formalin, and “crushed phenyl tabs” [23], organic acids, formaldehyde, and potassium permanganate [29]. The number of reports where unique disinfection biosecurity measures were implemented by their reported effectiveness is summarized in Table 3.7. Expanded descriptions for disinfection biosecurity measures and their effectiveness are reported in Supplemental Table 4 of Appendix A.

Two reports discuss disinfecting clothing during FMD outbreaks. Kass, et al. (2022) simply reported that staff clothing was disinfected during the 1982 FMD outbreak in Soviet Estonia without giving further details regarding products used, methods, or effectiveness. Wee, et al. (2008) described spray disinfectant being applied to the jeans of a worker who participated in culling activities during the 2002 FMD outbreak in Korea. In the report the authors speculate that the disinfection process used was insufficient to prevent subsequent contamination of the

worker's vehicle interior. Byomi (2015) and Ellis-Iverson et al. (2015) both report the use of boot dips, but neither provide evidence of the practice's effectiveness in reducing disease transmission.

Eight reports described vehicle disinfection strategies [21, 29, 34, 35, 37-40]. General vehicle disinfection was reportedly used as part of a successful site decontamination process on a sow farm in Asia [29]. However, general vehicle decontamination efforts either had no association with FMD transmission risk [34] or were not evaluated [39] in other reports. Four reports mention the use of decontamination strategies specific to vehicle wheels and/or tires (e.g., wheel dips, sprays, or washes, or disinfection mats or baths), but these strategies either appeared not to be associated with decreasing FMD transmission risk [21, 37] or were not evaluated for effectiveness [35, 38]. Lee et al. (2021) reported the presence of vehicle disinfection equipment on 61% of swine farms and 35% of cattle farms infected during FMD outbreaks between 2014 and 2019 in South Korea, but no details were given as to their use or effectiveness. Similar to other disinfection reports, details regarding methods, protocols, or products used during specific vehicle disinfection efforts as well as estimates of effectiveness are lacking.

The disinfection of barns was described in two reports. Poulin and Christianson (2006) described the cleaning of the entire barn space through pressure washing and organic acid rinses, emptying of the manure pit, changing lightbulbs, and fumigation of the entire barn with formaldehyde and potassium permanganate during the successful decontamination of a swine farm in Asia. Kass, et al. (2022) reported that barns were disinfected with lime and ash water during the 1952 FMD outbreak in Soviet Estonia, but no further detail was given about the method of application or estimated effectiveness.

In their case control study evaluating a 2019 FMD outbreak in Pakistan, Ali, et al. (2022) discussed two strategies for general premises disinfection. In a univariable model, they did not identify an association between disease risk and the farms that reported performing disinfection regularly, and while no consistent disinfection protocols or products were evaluated, the most commonly reported disinfectants included slaked lime, formalin, and “crushed phenyl tablets (phenylephrine hydrochloride)”. The authors also reported that a small proportion of the total enrolled farms (7/128, 5.5%) utilized disinfection dips at the farm entrance, but did not evaluate the measure for effectiveness, nor were any further details provided regarding disinfection target, protocol, or products used.

Three reports discussed other disinfection strategies or targets (e.g., staff, equipment, and supplies), but none were evaluated for effectiveness. Mielke, et al. (2023) mentioned the application of Virkon S to researcher’s shoes and equipment during an environmental sampling study; however, the timing and intended purpose of the application within the study design was unclear. Kass, et al. (2022) reported regular disinfection of staff and supplies being implemented during the 1982 FMD outbreak in Soviet Estonia but did not detail disinfection methods or what supplies were targeted. DiPietro, et al. (2023) reported that a small proportion of surveyed nomadic herders from Mongolia indicated that they utilized “sanitizing efforts” to prevent or respond to FMD (3/104), but did not provide details about the reported efforts.

Discussion

Numerous biosecurity practices identified in this review are plausibly effective, and the data presented here do not undermine that intuitive sense. However, the available data are not sufficient to support or refute their effectiveness or the specific critical control points necessary for effective implementation. We propose that field biosecurity measures be assessed for

potential usefulness utilizing three practical criteria. First, the proposed measure must plausibly interrupt a transmission route of the disease of interest. Second, the proposed measure should be effective in the field at mitigating disease risk. Third, the measure should ideally be suitable for practical and economic implementation in the field setting. The biosecurity measures identified in this review, along with other recommended best practices are generally accepted as meeting the first criterion, as evidenced by the recommendation of their implementation in guidance documents [41]. These measures also may plausibly be thought to mitigate risk, and in some cases, may not be overly onerous or expensive. However, reported data that support the second and third criteria are largely lacking.

From this review, no biosecurity measures that appeared in more than one report were identified as being consistently effective at mitigating disease risk in a field setting. Showering and changing outerwear was demonstrated to be consistently effective for preventing FMD transmission in a laboratory setting; however, no reports were identified to support the effectiveness of this biosecurity measure in the field [19, 20]. Handwashing and changing outerwear were also demonstrated to have variable efficacy in a laboratory setting, depending on viral strain and susceptible species, but again, no reports were identified to support this measure's effectiveness in the field [19, 20]. Utilizing spatial separation as a management strategy for groups of livestock within herds [22, 29, 30] and vehicle disinfection [29, 34, 39] were reported to be inconsistently effective at mitigating disease risk in field settings. Managing feral animal farm access and cleaning barns through pressure washing, organic acid rinses, and fumigation with formaldehyde and potassium permanganate were described as being effective for mitigating disease risk in a single report [29], but no estimate of effectiveness was given in other reports where these measures were mentioned [31, 32, 35]. Using sealed containers or

waterproof sheets during carcass transport [34], having a physical barrier to farm access [37], and having designated visitor parking away from animal areas [37] were all reported to be effective for mitigating disease risk in one report each. While plausibly effective, more evidence is needed to achieve a consensus regarding the effectiveness of these biosecurity measures. Allowing dogs to accompany farm staff [37] was also reportedly effective for mitigating disease risk but may exemplify a spurious relationship. None of the biosecurity measures describing the utilization of PPE or individual management were reported as being effective for mitigating disease risk [22, 31-33, 35-37]. Furthermore, the reporting detail regarding PPE use in most of the included reports was not sufficient for making meaningful comparisons of PPE effectiveness among reports. Additionally, in the Wee et al report from the 2002 outbreak in Korea, the PPE failure was arguably a failure of compliance since clothes worn under the PPE were worn home without sufficient disinfection [36]. Notably, the practice of isolating clinically ill animals was reported to be ineffective for mitigating disease [23] and also implicated in exacerbating disease spread [21, 22]. The same issues of insufficient reporting of protocols and poor implementation of plausible biosecurity measures that were identified regarding reports on PPE effectiveness, were also likely present in animal isolation reports. The inconsistent and limited evidence to support the effectiveness of specific biosecurity measures in field settings identified through this review hampers the ability of animal health officials and animal caretakers to plan for and respond appropriately during an FMD outbreak.

Because of its highly contagious nature and trade impacts, researchers are limited in their ability to study FMD in field-trial settings. In countries free of the disease such as the U.S. and United Kingdom (U.K.), high-containment bio-laboratories are needed to investigate FMD. However, these controlled environments cannot completely replicate all variables present in field

settings. We identified two laboratory studies that experimentally evaluated the efficacy of biosecurity measures for preventing the transmission of two different FMD strains [19, 20]. In both studies, researchers demonstrated that implementing certain biosecurity measures for animal caretakers can reduce the risk of indirect FMD transmission. While showering and changing outerwear appeared to be the most effective biosecurity measure evaluated, hand washing and changing outerwear was more effective than not implementing any biosecurity measures. The efficacy of hand washing and changing clothes in preventing the transmission of FMD varied based on FMD strain evaluated, susceptible species, and outcome used to assess FMD infection status. While useful in understanding transmission and biosecurity in high containment, the limitations of the laboratory environment make estimating the actual impact of handwashing, changing outwear, or complete showers in the field difficult. These laboratory results should be extrapolated to the field with caution as the incomplete implementation of biosecurity in the field setting could create a false sense of security in disease prevention. In a field setting, protocols often do not maintain the same level of stringency observed under laboratory conditions and can undergo protocol drift which can impact the protocol's actual effectiveness. An example of such protocol drift is often seen in milk producers in the U.S. with daily tasks such as preparing teats for milking [42]. Additionally, while cattle were the most commonly reported species in the field biosecurity measures reviewed here, no cattle were included in the laboratory studies identified through this review. Furthermore, only two strains of FMD were investigated in the laboratory studies. While this is a strength for assessing the impact of interventions for those strains, it limits the application of the study findings to field settings. Infectivity varies among FMD strains which could impact biosecurity measure effectiveness [43]. Consensus is also needed regarding which animal disease outcomes should be assessed to

determine whether biosecurity measures are effective. The choice of measured outcome (e.g., clinical signs, viremia, seroconversion) should be relevant to claims made regarding biosecurity efficacy/effectiveness (e.g., prevention of disease, transmission, infection, exposure).

In addition to the previously mentioned lack of consensus regarding measured outcomes and efficacy/effectiveness criteria, several other reporting issues precluded further analysis of the effectiveness of farm-level biosecurity measures against FMD. Few reports were identified that quantified the effectiveness of specific biosecurity measures. Most reports included in this review were observational studies or descriptive reports with small sample sizes and simple descriptions of biosecurity measures implemented without an assessment or estimate of effectiveness. Additionally, the implemented biosecurity measures, whether assessed or not, were generally not described in sufficient detail to allow a clear understanding of the practice implemented. These limitations increase the potential for the reported results to be type 1 and type 2 errors. A type 1 error may have occurred in reports where the authors are crediting the biosecurity measure with effects that were actually a result of chance or good luck, such as in the report that found dogs accompanying staff to work to be protective [37]. Additionally, type 2 errors may be present in reports that did not find a biosecurity measure to be effective when other studies, and biological plausibility suggest otherwise. For example, many reports referred to isolation or quarantine of animals but very few defined the distance the animals were quarantined from others or the duration of the quarantine. Isolation was not reliably associated with decreased risk, in some cases it was associated with increased risk; however, the details of how isolation was implemented are not sufficient to sort out what practices were actually reported or evaluated. Unclear and insufficient reporting is also a limitation for evaluating disinfection biosecurity measures. Future reports should include adequately detailed descriptions

of implemented biosecurity measures or protocols to allow for subsequent comparisons. To accomplish adequate reporting, standardized reporting guidelines to evaluate biosecurity measure effectiveness would be helpful. The STROBE-Vet Statement (Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary Extension) provides reporting guidance for observational studies conducted in all animal species [44]. Additionally, outbreak investigation reporting guidance has been developed for use during human disease outbreaks that could potentially be modified for veterinary use [45, 46]. In addition to reporting guidance to standardize study design reporting uniformity and transparency, consensus regarding reporting guidance for defining biosecurity measures, describing biosecurity measure protocol implementation, and assessing biosecurity measure outcome effectiveness will also be necessary to allow the comparison of biosecurity measure effectiveness among reports.

Field based research on biosecurity is a fundamentally difficult endeavor. Unlike experimental research in a controlled laboratory setting, exposure risk and magnitude is unknown so the study population of farms are a mix of those exposed and infected (biosecurity failure), exposed and uninfected (biosecurity success), and those unexposed (biosecurity not tested). For FMD, rare exposure between outbreaks provides few opportunities to test biosecurity practices, while assessment during outbreaks is difficult due to the demands of outbreak management and the variable farm risk. Individual farm risk may differ dramatically from farms with high risk which may overwhelm even good biosecurity to farms with low risk which may avoid infection in spite of poor biosecurity.

Robust assessment of field-biosecurity may be best served by long term prospective cohort studies of farms with well-defined and implemented biosecurity measures followed over time and through outbreaks to assess effectiveness. The necessary number of farms enrolled

would be large to account for the inherent variability in farm exposure. However, the level of biosecurity required to be effective against FMD is likely not practical or economic for everyday biosecurity. As such, establishment of well-defined enhanced biosecurity plans for “just in time” implementation at the start of a local outbreak may be an achievable alternative. This would require development of a cohort of motivated and willing producers for education on effective implementation of biosecurity measures. Immediately at the onset of an outbreak, collection of data on defined biosecurity implementation (daily records of implementation and deviations), local incidence risk, and active surveillance for disease occurrence would be required. Once disease was identified at a farm, active surveillance within the farm would be necessary to assess any biosecurity measures meant to control disease spread on the farm. These would be resource intensive studies for field evaluation of effective biosecurity measures. Application of target trial emulation practices would be necessary to strengthen the study design and subsequent results [47]. Future research in the form of case-control studies may also be helpful but will be hampered if well-defined and pre-planned biosecurity practices are not evaluated and substantial effort devoted to assuring control farm status.

It is also critical that the results of the biosecurity trials and research are adopted by the producers. Recent research has shown that currently, adoption of biosecurity planning by U.S. producers is low [48]. In their 2021 survey, Pudenz, et al. found that only 4% of U.S. cow-calf producers and 7% of feedlots have a biosecurity plan. This is not surprising given the rarity of large-scale national disease outbreaks affecting U.S. cattle in recent years. Producers cannot be expected to implement biosecurity measures that have no positive economic return. In FMD free countries the path toward better biosecurity should prioritize biosecurity measures that are effective against endemic diseases to demonstrate the value of utilizing biosecurity to decrease

disease risk. Despite the low level of biosecurity adoption in the U.S. cattle industry, FMD preparation plans continue to be developed in various academic, state, and federal settings. Reports included in this scoping review were limited to those published in English which may have eliminated some relevant reports from FMD-endemic areas. The elimination of a search update from the CAB database, may also have eliminated a few relevant reports; however, since no reports included from the original search were unique to the CAB database, its elimination from the search update is unlikely to be a major source of bias. Additionally, while only reports from peer-reviewed sources were considered for inclusion in this review, which served to decrease search time, conducting the topic search as part of a larger project ultimately increased the time necessary to complete the screening process. These methodology choices impacted the timeliness of review completion and could be decreased with a more limited search strategy. Lastly, the lack of defined criteria for what is or is not considered a farm-level biosecurity measure and what does or does not constitute effectiveness also presented challenges for data charting that impacted the timeliness of the review. Having clearly defined criteria for these and other terms would enhance repeatability of reviews focusing on the effectiveness of biosecurity measures.

Conclusion

The reports included in this review provide insight regarding biosecurity measures used to manage FMD in a large variety of geographic locations and farm types. The reports represent measures that producers are using in the field to mitigate the introduction and spread of FMD at the farm level globally. While the challenges of evaluating biosecurity measure effectiveness identified in this review hamper U.S. preparedness efforts, the lack of consensus and data to support the effective implementation of biosecurity measures also impacts farms globally.

A number of lessons learned are apparent from this review. There were various weakly evidenced descriptions of the efficacy or effectiveness of interventions that give some credibility to support the use of the reported biosecurity measures. However, it remains difficult to extrapolate the effectiveness of the reported measures to other regions and production types given the differences between FMD-endemic and FMD-free regions in disease spread and animal production systems. The scope of this review was focused on measures that could influence U.S. decision making but the information gap remains globally. Additionally, incomplete reporting regarding the description and implementation of many biosecurity measures contributes to the imprecision of biosecurity measure effectiveness estimates. Future reports of biosecurity measures implemented during FMD outbreaks would benefit from the utilization of current reporting guidance as well as the development of standardized reporting guidance for biosecurity descriptions, biosecurity measure implementation protocols, biosecurity effectiveness outcome assessment, and animal disease outbreak investigations. Accurate descriptions of biosecurity measure implementation and protocols are critical to allow the comparison of effectiveness among reports.

While current FMD preparation and response plans promote biosecurity measures that are “best practices” and may decrease the likelihood of FMD introduction or spread, clear evidence to support the effectiveness, or lack of effectiveness, of the recommended biosecurity measures is currently lacking in peer-reviewed literature. Ultimately, more studies, both in laboratory and field settings, in the U.S. and beyond, are necessary to validate field use of biosecurity measures with demonstrated laboratory efficacy, to build consensus regarding the effectiveness of biosecurity measures currently in use, and to inform which biosecurity measures have effectiveness that may vary depending on the outbreak strain of FMD and species affected.

Better reporting of implemented or evaluated biosecurity measures in the literature will allow producers, animal health officials, and veterinarians to make informed decisions in the face of an outbreak.

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Figures

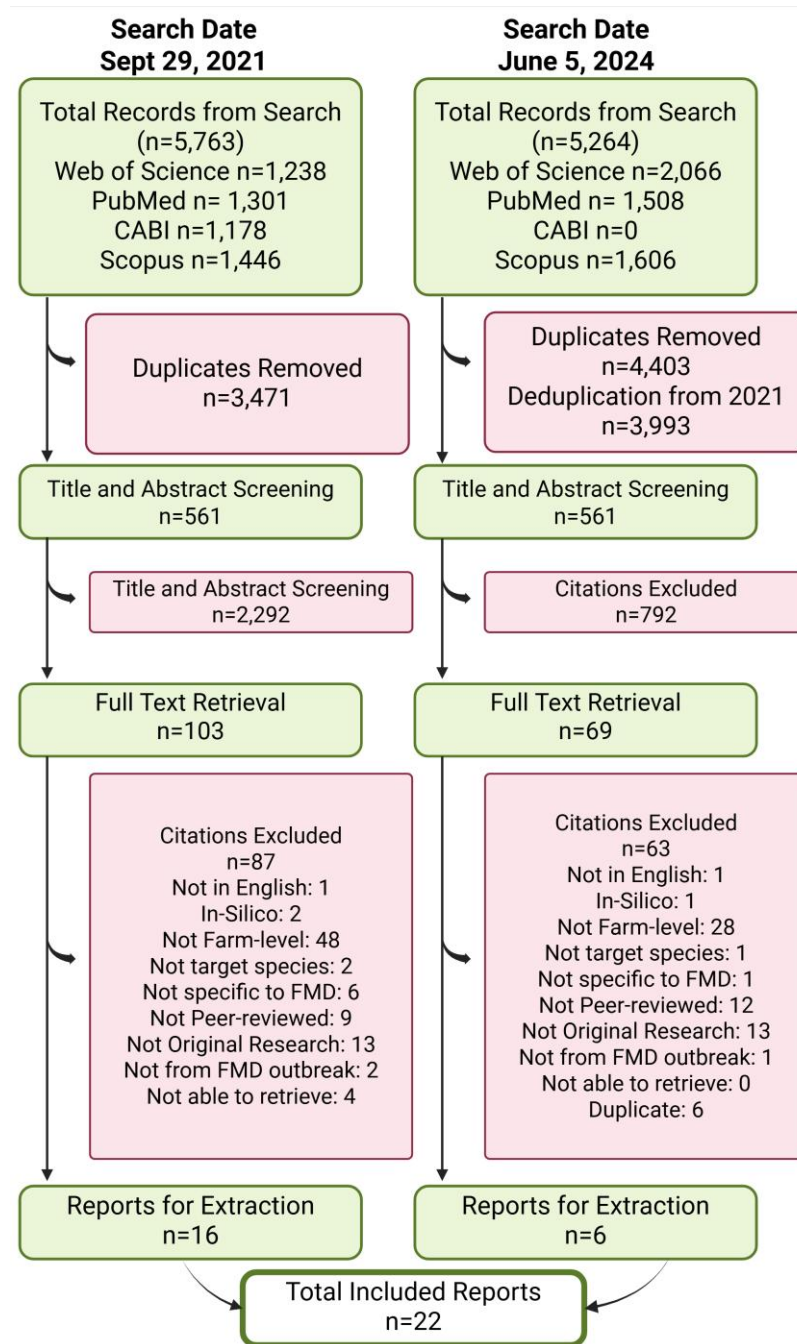


Figure 3.1: Flow diagram of the number of records and reports identified, screened for eligibility, and retained for inclusion in the review from an original and an update search.

Eligibility screening utilized a title and abstract screen followed by a full-text screen. Reasons for report exclusion during full-text screening are detailed.

Tables

Table 3.1 Search strategies by database and number of records returned by date.

The search strings utilized were optimized for each search engine's unique Boolean logic requirements.

Database and date range of coverage	Search String	Number of records from Sept 29, 2021	Number of records from June 5, 2024
CAB 1973 - present	(ab:("foot and mouth")OR title:("foot and mouth")) AND ab:(surveill* OR transmi* OR persist* OR biosecur* OR disinfect* OR "virus surviv*" OR "environment* surviv*" OR bird OR pest OR rodent OR wildlife) NOT ab:("hand foot and mouth") Language=English	1,778	Not included
Scopus 1800s - present	(TITLE-ABS ("foot and mouth")) AND ABS (surveill* OR transmi* OR persist* OR biosecur* OR disinfect* OR "virus surviv*" OR "environment* surviv*" OR bird\$ OR pest\$ OR rodent\$ OR wildlife) AND NOT ABS ("hand foot and mouth") AND (LIMIT-TO (LANGUAGE , "English"))	1,446	1,690
Web of Science 1800s - present	((TI=("foot and mouth") OR AB=("foot and mouth")) AND AB=(surveill* OR transmi* OR persist* OR biosecur* OR disinfect* OR "virus surviv*" OR "environment* surviv*" OR bird\$ OR pest\$ OR rodent\$ OR wildlife) NOT AB=("hand foot and mouth")) AND LA=(English)	1,238	2,066
PubMed 1950 – present	("foot and mouth" [Title/Abstract] AND(surveill* [Title/Abstract] OR transmi* [Title/Abstract] OR persist* [Title/Abstract] OR biosecur* [Title/Abstract] OR disinfect* [Title/Abstract] OR "virus surviv*" [Title/Abstract] OR "environment* surviv*" [Title/Abstract] OR bird* [Title/Abstract] OR pest* [Title/Abstract] OR rodent* [Title/Abstract] OR wildlife [Title/Abstract]) NOT ("hand foot and mouth" [Title/Abstract]) AND english [la])	1,301	1,508

Table 3.2: Key data items.

The key data items that were charted for all included reports included citation information, country, and year(s) of data collection. Animal species and use was charted as reported by the authors. Biosecurity measure descriptions were charted as reported by the authors, and subsequently categorized by reviewers. If available, biosecurity measure effectiveness was charted as reported by report authors, or if sufficient information was available, was summarized by reviewers.

Data Item	Description
Citation information	List of authors, article title, journal title, publication date
Location	Country of data collection as reported by the authors
Study date	Year(s) of data collection as reported by the authors
Animal species and use	Study population species (cattle, goats, sheep, swine, American bison) affected by implemented biosecurity measures. Use was charted for cattle as beef (includes “fattening”), dairy, both, or unspecified.
Biosecurity measure description	Descriptions of individual biosecurity measures were captured as described by the authors and subsequently categorized as follows: 1) Biosecurity measures for livestock and their products included management policies for susceptible livestock species of interest (e.g., isolation and quarantine) and their products (e.g., carcass, manure, and milk disposal) 2) Biosecurity measures for personnel and visitors included personal protective equipment use and management policies regarding workers and/or visitors (e.g., access to animal areas) 3) Biosecurity measures for fomites included management policies for vehicles (e.g., designated parking areas), non-livestock species management, and management strategies for other routes of indirect viral transmission 4) Disinfection measures included disinfection strategies for clothing, vehicles, and facilities to limit viral spread as reported by authors
Biosecurity measure effectiveness	Description of biosecurity measure effectiveness if reported by authors or as summarized by reviewers if sufficient information was available

Table 3.3: Report characteristics.

Summary of report characteristics including species and use of study population, country and timeframe (year(s)) of data collection, and reference.

Species (use)	Country; Year(s) of data	Reference
Cattle (beef)	Australia, 2017-2018	Manyweathers, et. al, 2020
	England, 2007	Ellis-Iverson, et. al, 2011
Cattle (dairy)	Egypt, 2012	Byomi, 2015
	Ethiopia, 2021-2022	Seifu, et. al, 2023
	Saudi Arabia, 1994	Hutber and Kitching, 2000
	Thailand, 2016-2017	Sansamur, et. al, 2020
Cattle (unspecified)	Cambodia, 2015	Young, et. al, 2016
	Ethiopia, 2021	Shurbe, et. al, 2022
	Pakistan, 2019	Ali, et. al, 2022
Cattle (beef and dairy) and Swine	Korea, 2014-2019	Lee, et. al, 2021
	USSR Estonia, 1952, 1982	Kass, et. al, 2022
Cattle (dairy), Goats, and Sheep	Kenya, 2012	Lyons, et. al, 2015
Cattle (dairy) and Swine	Korea, 2002	Wee, et. al, 2008
Cattle (unspecified), Goats, and Sheep	Mongolia, 2021	DiPietro, et. al, 2023
Cattle (unspecified), Goats, and Swine	Lao People's Democratic Republic, 2016	Miller, et. al, 2018
Cattle (unspecified) and Sheep	Cameroon, 2016	Mielke, et. al, 2023
Cattle (unspecified) and Swine	Japan, 2010	Hayama, et. al, 2015
	Lao People's Democratic Republic, 2010	Nampanya, et. al, 2012
Sheep	Australia, 2017-2018	Manyweathers, et. al, 2021
Sheep and Swine	United States (PIADC*), NR	Amass, et. al, 2004
	United States (PIADC*), NR	Amass, et. al, 2003
Swine	NR**, 2002	Poulin and Christianson, 2006

NR= Not Reported

*Plum Island Animal Disease Center

**No specific country reported by authors

Table 3.4: Number of reports where unique biosecurity measures for livestock and livestock products were implemented by their reported effectiveness.

A single report may discuss variable outcomes for individual biosecurity measures. Therefore, reports may belong to more than one effect category per row.

BIOSECURITY MEASURE	NUMBER OF UNIQUE REPORTS				
	Beneficial	Detrimental	Neutral	Effect Not Determined	Total (n=15)
ISOLATION OF INFECTED ANIMALS FROM THE REST OF THE HERD/GROUP	0	2	1	5	8
SEPARATION OF ANIMAL GROUPS WITHIN FARM	3	0	2	0	3
ISOLATION, QUARANTINE, OR INSPECTION OF INCOMING STOCK	0	0	1	3	4
MANAGING FARM AS A CLOSED HERD	0	0	0	2	2
COVERING CARCASSES FOR TRANSPORT	1	0	0	0	1
CARCASS DISPOSAL BY BURNING	0	0	0	1	1
FECES STORED INSTEAD OF SPREAD AS FERTILIZER	0	0	0	1	1
MILK DISPOSED OF OR PASTEURIZED BEFORE FEEDING TO OTHER ANIMALS	0	0	0	1	1

Table 3.5: Number of reports where unique biosecurity measures for personal protective equipment and individual management were implemented by their reported effectiveness.

A single report may discuss variable outcomes for individual biosecurity measures. Therefore, reports may belong to more than one effect category per row.

BIOSECURITY MEASURE	NUMBER OF UNIQUE REPORTS				
	Beneficial	Detrimental	Neutral	Effect Not Determined	Total (n=7)
FARM-SPECIFIC CLOTHING REUSABLE OR DISPOSABLE	0	0	2	1	3
FARM-SPECIFIC FOOTWEAR REUSABLE OR DISPOSABLE	0	0	1	1	2
GLOVES	0	0	0	1	1
RESTRICTION OF VISITOR ACCESS TO FARMS	0	0	0	3	3
FARM LOCKDOWN	0	0	0	1	1
BATHING	0	0	0	1	1
MINIMIZING CROSS CONTACT BETWEEN ANIMAL GROUPS	0	0	0	1	1

Table 3.6: Number of reports where unique biosecurity measures for fomite management were implemented by their reported effectiveness.

A single report may discuss variable outcomes for individual biosecurity measures. Therefore, reports may belong to more than one effect category per row.

BIOSECURITY MEASURE	NUMBER OF UNIQUE REPORTS				
	Beneficial	Detrimental	Neutral	Effect Not Determined	Total (n=6)
FERAL ANIMAL MANAGEMENT	1	0	0	2	3
ALLOWING DOGS ON FARM	1	0	0	0	1
DESIGNATED VEHICLE PARKING	1	0	0	0	1
BARRIER TO VEHICLE ENTRY	1	0	0	0	1
NOT SHARING EQUIPMENT BETWEEN FARMS	0	0	1	1	2

Table 3.7: Number of reports where unique disinfection biosecurity measures were implemented by their reported effectiveness.

A single report may discuss variable outcomes for individual biosecurity measures. Therefore, reports may belong to more than one effect category per row.

BIOSECURITY MEASURE	NUMBER OF UNIQUE REPORTS				
	Beneficial	Detrimental	Neutral	Effect Not Determined	Total (n=11)
CLOTHING	0	0	1	1	2
FOOT DIPS	0	0	2	0	2
DISINFECTION OF VEHICLES	1	0	1	1	3
WHEELS AND TIRES	0	0	2	2	4
POSSESSION OF VEHICLE DISINFECTION EQUIPMENT	0	0	0	1	1
BARN AND ANIMAL HOUSING	1	0	0	1	2
REGULAR DISINFECTION (TARGET NOT SPECIFIED)	0	0	1	0	1
DISINFECTION DIP AT ENTRANCE (TARGET NOT SPECIFIED)	0	0	0	1	1
DISINFECTION OF RESEARCHER EQUIPMENT	0	0	0	1	1
DISINFECTION OF STAFF	0	0	0	1	1
GENERAL DISINFECTION OF SUPPLIES (NOT SPECIFIED)	0	0	0	1	1
SANITIZING EFFORTS IN NOMADIC HERDS	0	0	0	1	1

Chapter 4 - Animal Disease Traceability: Evaluation of Simulated Foot-and-Mouth Disease Outbreak Metrics with Implementation of Improved Contact Tracing of Cattle

MaRyka R. Smith¹, Michael W. Sanderson^{1*}

¹Kansas State University, College of Veterinary Medicine, Diagnostic Medicine and Pathobiology, Center for Outcomes Research and Epidemiology, Manhattan, KS, USA

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Abstract

In the event of a Foot-and-Mouth Disease (FMD) introduction in the United States (US) animal health officials will need to rapidly trace infected animals and their contacts. Electronic identification (EID) and digital tracing of cattle could improve the speed and accuracy of tracing efforts. This study evaluated the impacts of improving cattle traceability during an FMD outbreak in the US.

InterSpread Plus (ISP) was used to simulate FMD outbreaks with a US national livestock population file and animal movement parameters. Scenarios were defined by starting location (California, Nebraska, Texas, New Mexico, New York, and Tennessee), farm type (dairy, feedlot, stocker, cow calf), detection day (8, 14, or 21), and tracing level. The tracing levels represented the current speed and accuracy in the US, a partial EID tracing or an ideal EID tracing implementation. A secondary objective investigated decreasing the geographical size of control areas and surveillance zones under the ideal tracing level. We assessed outcome metrics (infected premises (IPS), outbreak duration, and number of farms under surveillance or in control areas) using a calculation of difference between scenarios and bootstrap confidence interval estimation.

Improved tracing showed the largest potential for decreasing outbreak size when the outbreaks were detected on day 21. The distribution of IPs decreased consistently at the median and beyond with some scenarios showing decreases as low as the 10th percentile. Similar trends were seen in the duration of outbreaks and number of farms in surveillance zones. When the size of control areas and surveillance zones decreased, the number of IPs tended to increase while the number of farms under surveillance decreased in some scenarios and increased in others.

Our results support the value of improved cattle traceability that is rapid and accurate for decreasing the potential for large FMD outbreaks in the US. An improved traceability system could also decrease demands for human labor to conduct traces and surveillance during the outbreak, and improve business continuity of producers during and outbreak. More research into the economic trade-offs and EID feasibility are needed to determine the best implementation of EID tracing systems.

Introduction

Tracing the introduction of a disease back to its original herd or animal is not a novel concept. Reports of disease tracing can be found as early as 1275 wherein the source of “rot” in Europe was traced back to a “Spanish ewe” [1]. Later, in 1711, an introduction of Rinderpest to a farm in Venice was linked to a stray ox [1]. These were not isolated incidences, and many other accounts of the interest in tracing the origin of disease can be found in historical literature [1]. A key difference between the historical tracing of animals and modern tracing is the methods for identification of animals. Historical traces relied on human recollection of ownership, markings descriptions, hooves or hide branding, or physical collars or tags [1, 2]. In the modern era, these techniques may still be used, but great advancements have been made in the ability to individually identify animals and trace their origins, namely, electronic identification (EID) and computer record keeping [2, 3]. Ultimately, for a disease traceability system to be effective, it needs to perform at the same timescale as animal movement and disease transmission.

In the United States (US), traceability of disease in livestock, especially cattle, has been of interest beginning as early as the 1900s with a focus on brucellosis (*Brucella abortus*) and bovine tuberculosis (bovine TB) [4]. In 1917, the US Congress initiated the State-Federal Bovine Tuberculosis Eradication Program [5]. This program included testing all animals in a herd and slaughtering all reactors. The formal efforts to eradicate brucellosis in cattle began in 1934 with systematic sampling and depopulation of herds [6]. In the modern day, control of both diseases relies on routine surveillance and tracing the source of infected animals.

The surveillance and traceability efforts for brucellosis and bovine TB have been effective at disease control. Brucellosis has been eliminated from domestic livestock herds in the United States [6]. The only herds that remain positive for brucellosis are wildlife in Yellowstone

National Park with occasional infections in herds in the Greater Yellowstone Area (GYA) [6]. Bovine TB control efforts have heavily relied on tracing animals identified at slaughter to their herd of origin [7]. A recent study investigated the success of these traces and found as high as 83% success in finding the origin farm, with 70% of traces from adult cows resulting in the identification of more infected animals [7]. These two example diseases show the impact of tracing in disease control; however, both diseases spread at a very slow rate. Bovine TB-infected animals can take months to years to incubate the bacteria prior to developing clinical signs [8]. Similarly, the incubation period for brucellosis could range from weeks to months [9]. The systems can adequately complete traces for controlling the spread of these diseases but are likely insufficient for a rapidly progressing disease such as Foot-and-Mouth Disease (FMD). The failure to trace at-risk contacts quickly enough in an FMD outbreak is likely to result in continued transmission through animal contacts and larger outbreaks.

Over the years, the eradication programs have matured to reflect changes in technology and disease tracing policy. In 2004, the National Animal Identification System (NAIS) was the first iteration of a widespread approach to national animal traceability [10]. In 2010, the NAIS program was replaced by the current Animal Disease Traceability (ADT) program [10]. The ADT program requires that covered animals moving interstate have an official form of identification and are documented back to the state of origin [10]. The ADT program increased traceability for interstate movements for covered classes of cattle, but class exceptions and within-state movements remain under the authority of state and tribal governments [10]. In 2013, the final rule, 9 CFR, part 86, clarified the animals that must be properly identified on Interstate Certificates of Veterinary Inspection (ICVI) and provided for multiple exempt classes of cattle and bison. These exemptions increase producer compliance but allow many animal movements

to be undocumented. It remains that intra-state movements of exempt animals may occur with no traceability beyond optional producer records. In November 2024, there was an amendment to the final rule that required official identification of covered animals to be a permanent tag that is both electronically and visually readable [11]. These improvements assist in the fight against disease, but in the US, room exists to improve the speed and accuracy of the efforts [12]. In many instances of attempted animal tracing efforts, the records are incomplete which can result in delays or failure to complete a trace [12].

One of the most significant diseases of concern for traceability is FMD. FMD is a highly contagious and readily transmissible disease of cloven-hooved animals. Upon initial FMD infection, animals can become infectious to others within 4 days of exposure [13]. FMD virus can be shed in all bodily fluids of infectious animals [13]. The potential of transmission from sub-clinical animals prior to the appearance of clinical signs and transport of latent animals adds to the need for rapid and accurate tracing of the movements of infected and at-risk animals in the face of an FMD outbreak [14].

In an FMD outbreak in the US, government officials will be tasked with finding all diseased and at-risk animals and identifying where they have been in the previous 28 days. Because of the extensive movement of cattle in the US, these traces could include numerous farms spread widely across many states and counties [15]. Utilization of EID can aid in capturing the identity of an animal and storing that information quickly in a digital database. This data capture can occur at the speed of commerce with some EIDs being readable up to 30 feet away allowing animals to be scanned as they pass through chutes and gates in markets or on farms [16].

Previous research has shown that rapid tracing can have positive impacts on controlling outbreaks of FMD but has been limited to specific regions of the United States [17, 18]. A national model in 2023 also found tracing to be beneficial for outbreak control [19]. However, that study was limited by decreased movements of animals through markets that were not representative of the realities of livestock movement and production system of the US [20].

Tracing efforts are not the only method animal health officials will use to control an FMD outbreak. Areas of quarantine and movement control known as control areas and surveillance zones will be created around infected premises (IPs) to control the spread of FMD [21]. Currently, the United States Department of Agriculture (USDA) FMD Response Plan, also known as, “The Red Book,” calls for a 10 km radius circle to be drawn around the IP for the control area and a second circle from 10 km to 20 km to be designated the surveillance zone [21]. The improvement of trace accuracy and speed could aid in the rapid creation of these areas and zones and prevent the continued spread of disease beyond the impacted area. Further, improved tracing could reduce the business continuity impacts of an incursion of FMD by decreasing the number of premises that are not infected but experience barriers to business continuity such as limitations in their ability to procure supplies or get their products to market.

The purpose of this project was to simulate FMD outbreaks in the US and assess the potential impacts of more rapid and accurate traceability of cattle using representative US national production system parameters. The primary objective was to compare the number of IPs, outbreak duration, and number of farms impacted by surveillance efforts with varied improvements in the tracing of direct contacts of cattle. The secondary objective was to investigate the possibility of decreasing the size of control areas and surveillance zones from the current recommendation when an improved traceability system is used.

Materials and Methods

Modelling Program

InterSpread Plus (ISP) (Version 6.01.44), a spatially explicit, stochastic modelling software, was used to simulate the outbreaks of FMD [22]. The program allows for multiple parameters that describe animal movement, control efforts and the transmission of disease. Disease transmission is defined by many parameters including direct contacts, indirect contacts, airborne spread, and local spread. To begin a simulated outbreak, users load an “epidemic history” file that includes the farm identification number for the index case(s) and a defined day and farm identification number for the first detection. The outputs from ISP are plain-text files that can be exported for analysis by statistical software.

Basic Parameters and Population

The baseline parameter set was provided by the United States Department of Agriculture Center for Epidemiology and Animal Health (USDA-CEAH). The baseline parameter set describes the basics of the US production system and FMD-specific parameters. The parameters for livestock production system behavior were developed with National Animal Health Monitoring System (NAHMS) data and expert opinion when the data was incomplete. The FMD-specific parameters were developed from the current literature on FMD in field and laboratory settings. Expert opinion was also used to fill gaps in FMD virus knowledge. A sample of key parameters of interest are in Supplement 1.

The population file was generated by USDA-CEAH with information from National Agricultural Statistics Service (NASS) Census of Agriculture. Census data from 2020 was used for all dairy premises populations and data from 2012 was used for all other premises. Farms were placed geographically using the Farm Location and Agricultural Production Simulator

(FLAPS) to anonymize the data [23]. The population file includes beef and dairy cattle, bison, sheep, goats, and swine with subdivisions for size and specific farm types such as cow-calf, feedlot, and stocker operations. There is also a population of markets and processors with publicly available locations that serve as points of contact, mixing, and dispersal of infected animals. A total of 1,176,200 premises were included in the population. An overview of the population file is in Supplement 2 of appendix B.

Livestock herd movements in ISP are completed in three steps using stochastic processes to generate movements, and probability distributions of movement distances and destination farms. In the first step, movement from the infected origin farm is generated based on a Poisson process of the expected daily movement rate. If a movement is generated, a shipping distance and a farm type destination are selected, each from a probability distribution. If a destination farm of the chosen farm type is available within that shipping distance, the movement is completed. For movements through markets, the same process is followed to generate a movement, select a shipping distance and choose a market within that shipping distance band. Then, the model determines a farm type and shipping distance for the final destination of that movement through the market. The movement parameters were input and tested to ensure that all production types were making shipments to other farms and markets at expected rates. This was confirmed by comparison of the observed movement rates to the model parameter distributions as shown in Supplement 3.

The base efforts to control the outbreaks were surveillance, movement restriction, and depopulation. Upon the detection of the first IP, the control measures began. Surveillance measures were applied in the control areas and surveillance zones drawn around IPs and increased the likelihood of detection of a clinical farm. Movements from detected IPs were

stopped with 100% efficacy consistent with the use of state or federal quarantine orders, and other movements from all other farms were decreased. Depopulation was triggered when the farm was detected and was completed within a time period specified for the farm type. Farms are queued for depopulation based on the order of detection and farm type. Each day the number of farms depopulated is constrained by the daily capacity limit for that farm type. Capacity limits vary with operation type and size, e.g. large farms take more days to depopulate. The details for depopulation time and time to the completion of transmission potential from that farm are detailed in Supplement 1 of Appendix B.

Initiation of Outbreaks

Outbreaks are started in ISP with an “epidemic history” file that details the unique index farm identification infected on day 1 and the day the first farm becomes detected. To capture a range of detection days we modeled day 8, day 14, and day 21 detection. Outbreaks were not regionally limited; every farm and farm type in the US population file was eligible for infection in every scenario. The model parameters capture the networks of animal trade in the US by the random selection of movement destinations according to production type and defined distance probability distributions. This characteristic of the model aids in representing the spatial relationships that may drive outbreak spread in a real-world outbreak. Additionally, allowing all species to be infected and transmit is consistent with biological expectations and results in more realistic simulated outbreaks.

To gain insights into multiple regions of the US and multiple farm types, eight locations and four different farm types were selected. USDA NASS census data, research interest, and published literature were used to identify the areas of interest in each region. The index cases are detailed in Table 4.1.

Scenario Specific Parameters

Tracing Parameters

In ISP, the tracing parameter is defined by the speed, in days, to completion and the likelihood the movement is not traced (trace failure). There are parameters that define the speed and accuracy of tracing all of the species included in the population file. The tracing parameters of interest in this project consisted of the current tracing ability, a partial implementation of cattle EID tracing ability, and an ideal cattle EID implementation. The tracing parameters for all non-cattle species were kept constant across the scenarios. The tracing levels were developed with input from the USDA-CEAH and the United States National Animal Disease Traceability and Veterinary Accreditation Center (USDA-NADTVAC). The data for current tracing parameterization was primarily derived from data gathered in real-world brucellosis and bovine tuberculosis tracing efforts, along with expert opinion from USDA-NADTVAC.

The “current” level of tracing depended on the production type. For beef cattle traces, 85% were successfully completed (15% trace failure). Of successful traces, 10% were completed within 2 days, 41% completed in 4 days and 98% within 10 days with approximately. Successful completion of dairy cattle tracing was 85% in dairy heifer calf units and 87.5% in all other dairy farm types. Of successful dairy traces, 29% were completed within 2 days 77% within 4 days and 98% within 10 days.

Partial implementation of EID-based tracing improved the current tracing level but did not meet the complete capability of an entirely EID-based system. Beef and dairy cattle tracing speed was improved to 52% of the traces being completed within 2 days, 97% within 5 days and 99% by day 7. For all cattle, 90% of traces were successfully completed.

The “ideal” implementation of EID-based tracing had 99% successful completion and all traces completed within 1 day for all beef and dairy cattle. The full details of the traceability parameters are provided in Supplement 4.

Zones

The standard control area and surveillance zones used for this project are those described by the USDA FMD Red Book, wherein the control area has a 10 km radius from the detected IP and the surveillance zone extends 10 km beyond that (10 km to 20 km from the IP) [21]. The standard control area was modeled with all 3 tracing levels. We also evaluated a “reduced” zone size at the ideal level of tracing with a control area radius around a detected IP of 7 km and a surveillance zone that extended another 7 km beyond that (7 km to 14 km from the IP).

Analysis

Each iteration of ISP is a modeled introduction and outbreak of FMD. The model completes the outbreak when 60 days have passed since the last detection. The outputs from ISP are in the form of plain-text files with each change in a specific farm’s outbreak state (e.g. infected, detected, depopulated) being reported as a new line. In the surveillance zone and control area outputs, a farm is only reported on the first instance of being in a control area or surveillance zone. If the farm is later included in an overlapping zone or area before the expiration of the first it will not be reported again as its farm state did not change. If a farm were in an area or zone that expired, then a new zone or area was drawn it would be counted again. The number of markets and processors are not included in the count of IPs reported in this analysis but were included as infected and able to transmit infection during the simulation of the outbreak. All analysis and data manipulation were performed using R version 4.1.1 and R Studio 2024.09.0 [34, 35].

The number of IPs was calculated as the total number of farms of any species that were ever infected during a given iteration, regardless of the detection status of the farm. The duration of an outbreak was the time from outbreak initiation to the day the final detection was made. The number of farms impacted by control areas and surveillance zones were calculated by the number of farms that were ever in a control area or surveillance zone. Farms in control areas or surveillance zones may have never become infected but were subject to the control measures within the area or zone.

Using the *rogme* R package, the shift function was used to calculate the differences between selected scenarios [36]. For our primary objective, we compared current tracing to partial EID and ideal EID tracing. For the secondary objective, we compared ideal tracing with standard (current Red Book) control areas and zones to ideal tracing with reduced area and zone sizes. For all comparisons, we compared predetermined percentiles: 10th, 25th, median, 75th, and 90th, and utilized bootstrap sampling ($n=2,000$) to estimate a 95% confidence interval for the difference at each percentile.

We tested each introduction site scenario for convergence of number of IPS using current tracing and day 21 detection. The scenarios were run for an initial 100 iterations. The total number of IPs in each iteration was calculated then the median and 90th percentile ranked outbreaks at 100 iterations were compared to the median and 90th percentile outbreaks at 90 iterations. If there was less than 5% change at both metrics, the scenario was considered converged. In outbreaks that were small in size, the percent change could be larger than 5%, but if there were less than 10 farms difference from the 90th iteration to the 100th iteration, the model was still considered to be converged. If a scenario was not converged, another 50 iterations were run and the median and 90th percentile at 150 iterations compared to the median

and 90th percentile at 100 iterations. If the scenario met the 5% change or less at 150 iterations, the 100 iterations were considered sufficient for convergence.

Results

Convergence

All scenarios except the feedlot introduction in Nebraska were converged at 100 iterations at the median and 90th percentile number of IPs. After an additional 50 iterations, the feedlot introduction in Nebraska had less than 5% change in IPs from 100 to 150 iterations. Thus, the results from 100 iterations were used in all scenarios.

General Results

The simulated outbreaks tended to have a clear divergence in number of IPs (outbreak size) between those that started in a cow-calf or stocker operation and those that started in a dairy or feedlot, across the other variables. The scenarios that began in a New Mexico stocker operation, or a cow-calf operation in Nebraska or Tennessee had smaller outbreaks and often failed to sustain transmission beyond a few farms. Specifically, across the introduction sites, there were at least 29 and up to 39 iterations where less than 10 farms were infected using day 21 detection and current tracing. These small outbreaks did not respond as markedly as the larger outbreaks to tracing improvements. For the remainder of this report, we will refer to the groups of outbreaks collectively as large (feedlot and dairy) or small (cow-calf and stocker).

The day that outbreaks were detected was also an influential predictor of outbreak size. Across all introduction sites and tracing levels, the outbreaks that were detected on day 8 were the smallest, followed by day 14 and day 21 detections. The outbreaks detected on day 8 were seldom remarkable in their response to changes in tracing level until the outbreaks were in the 75th percentile or larger. The outbreaks detected on day 14 were more variable in their response

to tracing than those detected on day 8 but were still modest in their change. The limited size of the outbreaks that were detected early likely lead to decreased opportunity for tracing to be implemented in the control efforts. The impact of improved tracing was substantial for outbreaks detected on day 21. For these reasons, the day 21 outbreaks will be the focus of the remainder of the results section of this report. Key outbreak metrics are provided in figures. Detailed data for all day 21 outbreak metrics is included in tabular format in Supplement 5. The outbreak metrics from those detected on day 8 and 14 are included in Supplement 6.

Level of Tracing

Infected Premises (IPs)

In large outbreaks, the number of IPs in an outbreak decreased markedly with improved tracing. In all scenarios, the estimated number of IPs decreased when partial EID tracing was compared to current tracing. The bootstrap confidence interval (CI) for the differences excluded zero at the 10th percentile for Tennessee and New York dairy and Texas feedlot introductions. The California dairy introduction difference CI excluded zero at the 25th percentile, and the Nebraska feedlot introduction difference CI excluded zero at the median. Figure 4.1 shows the distribution, shift function, and bootstrap difference confidence intervals of the outbreaks that started in feedlots. Figure 4.2 shows the distribution, shift function, and bootstrap difference confidence intervals of the outbreaks that started in dairies. The most notable changes were in New York and Tennessee dairy introduction scenarios where 100-120 IP decreases were seen at the 10th percentile and over 1,600 fewer IPs at the 90th percentile.

In small outbreaks, the number of IPs decreased with improved tracing but not to the same magnitude as the large outbreaks. When partial EID tracing was implemented, the number of IPs at the 10th and 25th percentiles were similar to the current level of tracing. At the median

outbreak, the predicted decrease in number of IPs was less than 20 farms across all introduction sites. In outbreaks starting in a New Mexico stocker operation, the 75th percentile outbreak had an estimated 427 fewer IPs and the bootstrap difference confidence interval excluded zero. The confidence interval of the partial and current IP difference for the two cow-calf introduction scenarios did not exclude zero until the 90th percentile, when the predicted decreases was approximately 900 to 1,300 farms. Figure 4.3 illustrates the shift function and differences for the partial EID compared to the current tracing for small outbreak scenarios.

When comparing current to ideal implementation of EID tracing, the resultant number of IPs in large outbreak scenarios decreased dramatically. The bootstrap confidence intervals for the estimated differences excluded zero at the 10th percentile outbreak in all large outbreak scenarios except the Nebraska feedlot introduction which excluded zero at the 25th percentile. The outbreaks in dairies saw an estimated decrease of 140 to over 1,200 IPs at the median and up to 2,200 fewer IPs at the 90th percentile.

When ideal EID tracing was compared to current, the small outbreaks had a more marked decrease in the number of IPs. In Nebraska cow-calf and New Mexico stocker introductions, the difference confidence interval excluded zero at the 75th percentile with approximately 400 fewer IPs and over 1,300 fewer IPs at the 90th percentile outbreak. Outbreaks that began in a Tennessee cow-calf reached a confidence interval that excluded zero at the 90th percentile with an estimated 1,765 fewer farms infected.

Duration of Outbreaks

The changes in duration of outbreaks with improved traceability were less marked than the number of IPs. Similar to IPs, changes were small for the outbreaks with detection on day 8 and day 14 (Supplement 6) but more notable for detection on day 21. The overall trend was a

decrease in the time to the last detection of an IP, but the magnitude and significance of that decrease was highly variable.

In the large outbreak scenarios that utilized partial EID tracing, the duration of outbreaks was consistently decreased based on bootstrap difference confidence intervals. The difference confidence interval excluded zero at the 10th percentile except for the Nebraska feedlot. At the median, the Nebraska feedlot had an estimated 63 fewer days duration and the confidence interval did exclude zero. The largest decrease was seen in the Tennessee dairy scenario 90th percentile outbreak with 134 fewer days duration. For the small outbreak scenarios with partial EID implementation, the estimated differences indicated a decrease in outbreak duration but the confidence interval did not exclude zero or any percentile in any location. These results are detailed in figure 4.4.

In large outbreak scenarios with ideal EID tracing, the decreased duration of the outbreaks was evident at the 10th percentile for all but the Nebraska feedlot scenario which was decreased at the 25th percentile by approximately 16 days. Median reduction in duration ranged from 41 to 139 days. The small outbreaks were not notably shorter until the 75th percentile for the Nebraska cow-calf and New Mexico stocker scenarios and the 90th percentile for the Tennessee cow-calf scenario. The small outbreaks were 135-175 days shorter at the 90th percentile with ideal tracing.

Number of farms under surveillance

The number of farms under surveillance includes those that were in control areas and surveillance zones. They serve as a representation of the farms that are impacted by outbreak control efforts even if not infected.

In the large outbreak scenarios, the implementation of partial EID tracing resulted in significant decreases in the number of farms in control areas (0 to 10km from IP) at the 10th percentile for the dairy introductions and at the median for the feedlot scenarios. The largest change at the median outbreak was from outbreaks starting in a Tennessee dairy where an estimated 68,000 fewer farms were in control areas.

In the surveillance zones (10 to 20km from an IP), this same trend continued with significant decreases at the 10th percentile for dairy introductions and the median outbreak for feedlot introductions. The largest overall decrease was over 200,000 fewer farms in the surveillance zones at the 90th percentile outbreak that began in a New York dairy. The data for the number of farms in surveillance zones with partial EID implementation is shown in figure 4.5.

In the small outbreak scenarios, the use of partial EID tracing made very small decreases in the number of farms in control areas and surveillance zones that were not significant until the 90th percentile for most scenarios. The outbreaks that began in New Mexico stockers reached a significant change at the 75th percentile outbreak with an estimated 23,000 fewer farms in control areas and 38,000 farms in surveillance zones. This data is shown in figure 4.5.

When ideal tracing was implemented, the decrease in number of farms in control areas was sufficient to exclude zero from the confidence interval beginning at the 10th percentile for all introduction sites except the Nebraska Feedlot (Supplement 5). At the median, there were approximately 33,000 fewer farms in control areas in outbreaks that began in a Nebraska feedlot. The dairy introductions saw 79,000 to 164,000 fewer farms in control areas at the 90th percentile outbreak. The trend continued in the surveillance zones with all locations except Nebraska feedlots reaching significant decreases at the 10th percentile and Nebraska feedlot reaching

significance at the median outbreak. The New York dairy scenario remained the site with the largest change having an estimated 271,000 fewer farms in surveillance zones at the 90th percentile when ideal EID use was implemented.

In the small outbreaks, the effect of ideal EID tracing on farms under surveillance was less remarkable until the 75th to 90th percentile outbreaks. Across the 3 small outbreak scenarios, at the 90th percentile, there was an estimated decrease of 90,000 or more farms impacted by control areas and 150,000 fewer farms impacted by surveillance zones (Supplement 5).

Reduction of Control Areas and Surveillance Zone Size

The reduced control area and surveillance zone scenario was combined with ideal EID tracing for all introduction sites. These scenarios address the secondary objective which was to assess the potential for further decreasing the resources required for outbreak control. All scenarios in this objective utilize ideal EID tracing parameters and day 21 detection.

For all scenarios, the estimated number of IPs increased marginally when the areas under surveillance were decreased. In the large outbreak scenarios, this increase was significant in the Texas feedlot scenario at the 75th percentile and 90th percentile (figure 4.6). The New York dairy scenario at the 90th percentile was very close to excluding zero (figure 4.7). The small outbreaks had similar numbers of IPs with reduced control and surveillance zones. The 90th percentile in the New Mexico stocker introduction did show a decrease in number of IPs with reduction of zone size, this is likely an artifact of stochastic processes in the model, the wide confidence interval supports a high uncertainty around this estimation (figure 4.8).

The impact of reducing the control area and surveillance zones on the duration of outbreaks was less predictable. In the majority of outbreaks, regardless of introduction site, the

change in duration was minimal. When outbreaks began in a Nebraska feedlot, Tennessee dairy, or New Mexico Stocker, at the 90th percentile the increase in duration was less than 30 days. The Texas feedlot in the 90th percentile outbreak had the largest estimated change with up to 70 more days to control the outbreak when the area and zone sizes were decreased. The California dairy introduction had the next largest with 48 more days of the outbreak at the 90th percentile.

The changes in number of farms under surveillance were the most remarkable of the metrics we evaluated. In most scenarios there was a slight decrease in number of farms under surveillance in both the control areas and surveillance zones in the smaller outbreak percentiles. The surveillance zone shift function are shown in figures 4.8, 4.9, and 4.10.

When looking at the number of farms in control areas, the Tennessee dairy introduction saw a significant decrease was seen even at the 90th percentile. Conversely, in the Tennessee cow-calf and Texas feedlot scenarios an estimated increase with a wide confidence interval was seen in the 90th percentile. When looking at the farms in surveillance zones, a similar trend occurred with most smaller outbreaks seeing decreases and some larger outbreaks having the potential for increased farms affected. The Tennessee dairy remains a significant decrease in farms affected at the 90th percentile. In contrast, the Texas feedlot and Tennessee cow-calf are joined by the California dairy as sites that have increased estimated farms at the 90th percentile. The data for farms in surveillance zones are shown in Supplement 5.

Discussion

This study's primary objective was to assess the impacts of three different levels of US cattle traceability in simulated FMD outbreaks. We simulated a variety of introduction sites and farm types to estimate the potential range of effect on outbreak size, duration, and total farms that were under surveillance. The collective result of the simulations was a decrease in the

likelihood of large outbreaks across introduction sites and detection days. This was consistent with our hypothesis, that increasing the speed and accuracy of tracing could improve the ability to surveil at-risk premises and detect their infection more quickly resulting in enhanced implementation of disease control. Across all simulated scenarios, improved traceability decreased the 90th percentile outbreak and in most, decreased the median value or lower percentiles. In smaller outbreaks, there was less opportunity for improved tracing to be impactful in shifting the median or 10th percentile metrics. When outbreaks were larger, improved tracing reduced the outbreaks dramatically, in some cases even down to the 10th percentile. This is similar to the previous Smith, et. al, 2023 results but in greater magnitude [19]. The value of traceability accrues from both the percentage of traces completed, but also the speed with which they are completed. This is particularly important for a disease like FMD which is rapidly transmitted between animals and farms. Delayed completion of traces for FMD result in extended periods of infectivity for undetected and unquarantined herds and delays in implementation of control efforts. These delays may result in increases in outbreak size, as supported by the results of this study.

Our results were extended beyond the implementation of an imagined ideal EID traceability program to include a partial implementation with improved but imperfect tracing. This suggests that even the partial implementation of an EID program could decrease the potential for large and disastrous outbreaks. The partial implementation of an EID program could be more achievable in the short term. Allowing more reasonable goal setting by producers and animal health officials while still providing substantial benefit in the truncation of FMD outbreak risk.

The potential value of improved traceability includes decreased numbers of IPs, decreased duration of the outbreak, and a decrease in the number of premises that were under surveillance during the outbreak. The number of IP's is a key indicator of the cost of an outbreak due to costs to producers and government for quarantine and depopulation efforts [37, 38]. Duration of the outbreak is also an important metric of outbreak cost as it is related to the potential duration of time the country would be excluded from international markets and incurring economic export losses [38]. The number of premises under surveillance in the control area and surveillance zone also add to outbreak costs through government costs associated with surveillance, but also, and perhaps more substantially, to costs borne by premises under surveillance. Farms that are within control areas and surveillance zones are subject to limitations that impact their daily operations and business continuity. This could include decreased ability to move animals to market in a timely manner, increased difficulty to acquire feed and consumables, and costs associated with biosecurity efforts. In order to maintain the operational viability of the livestock industries, less interruption of business continuity in the process of outbreak control is important. Balancing the need for robust outbreak control with the need for ongoing business continuity is challenging. Improved traceability has potential to enhance control while at the same time decreasing the number of farms affected by control efforts and increasing overall industry business continuity.

The secondary objective of this study was to explore the effects of a decrease in the size of control areas and surveillance zones with the implementation of ideal EID traceability. The hypothesis for this objective was that an increased speed and accuracy in tracing could allow for smaller surveillance areas which would decrease resources requirements and increase business continuity. The potential cost savings in human labor needed to conduct surveillance and in

improved continuity of business operations could be highly valuable during and after an outbreak. Interestingly, the results of this project suggest that while decreased size of the control area and surveillance zone may be beneficial in some outbreaks, in others, the number of farms that must be surveilled increased. Additionally, across scenarios, when the control area and surveillance zone sizes were decreased, the number of IPs increased to some degree. We suspect that in the scenarios where the number of farms under surveillance was increased it was due to the increase in the number of IPs resulting in increased control areas and surveillance zones established and an increase in the total area under surveillance and in total farms in control areas and surveillance zones. The mixed results found here do not support that reduced zone sizes are a reliably beneficial practice to decrease the total number of farms under surveillance and supports the current recommendation for zone size.

The value of early detection was evident in the results of all scenarios. Consistently, across location and tracing level, early detection of the outbreak was highly impactful in determining the outbreak size. Outbreaks detected on day 8 were smaller than day 14 detections, and day 21 detections respectively. These results are consistent with previous findings by Smith, et. al, Carpenter, et. al, and Bates, et. al [19, 39, 40]. This supports the continued need for producer and veterinarian education to support early identification. While the value of improved tracing following identification of outbreaks by day 8 is limited, such an early detection may be optimistic and detection at day 14 or 21 may be more likely to represent reality and the potential value of traceability.

Given the small size of many of the outbreaks, tracing efforts had fewer opportunities to make impacts in the outbreak course. These outbreaks were consistent with published literature from other models of the US. For example, Tsao, et. al, in their 2020 publication found that the

areas of Tennessee and New Mexico that we selected had very few resultant IPs when their models were seeded in those counties [41].

This study does not provide a full explanation for the differences in the introduction scenarios that were observed. Comparison of the outputs are confounded by region and index farm type. Additional scenarios with multiple index farm types within each region would be helpful in sorting out this effect. We expect there are interactions occurring between the farm type direct and indirect contact rates, the density of farms in an area, and the local disease spread parameters. For example, dairies and feedlots are parameterized to have much higher rates of indirect contacts than stockers or cow-calf operations. Additionally, dairies have a higher direct contact rate as well. This study only evaluated improved tracing for cattle in a US FMD outbreak. Improved tracing for additional species could increase the overall effect on FMD outbreak impact. Despite these limitations, the results are consistent across regions and index farm type. The results are based on a synthetic population of farms generated from aggregate data. To the extent the synthetic farm file deviates from the true farm and geographic distribution the results could be biased, although the consistent effect across different regions suggests the general results are robust. Finally, the FMD parameters used represent aggregate estimates of infectivity based on the referred literature which is predominated by a few strains that have been more thoroughly researched. An FMD strain with lower relative infectivity might result in less notable value of tracing, similar to the effect noted here in smaller outbreaks. Similarly, an FMD strain with higher relative infectivity might result in a more notable value of tracing, similar to the effect noted here in larger outbreaks. In all cases, whether a more or less infective strain will be introduced, or whether an outbreak will be large or small is not known in advance, but traceability systems must be in place in advance to be useful.

Historically in the US, the implementation of EIDs or radio frequency identification (RFID) tags has been proposed multiple times but has been met with producer resistance [16]. This research supports the value and need for rapid and accurate traceability and the most likely means to achieve it is through the use of EID technology. More economic research is needed to estimate the cost to benefit ratio of improved traceability in the face of an outbreak. Clear economic value of traceability would support EID technology adoption. Further, economic analysis may be warranted on the trade-offs of a decrease in the radii of control areas and surveillance zones. While possibly useful when personnel for surveillance are limited, the risk of detrimental increases in IPs and farms under surveillance in large outbreaks is concerning so the practice cannot currently be recommended.

Conclusions

In the scenarios modeled, tracing was most impactful in decreasing the likelihood of large outbreaks. This was especially evident in outbreaks that had detection delayed to day 21 in the feedlot and dairy introductions. There was a large variability in outbreak size and magnitude of tracing impact depending on day of detection. The impacts of decreasing the size of control areas and surveillance zones was also highly variable and has the potential to be detrimental in large outbreaks. Ultimately, more research into the factors leading to the variability and potential economic impacts of these control strategies is needed for animal health officials to make the most informed decision.

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Figures

Feedlot Outbreaks Current Vs Partial Tracing: Number of Infected Premises

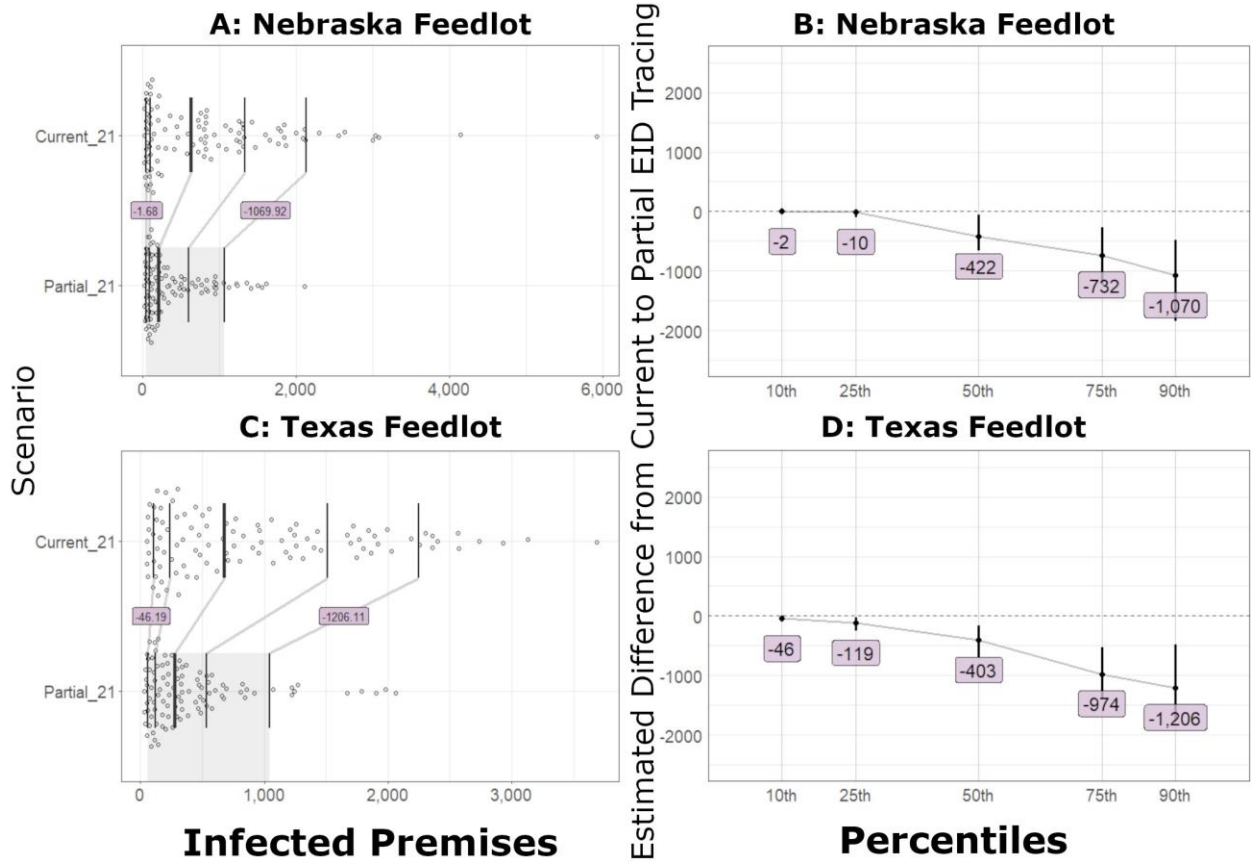


Figure 4.1: Number of infected premises for outbreaks that began in feedlots.

(A) Shift function overlaid on scatterplots of the number of IPs in Nebraska outbreaks detected on day 21 with current and partial tracing. (B) The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for Nebraska outbreaks. (C) Shift function for Texas outbreaks. (D) Bootstrap difference confidence intervals for Texas outbreaks.

Dairy Outbreaks Current Vs Partial Tracing: Number of Infected Premises

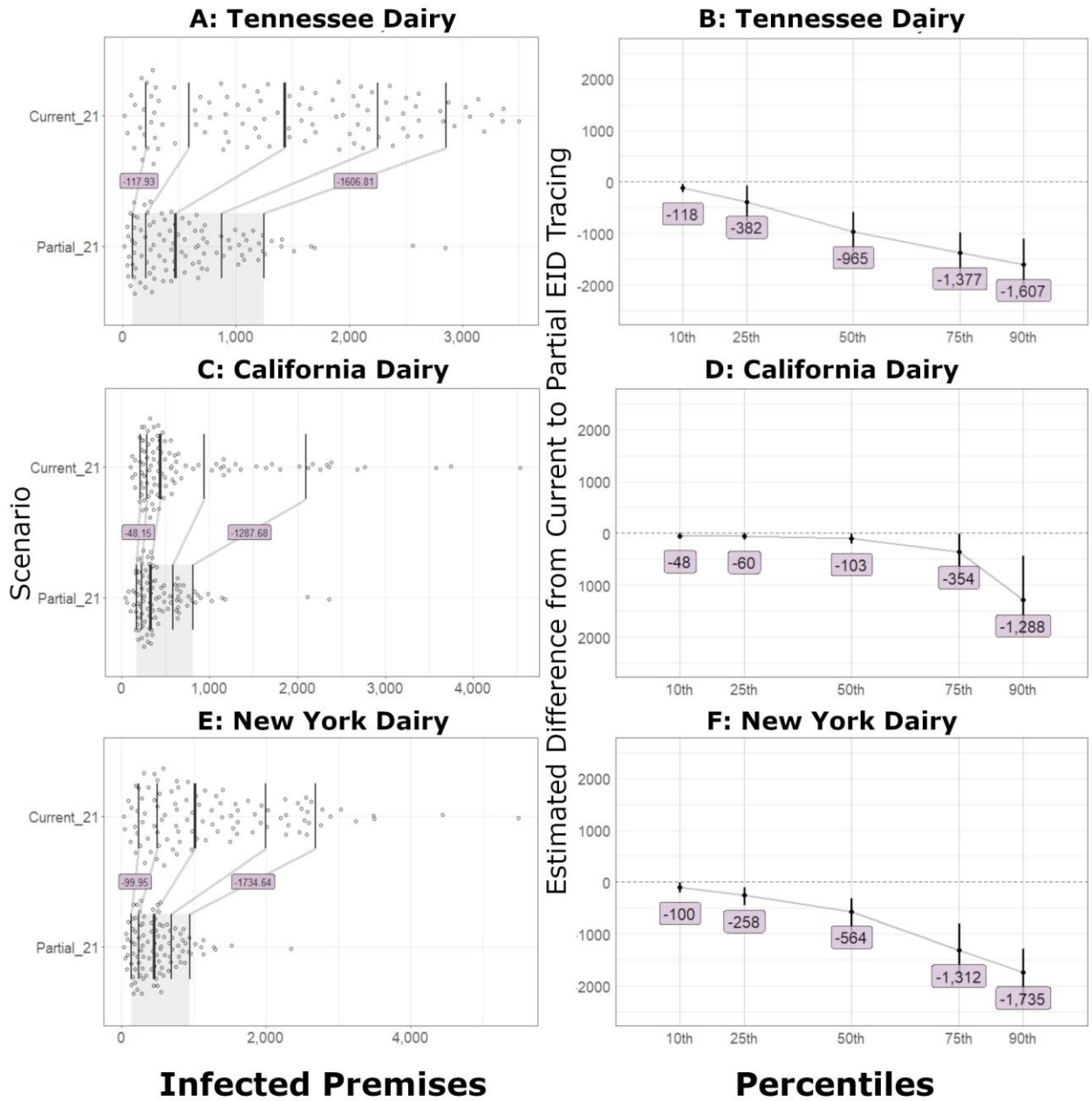


Figure 4.2: Number of infected premises for outbreaks that began in dairies.

(A) Shift function overlaid on scatterplots of the number of IPs in Tennessee outbreaks detected on day 21 with current and partial tracing. (B) The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for Tennessee outbreaks. (C) Shift function for California outbreaks. (D) Bootstrap difference confidence intervals for California outbreaks. (E) Shift function for New York outbreaks. (F) Bootstrap difference confidence intervals for New York outbreaks.

Small Outbreaks Current Vs Partial Tracing: Number of Infected Premises

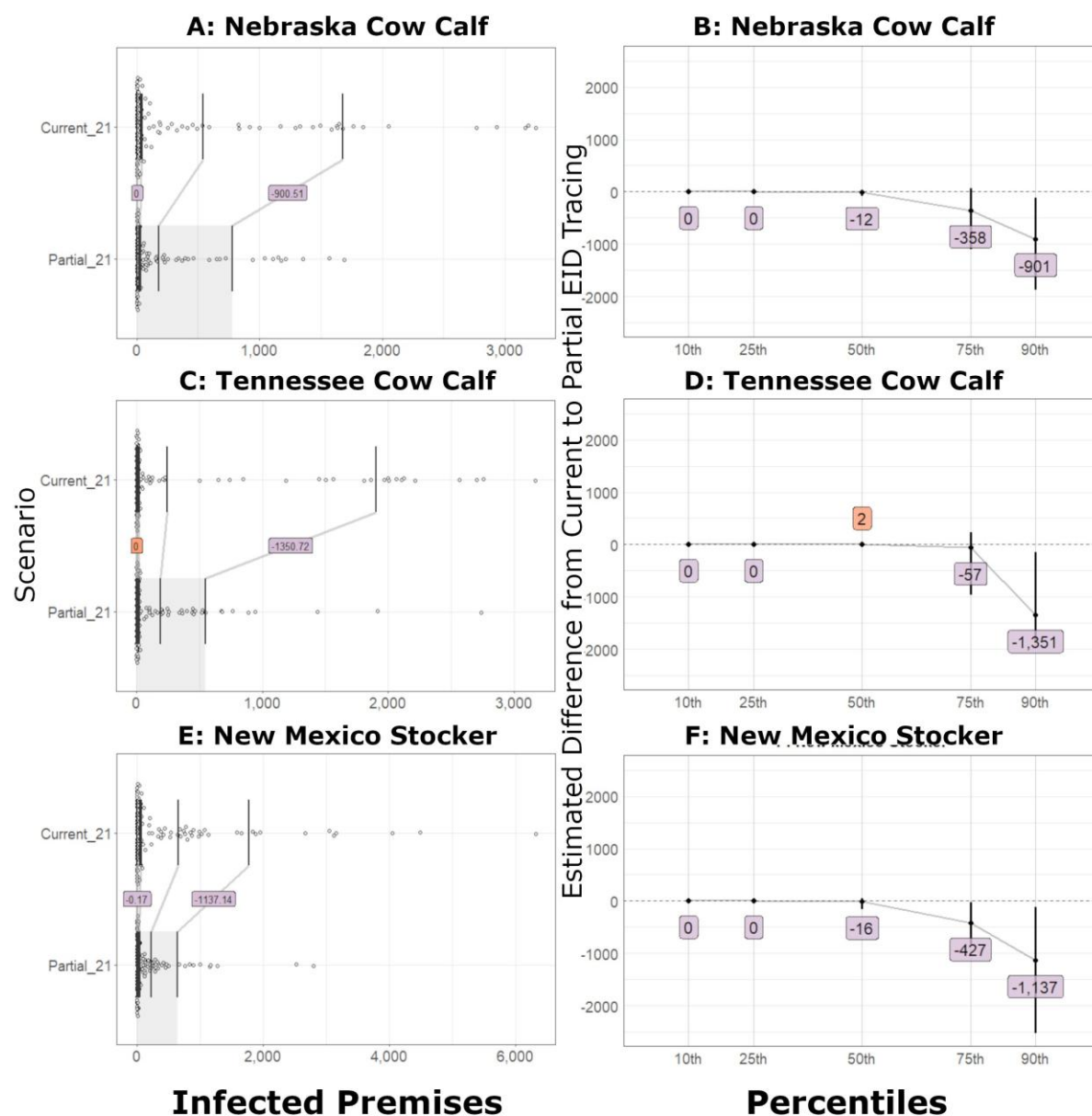


Figure 4.3: Number of infected premises for outbreaks that began in small outbreak scenarios.

(A) Shift function overlaid on scatterplots of the number of IPs in Nebraska Cow-Calf outbreaks detected on day 21 with current and partial tracing. (B) The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for Nebraska Cow-Calf outbreaks. (C) Shift function for Tennessee Cow-Calf outbreaks. (D) Bootstrap difference confidence intervals for Tennessee Cow-Calf outbreaks. (E) Shift function for New Mexico Stocker outbreaks. (F) Bootstrap difference confidence intervals for New Mexico Stocker outbreaks.

All Outbreaks Current vs Partial Tracing: Duration (days) of Outbreak

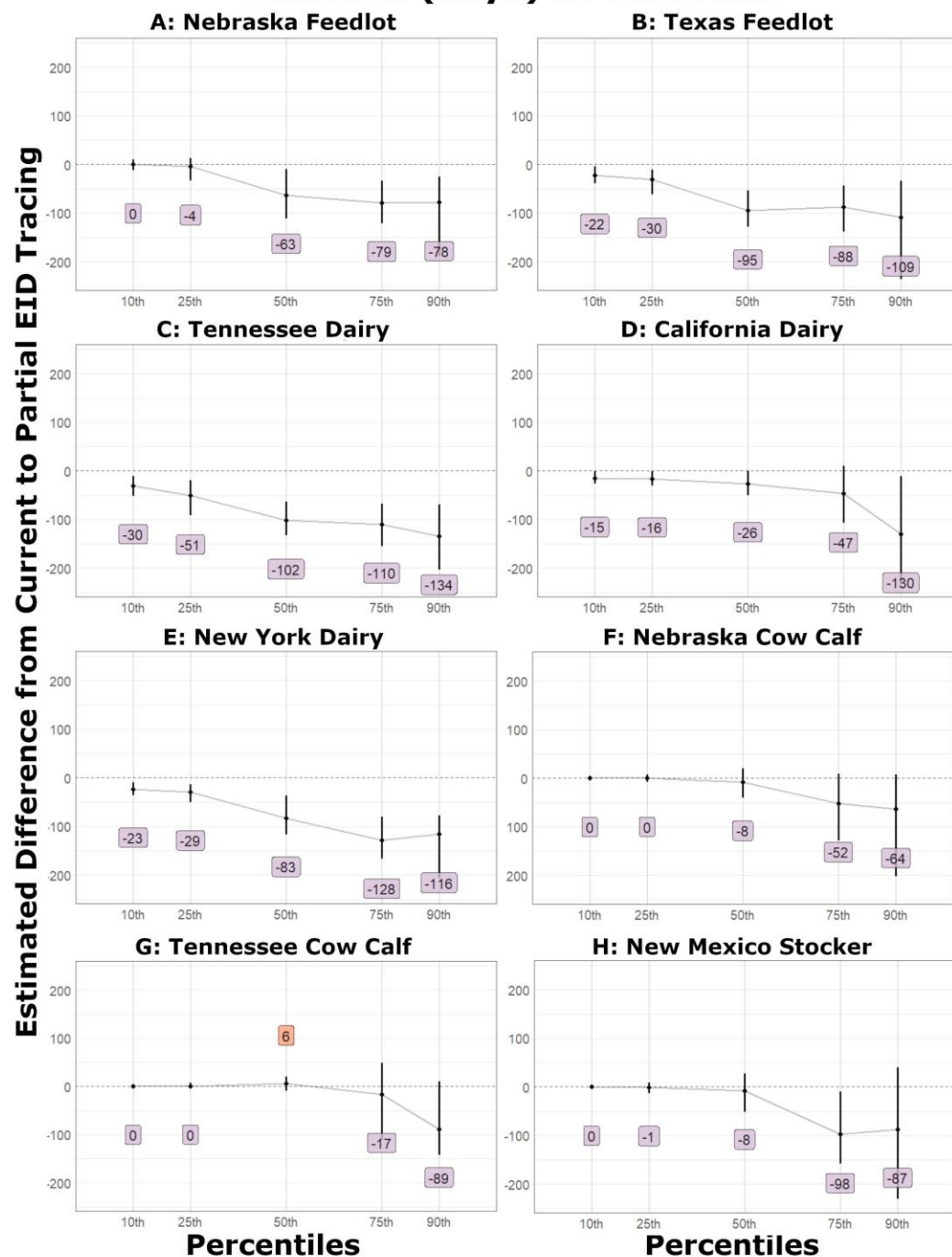


Figure 4.4: Shift function plots for duration of outbreaks in days.

The estimated difference and the bootstrap confidence interval. (A) Nebraska feedlot, (B) Texas Feedlot, (C) Tennessee Dairy (D) California Dairy, (E) New York Dairy, (F) Nebraska Cow Calf, (G) Tennessee Cow Calf, (H) New Mexico stocker.

All Outbreaks Current vs Partial Tracing: Number of Farms in Surveillance Zones

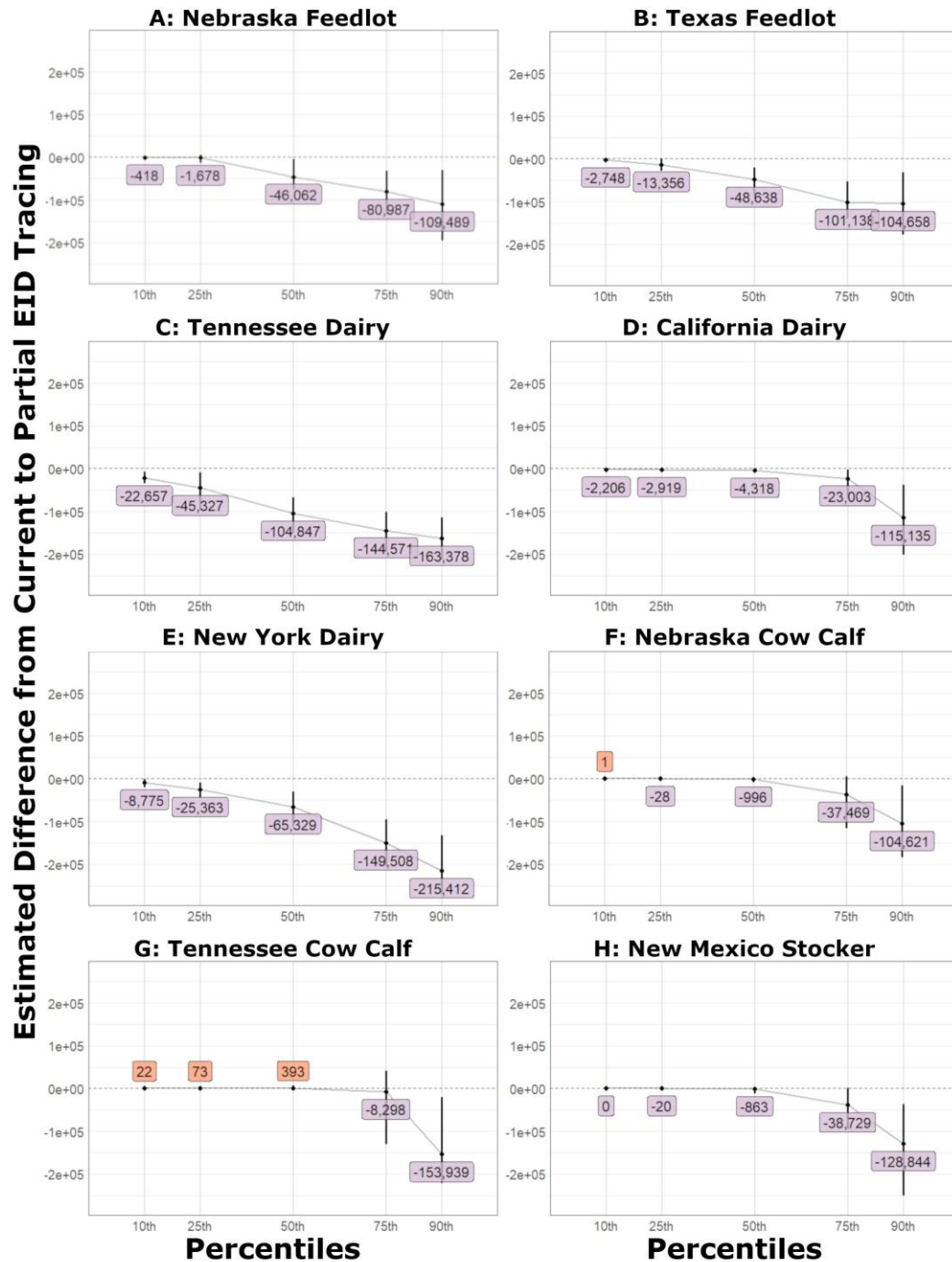


Figure 4.5 Shift function plots for number of farms in surveillance zones.

The estimated difference and the bootstrap confidence interval. (A) Nebraska feedlot, (B) Texas Feedlot, (C) Tennessee Dairy (D) California Dairy, (E) New York Dairy, (F) Nebraska Cow Calf, (G) Tennessee Cow Calf, (H) New Mexico stocker.

Feedlot Outbreaks with Ideal Tracing: Difference between Standard and Reduced Zones

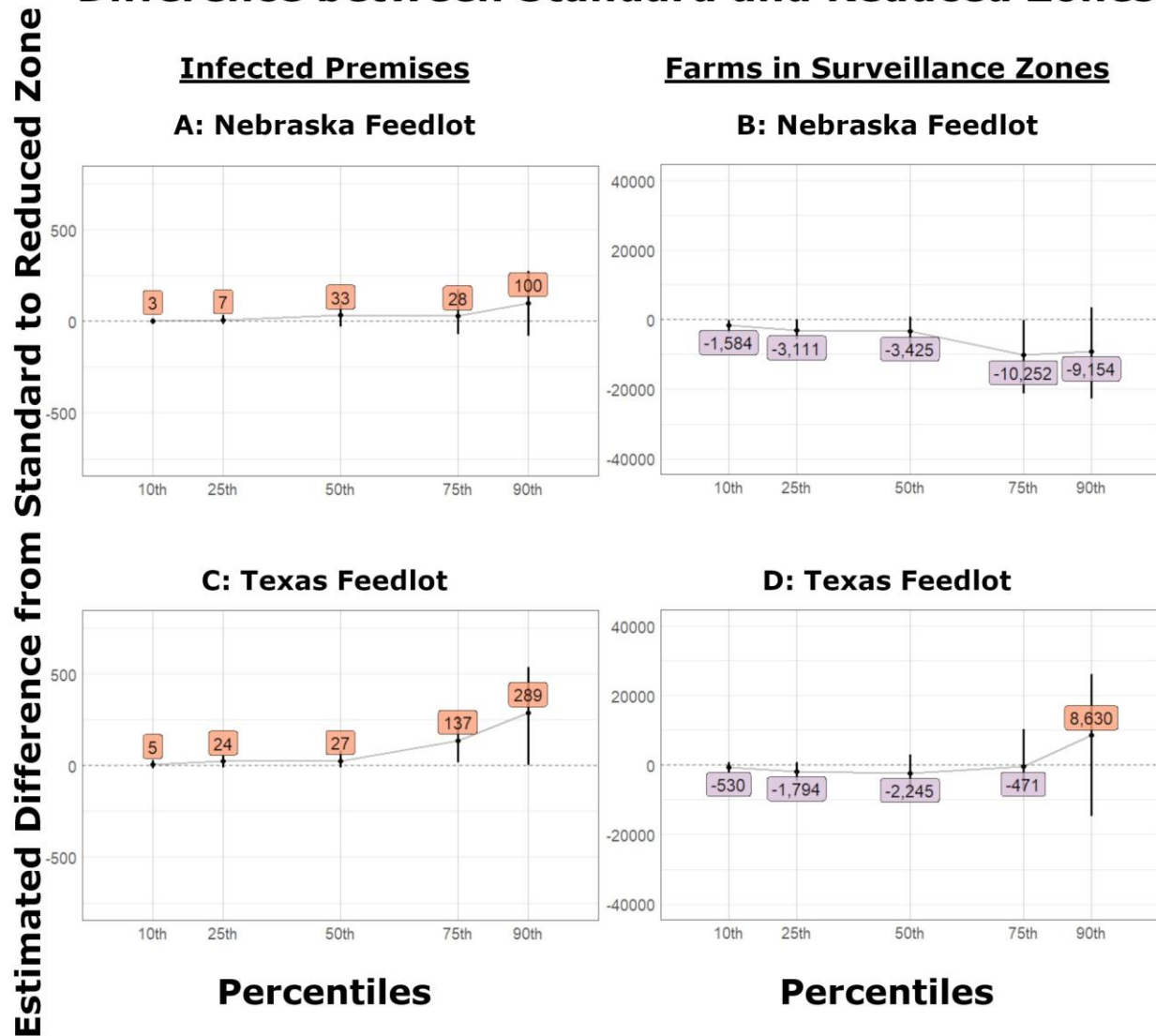


Figure 4.6 Change in number of IPs and farms in surveillance zones in outbreaks that began in feedlots and used reduced control area and surveillance zone radii.

The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for: (A) Nebraska Feedlot outbreaks infected premises, (B) Nebraska Feedlot outbreaks farms under surveillance, (C) Texas Feedlot outbreaks infected premises, (D) Texas feedlot outbreaks farms under surveillance.

Dairy Outbreaks with Ideal Tracing: Difference between Standard and Reduced Zones

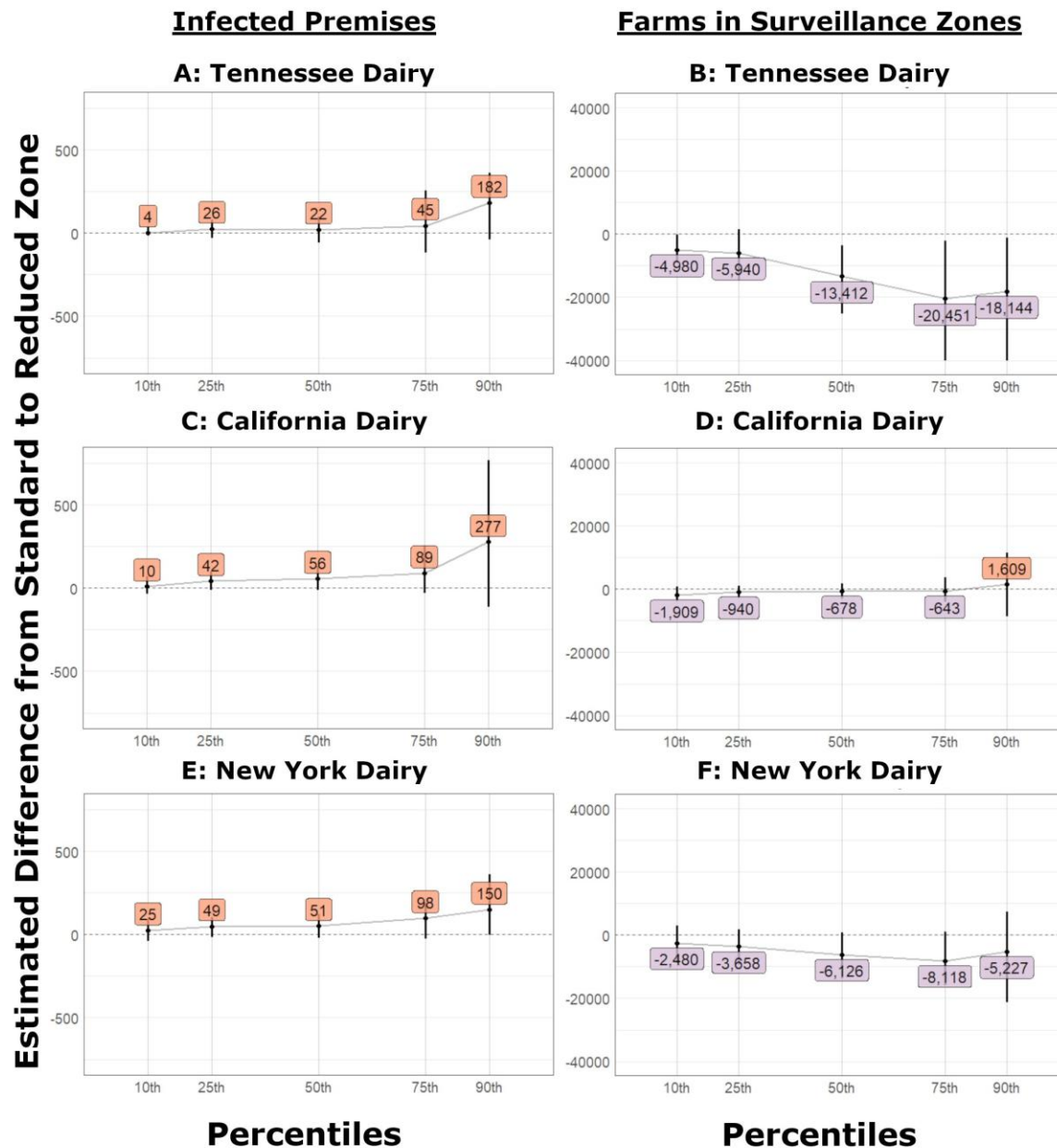


Figure 4.7 Change in number of IPs and farms in surveillance zones in outbreaks that began in dairies and used reduced control area and surveillance zone radii.

The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for: (A) Tennessee Dairy outbreaks infected premises, (B) Tennessee Dairy outbreaks farms under surveillance, (C) California Dairy outbreaks infected premises, (D) California Dairy outbreaks farms under surveillance, (E) New York Dairy outbreaks infected premises, (F) New York Dairy outbreaks farms under surveillance.

Small Outbreaks with Ideal Tracing: Difference between Standard and Reduced Zones

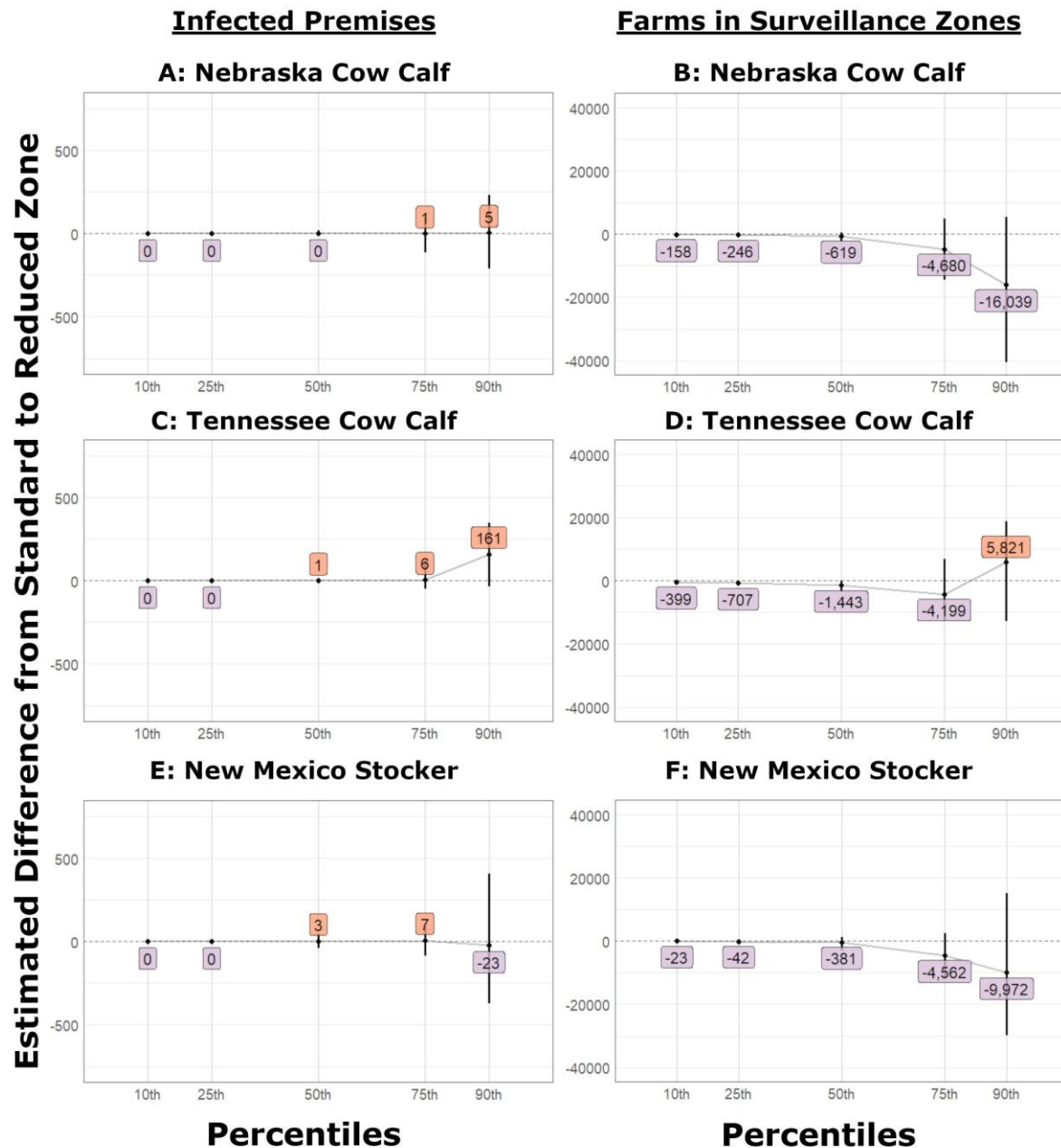


Figure 4.8 Change in number of IPs and farms in surveillance zones in small outbreak scenarios that used reduced control area and surveillance zone radii.

The estimated difference between the partial and current level of tracing and bootstrap confidence interval (vertical line) for: (A) Nebraska Cow Calf outbreaks infected premises, (B) Nebraska Cow Calf outbreaks farms under surveillance, (C) Tennessee Cow Calf outbreaks infected premises, (D) Tennessee Cow Calf outbreaks farms under surveillance, (E) New Mexico Stocker outbreaks infected premises, (F) New Mexico Stocker outbreaks farms under surveillance.

Tables

Table 4.1 Details for Index Case Selection

The index case is the first site of infection that initiated an outbreak. The model then used stochastic processes to determine the progression of the outbreak.

Details for Index Case Selection		
State	Farm Type (herd size)	Justification
California	Dairy (1,386)	California is the top dairy producing state in the US [24]. The selected farm was in the approximate location of Tulare County. Tulare County has the most dairy cattle in California [25].
New York	Dairy (1,859)	New York is the third largest dairy producing state in the US [26]. The selected farm was in the approximate location of Stueben County in rural, western New York.
Texas	Feedlot (37,693)	The Texas panhandle has over 100,000 head of cattle per county in the region [27]. A large feedlot was selected from that region. The Texas panhandle is also a common destination of cattle imported into the US [28, 29].
New Mexico	Stocker (6,053)	A stocker farm in the south-central region of New Mexico was selected based on models from Gorsich et. al, (2016, 2018) that estimated movement of imported cattle in the southern US [28, 29].
Nebraska	Feedlot (6,616)	A feedlot in northeastern Nebraska was selected to represent the Midwest for its proximity to other major livestock-producing states, Kansas and Iowa.
Nebraska	Cow-Calf (642)	Nebraska has approximately 6 million cattle and calves [30]. A farm in central NE was selected for its proximity to many beef producing counties in the state.
Tennessee	Dairy (694)	Tennessee was selected to represent the southeastern US. Tennessee ranks 33 rd for dairy production [31]. The selected farm was in the approximate location of White County, which is in central Tennessee and has the 5th most milk production [32].
Tennessee	Cow-Calf (386)	Tennessee was selected to represent the southeastern US. Tennessee ranks 22 nd for cattle and calves [31]. The selected farm was in the approximate location of Lincoln County, which has the most cattle and calves [33].

Chapter 5 - Assessment of Electronic Identification of Cattle and Digital Movement Reporting in Simulated United States Cattle Movement Networks

MaRyka Smith¹, Michael W. Sanderson^{1*}

¹Kansas State University, College of Veterinary Medicine, Diagnostic Medicine and Pathobiology, Center for Outcomes Research and Epidemiology, Manhattan, KS, USA

Abstract

In a disease outbreak, animal health officials in the United States (US) must identify the diseased and at-risk animals, at a speed that outpaces disease spread. Rapidly transmitted diseases such as Foot-and-Mouth Disease (FMD) likely require Electronic Identification (EID) and digital tracing technology to achieve the speed and accuracy needed for effective trace completion and application of control measures. Currently, the US only requires official EID of dairy cattle and some classes of beef cattle, resulting in an estimated less than 5% usage in beef cattle. Additionally, the US does not require all movements of animals to be reported and does not have a national database of all reported movements. This project's objectives were to create a simulated national cattle movement network to assess the traceability of farms with various levels of digital tracing implementation ranging from the current EID use to an industry-wide application of EID and digital reporting (DR).

A national cattle movement network was created for 30 days of movements using InterSpread Plus. In the network, farms, markets, processors and other premises are nodes and movements between premises are edges. A random sample of 100 cow-calf farms, 100 markets, and 100 feedlots were selected from the full network to be the “farms of interest” to assess the effectiveness of tracing.

To generate traceable networks, tagging was assigned as a source node characteristic using a binomial process to assign EID status. DR was assigned to destination nodes in the same manner. DR was assumed to be into a database accessible to officials conducting the trace. For a movement to be traceable, the source node must tag, and the destination node must report. The movements that were tagged and reported were included in the traceable network for comparison to the full network. The EID and DR probability rates began with a baseline level that represented the current usage in US cattle, and improved across increasing EID and DR rates to the highest level wherein 75% of all beef cattle farms tagged and 90% reported.

In the baseline level, there were zero traceable contacts across all three farm types tested. As EID and DR increased, the traceability increased incrementally. For the highest level of EID and DR, 63.4% of cow-calf farm contacts, 81.9% of market contacts, and 67.5% of feedlot contacts were traceable.

These results support increasing EID tag use and digital movement reporting to enable rapid, effective tracing and provide implementation targets to achieve specific levels of traceability. Untraceable contacts may cause delays in tracing the at-risk farms, which will ultimately delay and undermine the efficacy of control efforts, leading to potential increases in outbreak size and economic impact.

Introduction

Animal disease traceability (ADT) has been defined by the United States Department of Agriculture (USDA) as, “knowing where diseased and at-risk animals are, where they have been, and when they were there” [1]. An efficient and accurate tracing system improves the deployment of disease control resources which can impact the outcomes of a disease outbreak [1]. Rapid tracing can be facilitated by electronic identification (EID) of animals then reporting the movement of an animal including the source and destination data to a searchable electronic database. Currently in the United States (US), digital identification and data availability is limited for cattle movement records which leads to ineffective electronic traces and variable and often extended time periods required to manually complete trace events [2].

The USDA ADT program was implemented over 10 years ago and has resulted in substantial gains in the speed and accuracy of tracing cattle covered under the rule [2]. More recently, the 2024 ADT final rule now requires that covered animals have official identification tags that are both visually and electronically readable [3]. Beef calves less than 18 months of age are not covered by the rule requiring official identification, and therefore are less digitally traceable. Further, in many states, movements that do not cross state lines and movements directly to slaughter are exempt from reporting. These identification and reporting exemptions leave a potentially large number of movements digitally untraceable. Tracing the movement of animals that are digitally untraceable requires labor and time intensive manual methods.

In addition to the federal ADT rules, the US beef industry has shown increasing desire to improve cattle traceability in recent years. The 2016-2020 Beef Industry Long Range Plan listed improving traceability as a priority which prompted the World Perspectives, Inc, to complete a comprehensive study on the feasibility of cattle traceability [4]. The group found that despite

being a “globally-recognized leader” in beef production the US was lacking a robust traceability system for the domestic beef industry and estimated that 45-75 percent of producers adopting traceability technology could result in 35-90 percent of US beef being traceable [4]. The report stated this range was “Nationally significant and economically efficient.” However, no data was provided to support this conclusion. The next iteration of the Beef Industry Long Range Plan (2021-2025) described traceability as “critical and urgent” to protect the health and well-being of US cattle [5]. A goal of 75% of cattle producing states participating in a national traceability program was described in that plan. The potential utilization of improved traceability to increase beef exports and protect the domestic industry against the unmitigated spread of disease was also mentioned in the plan. The percentage of the producers that adopt EID is almost certainly linked to the percentage of US beef that is traceable but the relationship between the two variables has yet to be explored.

Previous research has shown the possible benefits of improving traceability for controlling diseases such as Foot and Mouth Disease (FMD). In an FMD outbreak model centered in the Texas high plains, Hagerman, et al. found that the ability to trace 90% of movements within 2 days decreased the median number of animals that had to be slaughtered, and median number of herds that were subjected to movement restrictions compared to a scenario with 30% effective tracing within 2 days [6]. They also found that 90% effective tracing within 2 days was the lowest cost option for disease control compared to delayed or reduced efficacy tracing. In a US national FMD model with scenarios initiated in 7 different introduction sites, Smith, et. al found that improved tracing of approximately 70% of cattle contacts within 2 to 3 days resulted in fewer infected premises and shorter outbreak duration [7]. If the tracing accuracy and speed were further increased to 99% of traces completed within 1 day, the outbreak

sizes and duration could be further reduced [7]. No estimate of the number of premises tagging and reporting movements to achieve those levels of traceability has been reported.

The objectives of this project were to create a simulated movement network of all cattle movements in the US, including the movements that are generally exempted from reporting then utilize the application of tagging and digital movement reporting at varying rates to generate traceable movement networks. The traceability of randomly selected cow-calf, feedlot, and market farms were compared between the full and traceable movement networks.

Materials and Methods

Objective 1: Network Simulation

Initialization of Model

Generation of the national cattle movement network utilized the program InterSpread Plus (ISP) (Version 6.01.44) [8]. ISP is a spatially explicit modelling software developed for modelling outbreaks of disease. Within a disease simulation, ISP models the risk of disease transmission via animal movements using stochastic processes to determine the source farm, the movement distance, and specific destination farm in a defined population.

The base parameter set and population file used in ISP were developed by the USDA Center for Epidemiology and Animal Health (USDA-CEAH) for the national FMD model. The population file from USDA-CEAH which was developed from agriculture census data collected by the National Agriculture Statistics Service (NASS), includes all FMD susceptible domestic livestock species.

Movements are modeled as the connection from one farm to another, the explicit animals involved are not reported. The rates of animal movements were defined using parameters developed from National Animal Health Monitoring System (NAHMS) studies and expert input

when data was incomplete. The movement rates from source farms are defined by a Poisson process specific to each farm type. The movement distance is defined by a look-up table that has the upper bound of each movement distance interval and probability associated with that distance interval. The destination farm type is defined by a look-up table of each possible destination farm type for a given source farm and the associated probability of shipment to that destination farm type. Movements through animal markets are generated at the source farm level and define the final destination based on the source farm type. All movements, including those to market are generated on a daily basis. A sample of the movement rates by farm type and region are shown in Supplementary materials 1 of appendix C.

Over 60 movement types are defined in the ISP parameter set. The majority of movement types define the direct movements from one farm to another, to markets, and to processors. The parameter set also defines movement types designed to capture indirect contacts between farms. Due to the sensitivity to changes in the parameter file, the indirect movements and those from non-cattle farms could not be removed prior to network simulation and were addressed in post-processing. ISP reports the movements in a plain-text format detailing the day of the outbreak, movement number, source farm identification, and destination farm identification. In the FMD model, the only movements that ISP tracks and reports are those that are from infected, but not yet detected, farms. To coerce ISP into reporting all direct movements, all cattle farms from the national farm population file were designated as infected sites at the initiation of the model. The model scenario parameters were altered to remove all FMD control measures including detection, movement restrictions, and surveillance generating a 30-day network of all simulated cattle movements. The completed simulated network will subsequently be referred to as the full network.

Post Processing of Movement Simulation Data

All post-processing of simulated movement data was performed using R version 4.1.1 and R Studio 2024.09.0 [9, 10]. The details of the post-processing methods described below are provided in the R code of Supplementary materials 2 in appendix C.

All movements that involved a non-cattle farm type as either the source or the destination were removed. Similarly, the indirect movements as defined in the parameter set were identified by their movement number and removed.

Market Movements

Market movements in ISP are simulated in two ways. ISP simulates markets as a “pass-through” movement where the source farm and the destination farm are specified, but not the identity of the market. Separately, ISP simulates market movements for the purposes of potential market contamination and subsequent transmission from the market. These “contamination” movements report the source farm and market identification but do not report a final farm destination.

For our network, market movements required an explicitly defined source, market, and final destination. For source farms making a “pass-through” movement, we utilized the information reported for the “contamination” movements to explicitly assign a market node. If the source farm had multiple markets contacted via “contamination” movements, the closest market geographically was assigned to the “pass-through” movements. If a farm making a “pass through” movement did not complete any “contamination” movements, the farm’s “pass through” movements were randomly assigned to a market within the source farm’s state. Two exceptions to the same-state assignment occurred. First, farms that were in the upper peninsula of Michigan were assigned to a market in Wisconsin. Second, since New Hampshire did not have

any markets and Maine, Vermont, and Massachusetts had very few, pass through movements were assigned to a market within the combined four-state area.

Model error messages: Failed movements and correction

In some cases, modeled movements “failed” in ISP and resulted in a warning message describing the failed movement. The warning message reported the source farm identification, movement type, destination farm type, and the reason for the movement failure. Most commonly, the reason for movement failure was the inability to find the designated destination farm type in the distance band that was selected.

The most common failed movement types were destined for a large feedlot. The ISP population only contains 43 large feedlots which are all located in the central or western states of the US. Thus, farms located outside of that area often failed to complete the generated movement because there was no large feedlot within the selected movement distance interval. The failed movements were recovered in post-processing by randomly assigning the destination to a feedlot in the same region as the source farm, or if no such feedlot of the selected size existed in the same region (defined in supplementary materials 1 of appendix C) then an appropriately sized feedlot in KS, TX, IA, NE, CO, or OK was randomly assigned. If movements failed due to the inability to find a market those movements were deleted from the network since no final destination was reported by ISP.

Network description

The size of the full network was assessed using the total number of movements and number of farms included. The overall average degree of the network, average path length (shortest number of movements between any two farms), density, reciprocity, diameter and transitivity were also calculated.

Objective 2: Utilization of Electronic Identification

All manipulation of the network for traceability assessment was performed using R version 4.1.1 and R Studio 2024.09.0 [9, 10].

Application of Tagging and Digital Reporting

Sixteen cattle farm types characterize the nodes in the generated cattle network. Table 5.1 details the farm types and the total number of nodes in the full network. There are 15 farm types that may serve as source farms for a movement, as livestock processors may only serve as destination. Electronic tagging (EID) was applied to individual source farms as a binomial process $\text{binomial}(n=1, p=\text{probability of tagging})$. Farms that were assigned to apply EID placed tags on all outgoing movements. There are no movements that are partially tagged. Digital reporting (DR) was applied to individual destination farms as a binomial process, $\text{binomial}(n=1, p=\text{probability of reporting})$. Farms that were assigned to DR reported all incoming tagged movements to an accessible database. This process is detailed in the R code of Supplementary materials 3 of appendix C.

Within the network, tagging farms may generate movements to non-tagging farms. When these non-tagging farms generate outgoing movements, a portion of those movements would contain tagged animals from an incoming tagged source. An example of this would be a cow-calf farm that tags and ships to a stocker farm that does not tag. The tagged animals that were in the movement to the stocker would remain tagged in later movements to a feedlot or other destination. To capture this complexity, a secondary tagging rate was applied to all non-tagging farms that both received and made movements. The secondary rate was calculated using Equation 1.

$$\text{outgoing tag probability} = \frac{\# \text{ tagged movements received}}{\# \text{ total movements received}}$$

Equation 1: Calculation of outgoing tag probability for non-tagging farms that received tagged movements and served as a source farm.

Finally, the outgoing movements from that farm were reassigned as tagged or not using the calculated rate in a binomial process *binomial*($n=1$, $p=\text{outgoing tag probability}$). The R code for this process is detailed in supplementary file 3 of appendix C.

Scenario Development

The baseline tagging and reporting scenario was developed using expert input from the Kansas Department of Agriculture traceability team, US CattleTrace, and other industry experts. This scenario was designed to represent the current use of EID, with most farm types being low EID adopters (1-2%) and the dairy cattle farm types having higher current utilization (95%). The DR rates to an accessible database were assigned similarly with most farm types low (1-5%) and dairy cattle higher (90%). Table 5.2 details the tagging and reporting rate used for each of the farm types in the network.

The improved EID/DR scenarios were developed to assess the impact of possible increased adoption of EID technology and reporting by producers on traceability success. Specific combinations of increased tagging and increased reporting were developed focused on implementation in the cow-calf sector, auction markets, and across all beef sectors. The dairy cattle EID and DR rates were held constant for all scenarios.

The cow-calf producer is the first step in an animal's life cycle in the beef production system, thus we hypothesized that EID and DR rate changes in this farm type may impact downstream traceability success. Increases of EID and DR rates were made for the cow-calf farms with additional increases in other farm types to represent how the industry as a whole

might respond to the EID and DR technology being more widely adopted. The EID rates for feedlots remained at the baseline for all cow-calf focused scenarios. These scenarios are detailed below in Table 5.3.

The change of cattle ownership at markets are presents a possible site for strategic intervention in application of tags. The scenario, Market 50/50 increased the EID and DR rate of markets to 50% and increased the DR rate of feedlots and processors to reflect wider adoption of the technology. The Market 90/90 scenario improved the EID and DR rate of markets to 90% and kept the DR rate of feedlots the same as Market 50/50 The EID and DR rates of all other farm types remained at the baseline. These scenarios are detailed in Table 5.4.

The next group of EID network scenarios were developed to assess the application of industry-wide tagging improvements. Changes in tagging and reporting were applied to all beef sectors in these scenarios. The All 50/75 scenario increased EID to 50% and DR to 75%. The All 75/75 scenario increased EID to 75% and DR to 75%. The final scenario, All 75/90 increased EID to 75% and DR to 90%. These scenarios are detailed in Table 5.5.

Lastly, two EID network scenarios were tested to assess the improvement of EID and DR rates separately. An All 90/50 scenario with 90% of all farms tagging and 50% of all farms reporting was completed. Then a contrasting, All 50/90 scenario, with 50% of all farms tagging and 90% of all farms reporting was tested. These scenarios are detailed in Table 5.6

Traceable Network Analysis

The digitally traceable networks were created by filtering the full network to only include the movements that were tagged and reported to an accessible database. The number of digitally traceable movements in the network represent the total number of movements that would be accessible to an animal health official for tracing, given the EID and DR rate of that scenario.

The traceable networks were assessed in the same metrics as the full network, described above, with the addition of the percent of movements included. The calculation for percent movements included is shown in Equation 2.

$$\text{percent of total movements} = \frac{\text{digitally traceable movements}}{\text{total movements in full network}}$$

Equation 2: Calculation of the percent movements traceable

Tracing Individual Farms of Interest (FOIs)

The R package, EpiContactTrace, was used to trace the incoming movements in the temporal contact chain to the Farms of Interest (FOIs) [11]. The function “Trace” was defined by the movement network being traced, the FOI as the starting node, the ending day, and the number of days to trace into the past. The resultant “ingoing” contacts were extracted for final evaluation.

Cow-calf and feedlot FOIs

To assess traceability, 100 randomly chosen cow-calf farms and feedlots were identified as FOIs. The farms that were eligible for selection had at least one contact in the full network during days 2 to 28. In an actual FMD outbreak, the 28 days of trace-back efforts would start from the first day clinical signs were observed [12]. To reflect this practice, we modeled trace back efforts the previous 28 days beginning on day 30 of the network for each FOI.

The tracing protocol for cow-calf and feedlot FOIs began by identifying the movements that had the FOI as the destination. Those movements were separated into direct farm-to-farm movements and movements from a market. Next, the movement file was filtered to only include direct farm to farm movements (no markets), after which the direct movements were traced for all possible incoming (including all upstream) movements to the FOI.

If an FOI had received a movement from one or more market(s), the movement file was filtered to only include one market at a time, while the incoming movements to that market were traced for the day the FOI contacted the market and the 6 previous days (1 week of contacts). The process was completed for all markets identified for the FOI. This captured the weekly behavior of markets in the US as closely as possible given ISP's daily movement generation.

The movements identified through direct and market tracing efforts were combined to determine the total number of incoming movements to the FOI. The movements were then converted to individual contacts by counting the unique farm identifiers present in the incoming movement record. This eliminated any duplication of movements from the same source to the FOI. From this point forward a movement will be defined as the connection between two farms, and a contact as the individual farm identified in tracing efforts. As an example, two movements from Farm A to Farm B would only represent 1 contact for Farm B.

The protocol described above was used for tracing FOIs in the full network and all derived digitally traceable networks. An example of this process as detailed in the R code is provided in supplementary material 4 of appendix C.

To capture a more realistic application of digital tracing in a disease outbreak scenario, a "1 phone call" tracing method was also developed. In this method, farms that had zero contacts in the initial EID/DR scenario standard protocol for tracing as described above would be investigated by making "1 phone call" to the producer to gain an oral report of any incoming movements from a market. The market contacts would then be traced in the EID/DR scenario for the time period relevant to the FOI's contact with the market. The contacts found after tracing from the market were then recorded as belonging to that FOI and combined with the rest of the results from the standard tracing protocol for that EID/DR scenario.

Market FOIs

The selection of 100 markets as FOIs followed a similar process to the cow-calf and feedlot, but also included the selection of a random market day to begin the tracing efforts. Markets that received shipments were filtered to only include days 7 to 30. Then, from the list of movements, each market had one day selected. Finally, 100 combinations of a market and its randomly selected day were selected to be FOIs. The markets were traced as though the random day selected was the day that animals with clinical signs were observed at the market.

The tracing protocol for market FOIs started by filtering the movement file to remove all markets except the FOI of interest. Then, the selected day and 6 previous days of movements into the market were traced. The movements were then converted to individual contacts by counting the unique farm identifiers present in the incoming movement record.

Analysis of FOI Tracing Outcomes

The number of contacts traceable for each FOI in the full network movement record represented the total number of contacts for that FOI. The calculation for the percent of contacts traceable for a given FOI in a specific EID/DR scenario is shown in Equation 3. The percent of contacts traceable was averaged over the 100 FOIs for each farm type.

$$\text{percent contacts traceable} = \frac{\# \text{ contacts traceable with EID/DR}}{\# \text{ contacts in full network}} * 100$$

Equation 3: Calculation of the Percent Contacts Traceable for a given FOI

If zero contacts were found for a given FOI in a given EID/DR scenario, that farm was considered digitally untraceable. The number of untraceable farms was calculated for each farm type and EID/DR scenario.

Results

Description of the Full Network

ISP generated 1,397,206 successful movements of cattle. There were 3,107 movements recovered from the failed movements warning file, of which 2,715 were feedlot movements. There were 339,410 pass-through market movements that were assigned an explicit market node. The number of movements that were unable to be reassigned and were thus omitted represented less than 0.04% percent of the total movements included in the network. After processing, the full network included 1,739,723 movements from 615,470 cattle farms, markets, dealers, or to processors. The average path length (shortest number of movements) between any two farms was 7.38 and the overall average degree (number of connections each farm has) was 5.65. The complete description of the full network metrics is shown in Table 5.7. Additional metrics of the full network and breakdown of the incoming and outgoing degrees by farm type is included in Supplementary material 5 of appendix C.

Number of Contacts Found for each FOI in the Full Network

The range of contacts identified in the full network for cow-calf FOIs was 1 to 560 contacts with a mean of 36.79 contacts, a median of 1 contact, and 75th percentile of 3.25 contacts. Of the 100 FOIs chosen, 77 had fewer than 5 contacts. Low contact numbers suggest that the FOIs had no market contacts and only limited direct farm-to-farm movements, primarily from farms that also had few incoming movements. The FOIs with higher numbers of contacts received one or more movements from market(s). Figure 5.1 demonstrates the distribution for number of contacts from cow-calf FOIs truncated at 25 contacts. Twenty cow-calf FOIs had greater than 25 contacts and are excluded from the graph.

The range of contacts for feedlot FOIs was 1 to 4,197 contacts. The average number of contacts was 519.1, the median 283 contacts, and 75th percentile was 597.2 contacts. Out of 100 feedlot FOIs, 88 had at least one contact with a market. Many of the feedlots had multiple contacts with markets resulting in the increased number of possible incoming contacts. Figure 5.2 demonstrates the distribution for number of contacts from feedlot FOIs.

The range of contacts for market FOIs was 12 to 498 individual farms over the 7-day tracing period. The average number of contacts was 108.2, the median was 80 contacts and the 75th percentile was 114 contacts. Figure 5.3 demonstrates the distribution for number of contacts from market FOIs.

Number of Movements in the Traceable Network per Scenario

The number of movements in the digitally traceable network increased with increasing EID and DR rates. In the baseline EID/DR scenario only 3.25% of all movements from the full network were present in the traceable network. The majority of movements were only present in traceable networks with both high rates of EID and high DR. The most remarkable increases in number of traceable movements occurred when the EID and DR rate increases were applied to the industry as a whole. The total number of movements in each EID/DR traceable network, and other network metrics are detailed in Table 5.7.

Untraceable Individual Farms

The number of FOIs that were digitally untraceable (none of full network contacts identified) decreased with the improved EID and DR rates. An untraceable FOI represents the failure of the first movement into that FOI to be tagged, reported, or both. If the first movement into the FOI is not in the digital database there are no other potential chains of contacts to search. In the real-world these FOIs would have to be manually contacted and traced. The percent of

untraceable farms are summarized in Table 5.8. A lower number indicates higher traceability success. There was no scenario where all FOIs were at least partially traceable (at least one contact found).

Percent of Contacts Traceable

The percent of contacts traceable varied widely among scenarios and FOI farm type. Market FOIs tended to have the most success in having at least partial traceability. In the baseline scenario, no contacts were found for any of the FOIs across all three types. The majority of the movements that were included in the baseline traceable network were dairy movements (data not shown). Increasing the EID and DR rates in the cow-calf-focused scenarios made only slight improvements in the downstream traceability of feedlots and markets. This was likely due to low EID/DR rates at the intermediate farm types and low levels of reporting at all farm types. The most successful was the cow-calf 50/75 scenario where an average of 36% of cow calf and 38% of the market FOI contacts were digitally traceable. Increasing the EID and DR rates at markets improved the traceability of market FOIs but had no impact on the traceability of cow-calf FOIs and a produced little improvement in traceability of feedlot FOIs. The most notable improvements in traceability were in the scenarios where EID and DR rates were improved for all farm types. At 50% EID and 75% DR there were nearly 50% of contacts traceable for market FOIs using digital tracing. As the EID improved to 75% and DR to 90% over 60% of cow-calf and feedlot contacts were digitally traceable and over 80% of market contacts were digitally traceable. Despite this marked improvement in traceability there were still individual FOIs across all three farm types that were digitally untraceable or had very few contacts traceable.

In the scenario with EID at 90% and DR at only 50% there were only about 50% of movements included in the traceable network and 21% to 38% of the average percent of contacts

traceable. In contrast, when 50% of farms used EIDs and 90% of farms reported, 67% of all movements were included in the digital database and nearly 50% to 70% of the average percent of contacts were found. The market FOI traceability nearly reached the goal of 70% of contacts being traceable in this scenario.

Cow Calf FOIs

The percent of contacts for each FOI that were traceable and the median percent of contacts traceable in each scenario is shown in Figure 5.4. The improvements in median digital traceability for the cow-calf FOIs was minimal for all cow-calf and market-focused scenarios. The highest median percent of contacts traceable in these scenarios was nearly 36% in the Cow-Calf 50/75 scenario. As the EID and DR rates increased in the all-farm type scenarios, median percent of contacts digitally traceable increased up to an average of 63% in the All 75/90 scenario. The description of the distribution of percent contacts found for cow-calf FOIs is shown in Table 5.9.

Feedlot FOIs

The distribution of the percent contacts for each feedlot FOI and the average percent of contacts traceable are shown in Figure 5.5. The mean percent of contacts traceable for feedlot FOIs was lower than that of cow-calf and market FOIs in all cow-calf focused scenarios. In the market-focused scenarios, the feedlot FOIs had higher percent contacts traceable than the cow-calf FOIs. However, the average was less than 1% of contacts traceable which is unlikely to make a difference in a real-world scenario. In the All 75/90 scenario, the feedlot FOIs had an average of 67.5% of contacts traceable. This was a 24.3% increase from the All 75/75 scenario. In the All 75/90 scenario, there were also increases at the 10th percentile of percent of contacts

traceable and up to an average of 55% of contacts traceable at the 25th percentile. The description of the distribution of percent contacts found for feedlot FOIs is shown in Table 5.10.

Market FOIs

The distribution of percent contacts traceable for market FOIs is shown in Figure 5.6. The mean percent of contacts that were traceable for market FOIs were consistently higher than those for cow-calf and feedlot FOIs. In the market-focused EID/DR scenarios, the traceability of market FOIs was notably higher than the cow-calf and feedlot FOIs at approximately 8% and 15%. These levels are still unlikely to be impactful in a disease tracing event. Market FOIs achieved the highest traceability of all FOI types in the All 75/90 scenario with over 80% of contacts traceable an increase of over 25% from the All 75/75 scenario. The description of the distribution of percent contacts found for market FOIs is shown in Table 5.11.

1 Phone Call Tracing

The “1 phone call” method was used to further investigate the traceability of cow-calf and feedlot FOIs. This method simulated the effect of animal health officials gathering an oral report of market movements received by cow-calf or feedlot FOIs that were digitally untraceable in a given EID/DR scenario. The increase in contacts found varied from 1.5-3%. In the market 90/90 scenario feedlot FOIs had a 16% increase in percent contacts traceable and the number of untraceable feedlot FOIs decreased from 96 to 14 farms. The “1 phone call” method also increased the traceability of cow-calf FOIs decreasing the number of untraceable farms by 4 to 19 farms across the scenarios tested. In the All75/90 scenario, the number of untraceable feedlot FOIs decreased to 4 with the average percent contacts traceable increasing to over 70%. The full results of the “1 phone call” scenarios are compared to the standard tracing method in Table 5.12.

Discussion

This study created a simulated movement network for all cattle movements in the US. Using that full movement network for comparison, tagging and reporting networks were generated and the potential traceability of randomly selected farms was assessed. The results of this study saw an improvement from 0% traceability for all FOIs in the baseline scenario to 60-80% traceable contacts for FOIs at the highest level of EID and DR use. The scenarios that focused on improving traceability from the cow-calf or market origins made small improvements in the traceability of all FOI types but likely are insufficient in outbreak control. The most remarkable improvements were in the scenarios, All 75/75 and All 75/90, where all farm types had increased EID and DR rates.

The hypotheses that drove the parameterization of the All 75/75 and All 75/90 scenarios were based on previous research by Smith, et. al, which suggested that tracing 70% of contacts within 2-3 days could be impactful in controlling an outbreak of FMD [7]. In the All 75/75 scenario where at least 75% of farms applied tags and reported incoming movements, the total number of movements in the digital database approached this threshold. However, the individual traceability of FOIs remained lower due to individual losses of contact chain connections. In the highest EID and DR scenario where at least 75% of farms tagged and 90% reported movements over 70% of movements were included in the digital database and markets met the goal of over 70% of contacts traceable. The cow-calf and feedlot FOIs remained slightly below 70%. This likely indicates that the goals for EID and DR adoption in the US need to be higher than previously estimated in the Beef Long Range plan and World Perspectives report to be effective disease control in an outbreak scenario.

This study utilized the current estimates of EID and DR use in the cattle industry with input from State Animal Health Officials and other industry experts to parameterize the baseline traceable network. The experts consulted by the authors expressed that currently, digital tracing often has a low probability for success, consistent with the poor performance of the baseline scenario. In order for the system to be viable it must save time, money, and labor when implemented. The higher levels of EID and DR use are likely what are needed to make the process useful for FMD tracing. Furthermore, the EID and DR rates need to increase simultaneously to result in effective digital tracing. The All 90/50 scenario represents the possible outcomes if EID rates are increased without increased DR. The traceable network that resulted from the All 90/50 scenario had fewer movements included than the All 50/90 scenario that represented an increase in DR without an increase in EID. Both of these scenarios had fewer movements in the traceable network than the All 75/75 scenario.

Trace-back efforts from each FOI type represents the traceability of movements going into that farm type. The cow-calf FOIs tended to be lowest in scenarios where EID and DR were improved at sites upstream in the production system. In comparison, the traceability of feedlot FOIs improved more markedly when the market EID and DR rates were improved. Ultimately, success of a digital trace is dependent on the continued connections from farm to farm; if the connections are broken, there is no information to identify the next incoming contact. The failure of the first movement to be traceable was seen across all scenarios, including those with industry-wide, high levels of EID and DR. In Figures 4-6 individual FOIs can be observed with 0% traceable contacts even at the All 75/90 scenario. In an outbreak, a producer is likely to be able to manually report their direct contacts to a surveillance team and ensure the connection to the first farm or market can be identified manually allowing initiation of an electronic trace from

the identified premises. That process would still come at the potential delay of the dispatch of the surveillance response team. We attempted to represent this scenario with the “1 phone call method” to support subsequent electronic tracing. Our discussion with State Animal Health Officials suggested that making phone calls to producers was commonplace in the current tracing efforts and would easily be implemented in an outbreak scenario. Additionally, in many states, markets are required to keep records of incoming animals and routine reviews of those records are conducted for compliance.

This project assumed that all reported movements were in a database that was completely accessible to the person completing the trace. Currently, there is not a centrally located database for reporting movements in the US that captures data from all states in an accessible format for all state and federal animal health officials. Instead, the US has multiple databases that may contain pieces of the information needed to conduct a trace. The first, the Animal Identification Management System (AIMS) contains the animal identification numbers allocated to manufacturers and to whom the tags were distributed [13]. This database may contain contact and premise information for the individual producer or the last distributor of the tag, such as the accredited veterinarian. It is the responsibility of the accredited veterinarian to maintain the final record of tag application in an accessible system [13]. Each state then utilizes a database of their choosing to manage various animal health programs, traceability, and other data. There is some overlap in the database that states choose, but many states do not use the same database(s). In some states, the adopted electronic certification of veterinary inspection (CVI) programs can retrieve the identification data directly from the accredited veterinarian’s submission form. To improve inter-state data availability, the Federal Animal Health Events Repository (AHER) maintains electronic records of animal health events including animal disease traceability data

[14]. States may choose to submit sightings of animals with official identification to the AHER database with the date and state where the animal was observed. A reported sighting in the AHER database can allow an animal to be traced to the last known state. To improve the efficiency of digital tracing, the states would need to agree on what system will be used and how the data will be input and applied. All the while, maintaining the data security of animal producers.

Concern for data privacy and security is likely influencing the reluctance from producers to adopt official EID and DR technology. The USDA has released documents for producers stating that the confidentiality of the data is protected by law and any identifying information is only accessible to officials that have security permissions and are conducting a disease trace [15]. The current legal requirement is that animals covered by the ADT rule must have an official form of identification that is both visually and electronically readable for non-exempt movements [16, 17]. There are other electronic tags commercially available that do not meet official requirements but can be privately used. The unofficial tags can be used for record keeping in on-farm or breed registry data management systems to track animal health and performance data but the data from unofficial tag use is often inaccessible to animal health officials.

The USDA FMD Response Plan calls for collecting trace-back and trace forward information for at least 28 days before the appearance of clinical signs in the FMD infected animals [11]. In this project, there is no infection or clinical signs, thus the assigned day for beginning a trace was always day 30. Additionally, only the trace-back of contacts was used to achieve this project's objective of assessing the traceability of farms with various levels of EID and DR. The tracing protocol used identified the contacts as possible sources of infection of an

FOI. Trace forward would identify farms that the FOI sent cattle to and so could be a source of infection in that farm. We believe that process would result in similar traceability results. To capture the success of tracing as defined by identification of the exact source of infection and potential dangerous contacts identified as forward contacts, a more complex model with transmission of disease dynamics overlaid with a movement network would be needed.

The simulated network generated the movements based on the movement rates between farm types and movement distances to randomly generate the source and destination farms in the network. In this process, the generated network does not explicitly capture relational movements that exist between farms. However, for the 30-day duration of the network, we believe the simulated network captures shipment rates between production types and is fit for the purpose of assessing tracing of the contacts of a selected FOI.

While fully synthetic, the network in this study captured individual farm to farm connections. This is a contrast to other studies which have collected data but only estimated movements on a state, county, or grid scale and did not capture within state movements [18, 19]. Both the Cabezas, et al., and the Buhnerkempe, et al., study utilized Interstate Certificates of Veterinary Inspection (ICVI) to estimate the number of movements that occurred with some inference from the ICVI data to estimate data gaps. The network generated in this study includes the within-state movements that do not require an ICVI and would not have been included in the other research efforts.

The simulated network in this does not model the movement of individual animals, only the connection from source to destination. This leads to ambiguity about what animals are being shipped. This may lead to an underestimation of the movements of cattle that are traceable. In a real-world example, a cow-calf producer may ship their calf crop in one large sale lot to a market

once per year. They might also take multiple small shipments of cows or bulls to be culled to market. Currently, the calves would be exempt from individual identification but the cows and bulls would be required to have an individual, official EID tag. Our current model does not capture those unique EID requirement variations in shipments from one farm, but does capture the effects of overall increased tagging and reporting across shipment types.

In the traceable networks, EID and DR status of farms was a fixed attribute and farms did not change their tagging status for movements during the 30-day period. The movement of tagged animals through non-tagging intermediate farms was simulated with a single estimate of the probability of outgoing movements being tagged estimated by the proportion of incoming movements that were tagged. In the 30-day sample of movements that were used, this assumption is reasonable. Further, the tags were applied to the entire movement which, in reality, could be mixed tagged and non-tagged animals. A partially tagged movement was not captured in the simulation. Future simulations could be improved by adding a tagging characteristic to individual animals within a movement. This could better capture the differences in EID and DR rates between different animal types within a farm.

The applications of improving traceability are not limited to animal disease traceability and outbreak control. Producers could leverage the verifiable history of their animals to achieve added value at market through product labels that reflect location of origin, production practices, or other characteristics desirable to consumers. The increase in consumer demand for knowledge about the products they are consuming can be readily captured with improved traceability. Those benefits can accrue to the individual producer that applies the tags and tracks the data, however benefits to the industry of rapid disease tracing will require implementation by a high percentage of farms. Other industry benefits could be improved value in export markets to countries that

recognize traceability as an asset. The applications of improving traceability are not limited to animal disease traceability and outbreak control. Producers could leverage the verifiable history of their animals to market through specific location of origin channels, product labeling, and other value-added product markets. The increase in consumer demand for knowledge about the products they are consuming can be readily captured with improved traceability. Those benefits can accrue to the individual producer who applies the tags and tracks the data, benefits to the industry of rapid disease tracing will require implementation by a high percentage of farms. Other industry benefits could be improved value in export markets to countries that recognize traceability as an asset.

Conclusion

This study showed that the current estimated rates of EID use and DR in cattle resulted in digital tracing failure for all 3 FOI types, supporting that the current rates are not effective for completing animal disease traces in an outbreak of a disease such as FMD. However, by increasing the EID use to 75% and DR to 90% the likelihood for success can be increased to an average percent of contacts found to 60-80% which could be highly impactful in outbreak control. These results support the need for not only improving EID use but improving the DR database infrastructure for digital tracing within and across state lines. The value of EID use for producers can extend beyond disease control and be applied to potential value-added marketing of their products and on-farm data management. Future work could incorporate individual animal EID and DR within a given farm to assess the impact of mixing tagged and non-tagged animals. More research is needed on the economic trade-offs, costs, and market benefits to support the adoption of this technology at the national scale.

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Figures

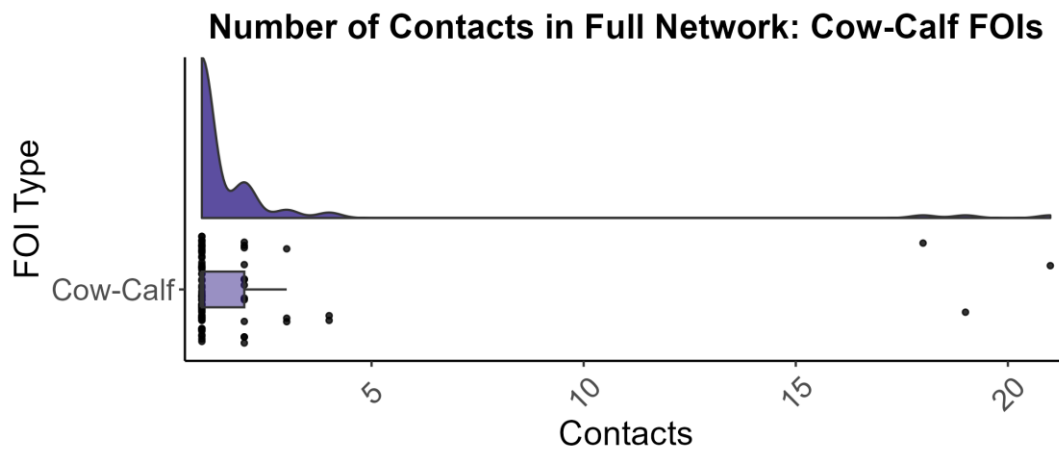


Figure 5.1: Distribution of contacts in the full network for cow-calf farm FOIs

The distribution has been truncated to those that have less than 25 contacts in this figure (n=80). The range of all cow-calf FOI contacts in the full network extended to 560 contacts.

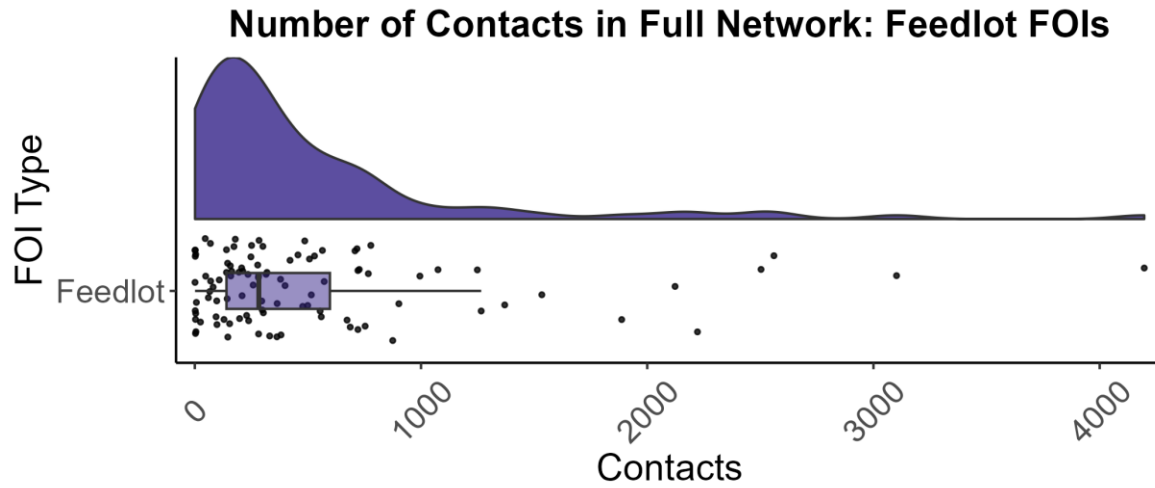


Figure 5.2: Distribution of contacts in the full network for feedlot FOIs.
No truncation applied (n=100).

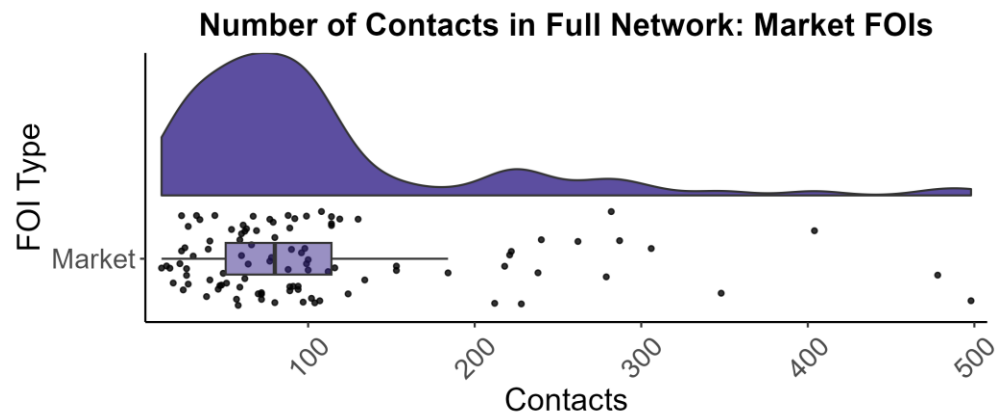


Figure 5.3: Distribution of contacts in the full network for market FOIs.
No truncation applied (n=100)

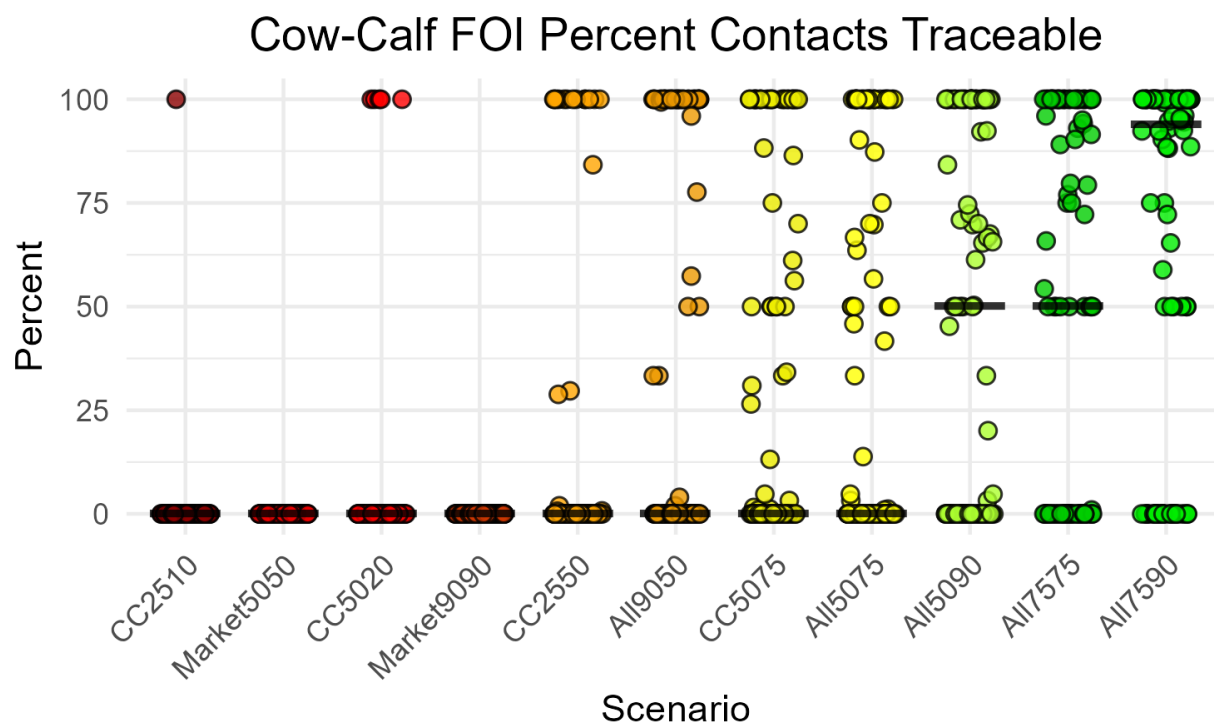


Figure 5.4: The percent of contacts from Cow-Calf FOIs that were traceable in each scenario
The percent of contacts from cow-calf FOIs that were traceable (colored circles) in each scenario. The black line is the median percent of contacts traceable in that scenario.

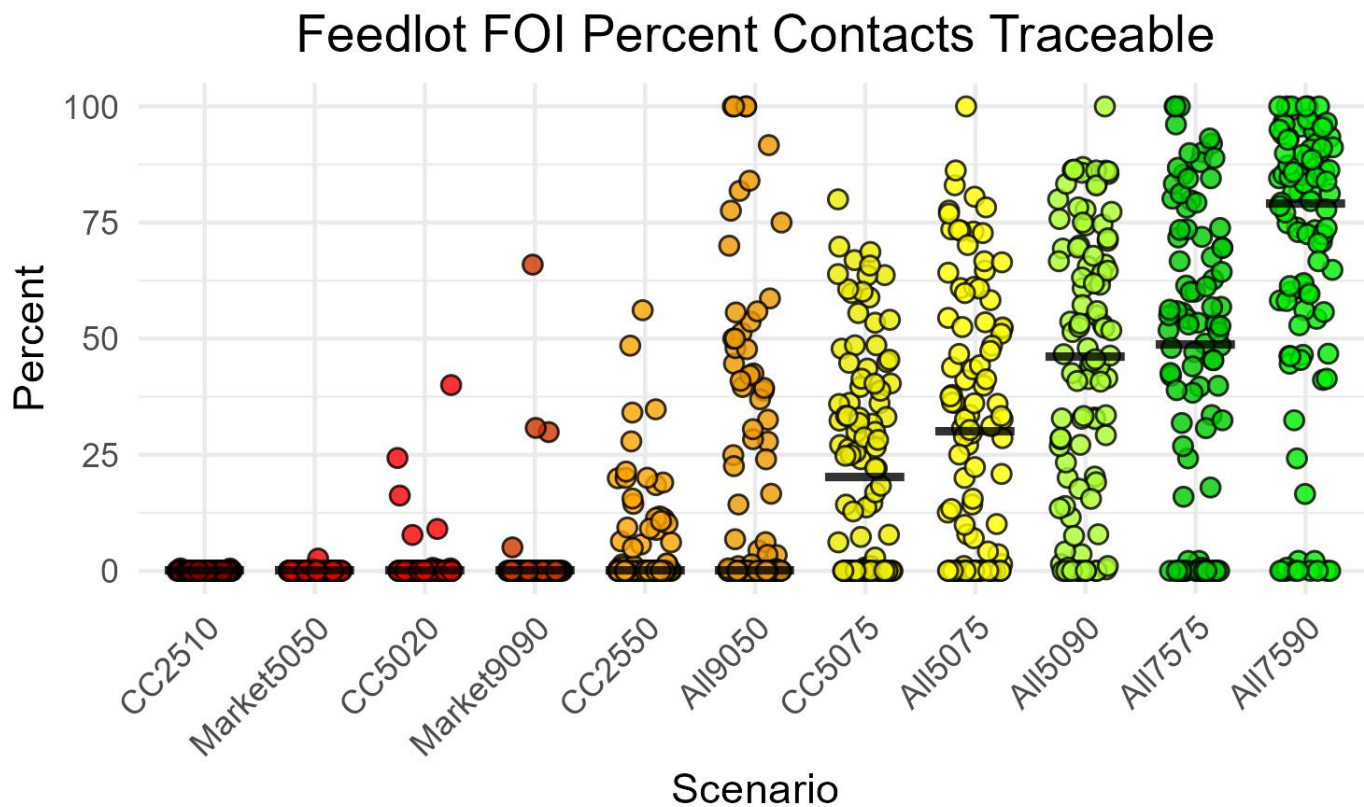


Figure 5.5: The percent of contacts from feedlot FOIs that were traceable in each scenario.

The percent of contacts from feedlot FOIs that were traceable (colored circles) in each scenario. The black line is the median percent of contacts traceable in that scenario.

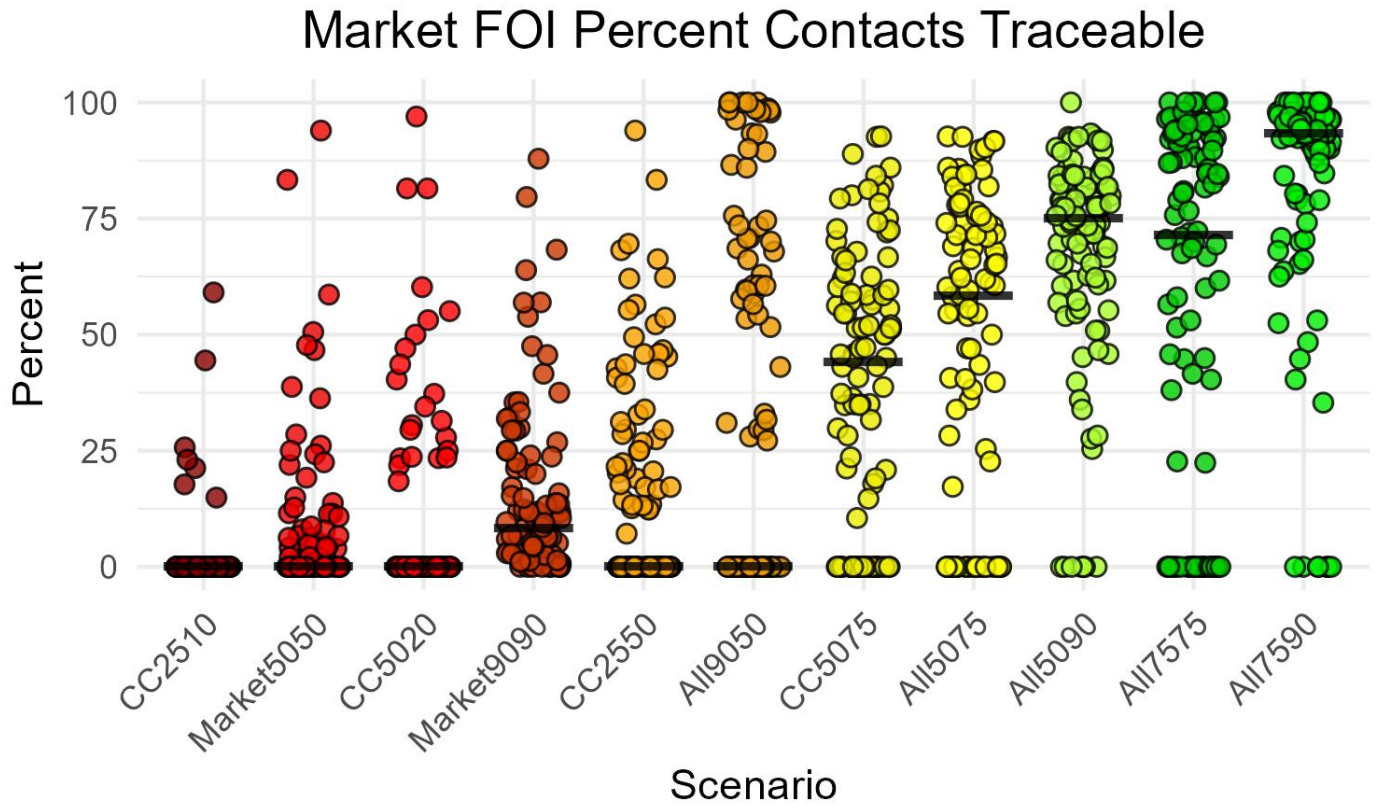


Figure 5.6: The percent of contacts from market FOIs that were traceable in each scenario

The percent of contacts from market FOIs that were traceable (colored circles) in each scenario. The black line is the median percent of contacts traceable in that scenario.

Tables

Table 5.1: Farm types included in the simulated movement network and number of farms represented of each type. Represented farms are farms that had at least one contact in the full network.

In the network, farms serve as nodes for the source and destination of a movement.

Farm Type	Number of Farms Represented in Network
Small Cow Calf	438,995
Large Cow Calf	45,927
Small Dairy Heifer/Calf	1,498
Medium Dairy Heifer/Calf	1,371
Large Dairy Heifer/Calf	474
Small Dairy	29,836
Large Dairy	3,451
Cattle Dealer	3,031
Small Feedlot	26,108
Medium Feedlot	416
Large Feedlot	43
Livestock Market	1,098
Large Stocker/Backgrounder	1,870
Small Stocker/Backgrounder	60,688
Small Processor	625
Large Processor	39

Table 5.2: The tagging and reporting rates for each farm type in the baseline scenario.

Tagging with an EID is a characteristic applied to outgoing movements and digital reporting (DR) is applied to incoming movements.

Scenario Name	Probability of tagging outgoing shipment		Probability of reporting incoming shipment	
Baseline	S Cow Calf	0.01	S Cow Calf	0.01
	L Cow Calf	0.02	L Cow Calf	0.01
	Dairies (all)	0.95	Dairies (all)	0.9
	Stockers	0.02	Stockers	0.01
	Dealers	0.02	Dealers	0.01
	S/M Feedlot	0.01	S/M Feedlot	0.01
	L Feedlot	0.02	L Feedlot	0.05
	Market	0.1	Market	0.01
			Processor	0.02

Table 5.3: The tagging and reporting rates for each farm type in the cow-calf focused scenarios.

Tagging with an EID is a characteristic applied to outgoing movements and digital reporting (DR) is applied to incoming movements.

Scenario Name	Probability to tag outgoing shipment		Probability to report incoming shipment	
Cow-Calf 25/10	S & L Cow Calf	0.25	S & L Cow Calf	0.1
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.2	Stockers/ Dealers	0.1
	S/M Feedlot	0.01	S/M Feedlot	
	L Feedlot	0.02	L Feedlot	
	Market	0.1	Market	
			Processor	0.2
Cow-Calf 50/20	S & L Cow Calf	0.5	S & L Cow Calf	0.2
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers		Stockers/ Dealers	0.2
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	
Cow-Calf 25/50	S & L Cow Calf	0.25	S & L Cow Calf	0.5
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.1	Stockers/ Dealers	0.5
	S/M Feedlot	Baseline	S/M Feedlot	
	L Feedlot		L Feedlot	
	Market	0.5	Market	
			Processor	
Cow-Calf 50/75	S & L Cow Calf	0.5	S & L Cow Calf	0.75
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.1	Stockers/ Dealers	0.75
	S/M Feedlot	Baseline	S/M Feedlot	
	L Feedlot		L Feedlot	
	Market	0.5	Market	
			Processor	

Table 5.4: The tagging and reporting rates for each farm type in the market focused scenarios.

Tagging with an EID is a characteristic applied to outgoing movements and digital reporting (DR) is applied to incoming movements.

Scenario Name	Probability to tag outgoing shipment		Probability to report incoming shipment	
Market 50/50	S & L Cow Calf	Baseline	S & L Cow Calf	Baseline
	Dairies (all)		Dairies (all)	
	Stockers/ Dealers		Stockers/ Dealers	
	S/M Feedlot		S/M Feedlot	0.1
	L Feedlot		L Feedlot	0.1
	Market	0.5	Market	0.5
			Processor	0.2
Market 90/90	S & L Cow Calf	Baseline	S & L Cow Calf	Baseline
	Dairies (all)		Dairies (all)	
	Stockers/ Dealers		Stockers/ Dealers	
	S/M Feedlot		S/M Feedlot	0.1
	L Feedlot		L Feedlot	0.1
	Market	0.9	Market	0.9
			Processor	0.2

Table 5.5: The tagging and reporting rates for each farm type in the scenarios developed to assess industry-wide improvement

Tagging with an EID is a characteristic applied to outgoing movements and digital reporting (DR) is applied to incoming movements.

Scenario Name	Probability to tag outgoing shipment		Probability to report incoming shipment	
All 50/75	S & L Cow Calf	0.5	S & L Cow Calf	0.75
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.5	Stockers/ Dealers	0.75
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	
All 75/75	S & L Cow Calf	0.75	S & L Cow Calf	0.75
	Dairies (all)	Baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.75	Stockers/ Dealers	0.75
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	
All 75/90	S & L Cow Calf	0.75	S & L Cow Calf	0.9
	Dairies (all)	Baseline	Dairies (all)	
	Stockers/ Dealers	0.75	Stockers/ Dealers	
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	

Table 5.6: The tagging and reporting rates for each farm type in the scenarios developed to assess tagging and reporting separately.

Tagging with an EID is a characteristic applied to outgoing movements and digital reporting (DR) is applied to incoming movements.

Scenario Name	Likelihood to tag outgoing shipment		Likelihood to report incoming shipment	
All 90/50	S & L Cow Calf	0.9	S & L Cow Calf	0.5
	Dairies (all)	baseline	Dairies (all)	Baseline
	Stockers/ Dealers	0.9	Stockers/ Dealers	0.5
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	
All 50/90	S Cow Calf	0.5	S Cow Calf	0.9
	L Cow Calf		L Cow Calf	
	Dairies (all)	Baseline	Dairies (all)	
	Stockers/ Dealers	0.5	Stockers/ Dealers	
	S/M Feedlot		S/M Feedlot	
	L Feedlot		L Feedlot	
	Market		Market	
			Processor	

Table 5.7: Full and Traceable Network Metrics

These metrics describe the full generated cattle movement network. The average path length is the shortest number of movements between any two farms and the overall average degree is the average number of movements each farm has.

Scenario	Edges	% of movements traceable	Vertices	Avg Path Length	Overall Avg Degree	Density	Reciprocity	Diameter	Directed Transitivity
Full	1,739,723	100%	615,470	7.38	5.65	4.6×10^{-6}	0.0108	28	0.00706
Baseline	57,374	3.25%	29,692	16.73	3.86	6.5×10^{-5}	8.7×10^{-4}	54	0.13
CC 25/10	114,243	6.47%	66,647	14.132	3.43	2.57×10^{-5}	0.0015	49	0.0056
CC 50/20	222,609	12.60%	147,384	12.988	3.021	1.025×10^{-5}	0.0018	42	0.0022
CC 25/50	506,533	28.67%	227,293	8.99	4.46	9.80×10^{-6}	0.006	28	0.0055
CC 50/75	912,783	51.67%	412,376	8.084	4.43	5.37×10^{-6}	0.008	23	0.0047
Mrkt 50/50	178,731	10.12%	56,569	9.26	6.32	5.59×10^{-5}	0.0091	30	0.0072
Market 90/90	251,342	14.23%	74,732	8.267	6.723	4.5×10^{-5}	0.0146	25	0.0062
All 50/75	1,000,414	56.63%	425,497	7.99	4.70	5.53×10^{-6}	0.0085	25	0.059
All 75/75	1,227,896	69.50%	496,758	7.768	4.943	4.98×10^{-6}	0.00867	25	0.0061
All 75/90	1,455,536	82.39%	552,430	7.5151	5.2695	4.77×10^{-6}	0.010	26	0.0065
All 90/50	892,544	50.52%	403,231	8.56	4.43	5.49×10^{-6}	0.00597	26	0.00519
All 50/90	1,185,613	67.11%	477,008	7.72	4.97	5.21×10^{-6}	0.0097	23	0.0063

Table 5.8: The total number of FOIs that had zero traceable contacts in each scenario

An untraceable FOI represents the failure of the first movement into that FOI to be tagged, reported, or both. A lower number indicates higher traceability success. There are 100 FOI possible for each type.

Scenario	# Untraceable Cow-Calf FOI	# Untraceable Feedlot FOI	# Untraceable Market FOI
Baseline	100	100	100
Cow-Calf 25/10	99	98	93
Cow-Calf 50/20	95	92	77
Cow-Calf 25/50	81	68	51
Cow-Calf 50/75	51	38	29
Market 50/50	100	98	52
Market 90/90	100	96	9
All 50/75	51	29	29
All 75/75	43	27	29
All 75/90	31	9	7
All90/50	56	55	51
All 50/90	40	12	7

Table 5.9: The mean and percentiles of percent of contacts traceable by scenario for cow-calf FOIs

The percent of contacts traceable is the observed contacts for each FOI in each EID/DR network divided by the full network contacts for that FOI multiplied by 100 gives the percent of contacts traceable for that FOI.

Cow-Calf Percent Traceable Contacts						
	Mean	10th	25th	Median	75th	90th
Baseline	0%	0%	0%	0%	0%	0%
Cow-Calf 25/10	1.0%	0%	0%	0%	0%	0%
Cow-Calf 50/20	5.0%	0%	0%	0%	0%	0%
Cow-Calf 25/50	14.5%	0%	0%	0%	0%	100%
Cow-Calf 50/75	35.9%	0%	0%	0%	100%	100%
Market 50/50	0%	0%	0%	0%	0%	0%
Market 90/90	0%	0%	0%	0%	0%	0%
All 50/75	37.7%	0%	0%	0%	100%	100%
All 75/75	48.8%	0%	0%	50.0%	100%	100%
All 75/90	63.4%	0%	0%	93.8%	100%	100%
All 90/50	38.0%	0%	0%	0%	100%	100%
All 50/90	49.6%	0%	0%	50.0%	100%	100%

Table 5.10: The mean and percentiles of percent of contacts traceable by scenario for Feedlot FOIs

The percent of contacts traceable is the observed contacts for each FOI in each EID/DR network divided by the full network contacts for that FOI multiplied by 100 gives the percent of contacts traceable for that FOI.

Feedlot Percent Traceable Contacts						
	Mean	10th	25th	Median	75th	90th
Baseline	0%	0%	0%	0%	0%	0%
Cow-Calf 25/10	0%	0%	0%	0%	0%	0%
Cow-Calf 50/20	1.0%	0%	0%	0%	0%	0%
Cow-Calf 25/50	4.6%	0%	0%	0%	2.4%	18.5%
Cow-Calf 50/75	22.6%	0%	0%	20.2%	39.8%	59.9%
Market 50/50	0%	0%	0%	0%	0%	0%
Market 90/90	1.3%	0%	0%	0%	0%	0%
All 50/75	30.4%	0%	0%	30.0%	52.4%	73.1%
All 75/75	43.2%	0%	0%	48.7%	70.1%	86.9%
All 75/90	67.5%	2.0%	55.4%	78.9%	90.3%	96.1%
All 90/50	19.2%	0%	0%	0%	38.9%	59.8%
All 50/90	44.2%	0%	18.7%	46.0%	69.4%	83.5%

Table 5.11: The mean and percentiles of percent of contacts traceable by scenario for market FOIs

The percent of contacts traceable is the observed contacts for each FOI in each EID/DR network divided by the full network contacts for that FOI multiplied by 100 gives the percent of contacts traceable for that FOI.

Market Percent Traceable Contacts						
	Mean	10th	25th	Median	75th	90th
Baseline	0%	0%	0%	0%	0%	0%
Cow-Calf 25/10	2.1%	0%	0%	0%	0%	0%
Cow-Calf 50/20	9.6%	0%	0%	0%	0%	37.6%
Cow-Calf 25/50	17.5%	0%	0%	0%	29.5%	52.4%
Cow-Calf 50/75	38.2%	0%	0%	44.1%	59.8%	78.4%
Market 50/50	8.3%	0%	0%	0%	6.9%	25.1%
Market 90/90	15.3%	0.8%	2.9%	8.2%	21.5%	37.9%
All 50/75	46.7%	0%	0%	58.3%	74.4%	84.6%
All 75/75	56.4%	0%	0%	71.4%	92.1%	96.3%
All 75/90	81.9%	48.0%	79.9%	93.3%	96.2%	98.1%
All 90/50	34.8%	0%	0%	0%	70.2%	97.9%
All 50/90	67.2%	33.3%	60.7%	75.0%	83.0%	89.9%

Table 5.12: Results of “1 phone call” tracing method

The percent of contacts traceable with standard tracing is the same data as presented in table 10. Similarly, the data for the number of untraceable farms with standard tracing is from table 9. The 1 Phone Call method of tracing simulated the producer orally reporting the contacted market(s) and repeating the tracing for an FOI from that market and reporting the new number of contacts traceable.

Scenario		100 Cow Calf		100 Feedlots	
		Percent Contacts	# Farms Untraceable	Percent Contacts	# Farms Untraceable
Cow-Calf 50/20	Standard Tracing	5	95	0.98	92
	1 Phone Call	6.32	91	5.74	48
Market 50/50	Standard Tracing	0	100	0.04	98
	1 Phone Call	1.56	89	8.32	31
Market 90/90	Standard Tracing	0	100	1.31	96
	1 Phone Call	3.05	81	17.1	14
All 75/75	Standard Tracing	48.8	43	43.2	27
	1 Phone Call	51.55	38	53.58	8
All 75/90	Standard Tracing	63.4	31	67.5	9
	1 Phone Call	66.31	27	71.08	4

Chapter 6 - Dissertation Conclusions

The objectives of this dissertation were to improve the preparedness of the US for an introduction of a foreign animal disease. FMD was chosen as the example disease due to its potential for economic devastation, high transmission rate, and wide range of susceptible species. The improvement in disease preparedness is achieved through the education of veterinarians, the identification of data gaps in biosecurity research, the quantification of animal disease traceability impacts in an outbreak, and the quantification of animal disease traceability infrastructure needs.

The ability for the US to respond quickly to an outbreak of FMD, or any foreign animal disease, will be contingent on the rapid detection of the first case and the efficacy of control actions that are implemented. This means that producers and veterinarians need to be adequately educated in FMD clinical signs to recognize them and call appropriate officials. Then they will need to be prepared for the regulatory processes that will occur after reporting the suspicion for FMD. Veterinarians should not hesitate to report suspicious clinical signs in animals to the state and federal animal health officials as surveillance for foreign animal diseases happen regularly each year.

Upon the confirmation of an introduction of FMD, the control measures will need to be carefully balanced with the need for continuity of business to prevent excess economic impact to the livestock industries. The implementation of strict control measures including quarantine and isolation of farms may reduce the transmission of virus but will also impact a producer's ability to deliver supplies to their operation or ship their finished products to market. The results of the biosecurity review in this dissertation aid in the preparation for continuity of business planning. This dissertation also assessed the potential to decrease the surveillance areas used during an

outbreak but found it to be highly variable in outbreak impacts and thus cannot recommend the practice.

In times of FMD freedom there is also a balancing act of implementing measures to control a disease that is not present but being adequately prepared to step up disease control and prevention measures. As an example, the utilization of strict decontamination of every vehicle onto and off of a farm would cost more than the current benefit of disease transmission reduction. Yet, if the supplies were readily available decontamination plans could swiftly be implemented in the face of disease. On the other hand, measures that require significant infrastructure, such as animal disease traceability systems, need to be in place and operational before the disease is introduced. The results of this dissertation highlight the potential biosecurity measures that can be developed and the potential goals for improving traceability infrastructure prior to an FMD outbreak.

The implementation of improved animal disease traceability will be a process that requires producer and market support. If there is no economic incentive or disease that demands a change in traceability, the system will be reluctant to change. More research is needed into the other benefits of improving traceability that extend beyond controlling disease.

Ultimately, we cannot predict if, when, or even what specific strain of FMD will be introduced to the US. This dissertation has added to the body of knowledge surrounding biosecurity measures for FMD mitigation, FMD outbreak control through animal disease tracing, and the improvements in digital movement tracing that need to occur to have effective FMD tracing. It has also identified knowledge gaps in biosecurity measure efficacy and economic costs for implementation of biosecurity and traceability. We must continue to conduct research that furthers the best of our knowledge on how to prevent, control, and recover from an outbreak.

Appendices and Supplementary Materials

MaRyka Smith

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Kevin Isaacs KAWI (he/him)
Publications Coordinator

Appendix A - Chapter 3 Supplementary Materials

Appendix A.1 Table 1: Livestock and product management: description and effect of biosecurity measures for managing livestock, and livestock products at the report level

Biosecurity measure	Description of implementation and effectiveness	Reference
Isolation of infected animals from the rest of the herd	Isolation, Quarantine, Animal Separation (n=13)	
	Detrimental	
	Authors report the presence of “isolation pens located near highway and not separated from other farm units... contributed to the spread of the disease”.	Byomi, 2015
	Authors reported that groups of cattle were moved to an isolation paddock after identification of the index case in each group. Authors suggest that the movement of infected cattle led to exposure and subsequent infection of other cattle on the farm, contributing to outbreak propagation.	Lyons, et. al, 2015
	Neutral	
	53/64 case farms and 44/64 control farms reported isolating sick animals. This practice was significant in a univariable model ($p = 0.091$), but not retained in the final multivariable model.	Ali, et. al, 2022
	Not Evaluated	
	Farmers reported “separating sick animals from unaffected animals upon noticing clinical signs consistent with FMD”. No isolation protocol was specified. Authors noted that “disinfection of clothing and equipment after treating FMD-infected animals was rarely practiced”.	Nampanya, et. al, 2012

	31.7% (20/63) households surveyed reported isolating clinically unwell animals until recovered. Biosecurity measure was not assessed for effectiveness due to significant collinearity with other variables.	Miller, et. al, 2018
	32% (9/28) of cattle owners who reported having at least one case of FMD in the previous six months reported using isolation as a disease management strategy.	Shurbe, et. al, 2022
	Nomadic herders reported that isolation of infected animals is implemented during outbreaks.	DiPietro, et. al, 2023
	Smallholder cattle farmers (n=240) reported always (52.1%), sometimes (25.4%), or never (22.5%) separating sick from healthy cattle. No isolation protocol was specified.	Young, et. al, 2016
Separation of animal groups on farm	Beneficial	
	Pens of immune animals were an “effective barrier” against within-herd FMD transmission.	Hutber and Kitching, 2000
	Apparently healthy piglets were transferred to a new farm and never became clinical or tested positive for FMD.	Poulin and Christianson, 2006
	Keeping small ruminants on a separate grazing pasture “a few kilometers” from the cattle sufficient to prevent contact between them. No clinical FMD cases were reported in the small ruminants.	Lyons, et. al, 2015
	Neutral	
	Physical and spatial boundaries sufficient to slow but not prevent within-herd FMD transmission.	Hutber and Kitching, 2000
	Separation of clinically healthy sows from infected farm not sufficient to prevent subsequent outbreaks of clinical disease.	Poulin and Christianson, 2006
	Neutral	

	No significant difference in disease risk found between the 2/64 case farms and 3/64 control farms that reported utilizing a quarantine measure for new herd introductions (univariable p-value = 0.763). Quarantine protocol not defined. Not Evaluated	Ali, et. al, 2022
Isolation, quarantine, or inspection of incoming stock	72.0-88.7% of survey respondents inspected and/or isolated incoming stock. No specific protocols were defined, actions included inspection for disease, isolation, and certification of inspection by veterinary professional.	Manyweathers, et. al, 2020
	64.9-84.1% of survey respondents inspected and/or isolated incoming stock. No specific protocols were defined, actions included inspection for disease, isolation, and certification of inspection by veterinary professional.	Manyweathers, et. al, 2021
	Smallholder cattle farmers (n=240) reported always (26.3%), sometimes (25.8%), or never (47.9%) isolating incoming stock for 2 weeks.	Young, et. al, 2016
Closed herd	Not Evaluated 3.1% of 93 dairy farmers who were “aware of FMD” reported that they practiced not bringing new cattle onto their farms as a prevention measure. 6.3% of 93 dairy farmers who were “aware of FMD” reported that they prevented other cattle from entering their farms. 9.6% of 93 dairy farmers who were “aware of FMD” reported that they practiced keeping cattle within the farm compound.	Seifu, et. al, 2023
	19.2% of 240 smallholder cattle farmers reported keeping their cattle from having direct contact with other farmers’ cattle as a prevention measure. 78.3% of 240 smallholder cattle farmers reported keeping their cattle in a fenced area as a prevention measure.	Young, et. al, 2016
Animal Products and Wastes (n=2)		
Beneficial		

Carcass transport	Covering carcasses with waterproof sheets or using disinfected trucks with sealed containers to transport carcasses from farms to burial sites was not significantly associated with increased transmission risk in a multivariable model (Operational burial sites within 500m p-value = 0.98; Operational transportation roads within 200m p-value = 0.34). Not Evaluated	Hayama, et. al, 2015
Carcass disposal	Dead calves were burned on bonfires.	Kass, et. al, 2022
Feces	Manure from sick cows was stored and not immediately used for fertilizer.	
Milk	Milk from infected cattle was added to manure for disposal or pasteurized and fed to other animals.	

Appendix A.2 Table 2: Personal protective equipment and individual management: description and effect of biosecurity measures for managing farm personnel and visitors at the report level

Biosecurity measure	Description of implementation and effectiveness	Reference
Personal Protective Equipment (n=3)		
Neutral		
Clothing	Use of disposable work suit (material not specified) during culling activities likely insufficient to prevent viral contamination of clothing.	Wee, et. al, 2008
	No association identified between providing farm staff with farm-specific clothing (material not specified) and being a case farm (univariable p-value = 0.47).	Ellis-Iverson, et. al, 2011
Not Evaluated		

	Use of protective clothing (material not specified) by stockpersons and other employees on a dairy farm was reported. Farm was located in a district that did not have an FMD case during the 1982 outbreak.	Kass, et. al, 2022
	Neutral	
Footwear	No association identified between providing farm staff with farm-specific footwear (material not specified) and being a case farm (univariable p-value = 1.00).	Ellis-Iverson, et. al, 2011
	Not Evaluated	
	Use of boot covers during culling activities was reported. Boot covers and boots were destroyed following activities, and worker returned home without footwear.	Wee, et. al, 2008
Gloves	Not Evaluated	
	Workers reportedly wore rubber gloves while milking cows with FMD lesions.	Kass, et. al, 2022
	Individual Management (n=6)	
	Not Evaluated	
Restricting visitor access to farms	25.4% of surveyed beef producers always restrict visitor farm access.	Manyweathers, et. al, 2020
	23.1% of surveyed beef producers never restrict visitor farm access and 39.3% of respondents never require visitors to undergo specific biosecurity practices.	
	32.3% of surveyed sheep producers regularly restrict visitor farm access. 53.6% of surveyed sheep producers did not require visitors to follow biosecurity practices.	Manyweathers, et. al, 2021

2.1% of 93 dairy farmers who were “aware of FMD” reported that they practiced not allowing visitors on their farms.

Seifu, et. al, 2023

Not Evaluated		
Farm lockdowns	During both the 1952 and 1982 FMD outbreaks farm personnel were confined to the infected premises for extended periods. Farm access by non-employees was prohibited. Movement restrictions were enforced by militia and breaches were punishable by imprisonment.	Kass, et. al, 2022
Not Evaluated		
Bathing	Use of public bath reported as part of decontamination protocol. No specific protocol reported.	Wee, et. al, 2008
Not Evaluated		
Minimizing cross-contact	Stockmen assigned to single cattle groups during the outbreak period.	Lyons, et. al, 2015

Appendix A.3 Table 3: Fomite management: description and effect of biosecurity measures for managing fomites at the report level

Biosecurity measure	Description of implementation and effectiveness	Reference
Non-livestock (n=4)		
Beneficial		

Feral animal management	Rodent control program strengthened to prevent mechanical reintroduction as one component of a successful FMD eradication and site decontamination process.	Poulin and Christianson, 2006
	Not Evaluated	
	18.7% of surveyed beef producers never, rarely, or occasionally control feral animals on their farm (vs most of the time or always)	Manyweathers, et. al, 2020
	29.6% of surveyed sheep producers have control plans for feral animals on their farm.	Manyweathers, et. al, 2021
Beneficial*		
Dog Permission	Allowing dogs to accompany staff onto livestock areas was less likely on case farms than control farms (univariable p-value = 0.05).	Ellis-Iverson, et. al, 2011
	None of the 5 case farms allowed dogs, 12 of 22 control farms did.	
Vehicles (n=2)		
Beneficial*		
Designated parking	Case farms were less likely than control farms to have visitor car parking areas away from animal areas (univariable p-value = 0.03).	Ellis-Iverson, et. al, 2011
Beneficial*		
Barrier to vehicle entry	Case farms were less likely than control farms to have gates/fences at the entrance to livestock areas (univariable p-value = 0.14).	Ellis-Iverson, et. al, 2011
Equipment (n=2)		
Neutral		

Equipment management	No significant association with disease risk found between the 1/64 case farms and 2/64 control farms that reported sharing equipment (univariable p-value = 0.56).	Ali, et. al, 2022
	Not Evaluated	
	4.2% of 93 dairy farmers who were “aware of FMD” reported that they practiced not sharing equipment as an FMD prevention measure.	Seifu, et. al, 2023

*Association of risk factor and case status were reported by authors to be significant based on a univariable p-value

Appendix A.4 Table 4: Disinfection: description of on-farm disinfection measures and their effectiveness to control FMD introduction or spread at the report level

Disinfection		
target or strategy	Description of implementation and effectiveness	Reference
Clothing and Footwear (n=4)		
Neutral		
Clothing	Jeans worn under a disposable work-suit during culling event sprayed with “disinfectant” and wrapped in vinyl during personnel decontamination process. Process appears to be insufficient for preventing contamination of the interior of the worker’s vehicle.	Wee, et. al, 2008
	Not Evaluated	
	During the 1982 FMD outbreak, the staff’s clothing was disinfected on a regular basis (product or protocols not specified).	Kass, et. al, 2022
Foot Dips	Neutral	

	Use of foot dips not sufficient to prevent FMD outbreak on farm (product utilized not specified).	Byomi, 2015
	No association identified between utilizing boot dips (product and protocol not specified) and being a case farm (univariable p-value = 0.30).	Ellis-Iverson, et. al, 2011
Vehicles (n=8)		
Beneficial		
	The internal feed truck was washed weekly (products and protocol not specified) during a successful site decontamination process.	Poulin and Christianson, 2006
Neutral		
Vehicles	Disinfection of vehicles transporting carcasses from farms to burial sites (products and protocol not specified) was reported in conjunction with other biosecurity measures. The presence of transportation roads within 200 meters of burial sites within 500 meters was not significantly associated with FMD transmission risk to farms (Operational burial sites within 500m p-value = 0.98; Operational transportation roads within 200m p-value = 0.34).	Hayama, et. al, 2015
Not Evaluated		
	86.1% (385/447) of both case (n=140) and control (n=307) farms reported using disinfectant for vehicles (product not specified).	Sansamur, et. al, 2020
Neutral		

	Use of wheel dips not sufficient to prevent FMD outbreak on farm (product utilized not specified).	Byomi, 2015
	No association identified between utilizing wheel washes (product and protocol not specified) and being a case farm (univariable p-value = 1.00).	Ellis-Iverson, et. al, 2011
	Not Evaluated	
Wheels and tires	During both the 1952 and 1982 FMD outbreaks, disinfection mats were reportedly used on the roads and at farm entrances for vehicles to drive over. Drivers would also exit and disinfect shoes.	Kass, et. al, 2022
	Products used were not specified.	
	During the 1982 FMD outbreak, a disinfection bath was utilized on a dairy farm that would completely wet the wheels and tires of feed delivery vehicles. The farm was located in a district that did not have an FMD case during the outbreak.	
	Authors report that a solution of one tablet of Virkon S diluted in 500 mL of water was sprayed on car tires during an environmental sampling study.	Mielke, et. al, 2023
	Not Evaluated	
Vehicle disinfection equipment	61.2% (126/206) of swine farms infected between 2014 and 2019 reported having vehicle disinfection equipment.	Lee, et. al, 2021
	35.3% (6/17) of cattle farms infected between 2014 and 2019 reported having vehicle disinfection equipment.	
Barns (n=2)		

Beneficial		
Barns	During a successful site decontamination, swine barns and manure pits were thoroughly cleaned and rinsed with organic acids. After which, they were then fumigated with formaldehyde and potassium permanganate.	Poulin and Christianson, 2006
Not Evaluated		
	During the 1952 outbreak, barns were reportedly disinfected with lime and ash water.	Kass, et. al, 2022
General site (n=1)		
Neutral		
Regular disinfection	No significant association with disease risk found between the 12/64 case farms and 15/64 control farms that reported performing disinfection regularly (univariable p-value = 0.564). The most usual materials used for disinfectants were reported to be slaked lime, formalin, and crushed phenyl tablets.	Ali, et. al, 2022
Disinfection dip at entrance	Not Evaluated	
	7/128 (5.5%) of the total case and control farms had a disinfection dip at the farm entrance. Specific products and dip use were not specified.	Ali, et. al, 2022
Other (n=3)		
Not Evaluated		

Researcher equipment	Authors report that a solution of one tablet of Virkon S diluted in 500 mL of water was sprayed on researcher equipment during an environmental sampling study.	Mielke, et. al, 2023
Not Evaluated		
Staff	During the 1982 FMD outbreak, farm staff were reportedly disinfected on regular basis (product or protocols not specified).	Kass, et. al, 2022
Not Evaluated		
Supplies	During the 1982 FMD outbreak, farm supplies were reportedly disinfected on regular basis (product or protocols not specified).	Kass, et. al, 2022
Not Evaluated		
Sanitizing Efforts	“Sanitizing efforts” were reportedly used by 3/104 surveyed nomadic herders to prevent or respond to FMD.	DiPietro, et. al, 2023

Appendix B - Chapter 4 Supplementary Materials

Supplement 1

```
[Infectivity1]
TimePeriodStart=1
TimePeriodStop=90
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nursery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine][]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1][]=BetaPert 7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nursery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine][]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
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```

TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
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TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][in_atlantic_coast_climate_zone|in_northwest_climate_zone|in_west_climate_zone)&!(vaccinated_bison_cattle
|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 1
Infectivity[][in_central_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_s
wine_2|vaccimmune_swine)]=Constant Constant 0.9
Infectivity[][in_new_england_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinat
ed_swine_2|vaccimmune_swine)]=Constant Constant 0.85
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[Infectivity2]
TimePeriodStart=91
TimePeriodStop=182
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_c
alf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dai
ry|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_fe

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eder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nurs
ery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][[]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_
bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][[]=BetaPert
7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|da
iry_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat_
other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|f
arrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nu
rsery_s|other_swine_l|other_swine_s|dealer_swine][[]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|pr
ocessor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][[]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[[ (in_atlantic_coast_climate_zone|in_central_climate_zone|in_new_england_climate_zone|in_northwest_climate_
zone|in_west_climate_zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vacc
immune_swine)]]]=Constant Constant 1

[Infectivity3]

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TimePeriodStart=183
TimePeriodStop=274
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][]=BetaPert 7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3

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TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][in_atlantic_coast_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.9
Infectivity[][in_central_climate_zone|in_west_climate_zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.85
Infectivity[][in_new_england_climate_zone|in_northwest_climate_zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.95

[Infectivity4]
TimePeriodStart=275
TimePeriodStop=365
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine]=BetaPert 7 10 14
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nursery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine]=BetaPert 30 34 42
ResetInfectionDelay[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nursery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine]=BetaPert 150 180 210

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ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][in_atlantic_coast_climate_zone|in_central_climate_zone|in_new_england_climate_zone|in_northwest_climate_
zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)][]=Cons
tant Constant 1
Infectivity[][in_west_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swin
e_2|vaccimmune_swine)][]=Constant Constant 0.95

[Infectivity5]
TimePeriodStart=366
TimePeriodStop=455
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_c
alf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dai

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ry|goat_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][[]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][[]=BetaPert 7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][[]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][[]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup 1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup 1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][[(in_atlantic_coast_climate_zone|in_northwest_climate_zone|in_west_climate_zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]]]=Constant Constant 1
Infectivity[][in_central_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]]]=Constant Constant 0.9

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Infectivity[][in_new_england_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinat
ed_swine_2|vaccimmune_swine)][]=Constant Constant 0.85

[Infectivity6]
TimePeriodStart=456
TimePeriodStop=547
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_c
alf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dai
ry|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_fe
eder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nurs
ery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine][]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_
bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1][]=BetaPert
7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|da
iry_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_
other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|f
arrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nursery_1|nu
rsery_s|other_swine_1|other_swine_s|dealer_swine][]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|pr
ocessor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17

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TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][in_atlantic_coast_climate_zone|in_central_climate_zone|in_new_england_climate_zone|in_northwest_climate_
zone|in_west_climate_zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vacc
immune_swine)]=Constant Constant 1

[Infectivity7]
TimePeriodStart=548
TimePeriodStop=639
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y
ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_c
alf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dai
ry|goat_other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_fe
eder_s|farrow_to_finish_1|farrow_to_finish_s|farrow_to_wean_1|farrow_to_wean_s|grower_finisher_1|grower_finisher_s|nurs
ery_1|nursery_s|other_swine_1|other_swine_s|dealer_swine]=BetaPert 30 34 42
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_
bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine|processor_swine_1]=BetaPert
7 10 14
ResetInfectionDelay[bison|dealer_bison|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heifer_calf_1|dairy_heifer_calf_m|da
iry_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s|dealer_cattle|goat_dairy|goat_
other|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_1|farrow_to_feeder_s|f

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arrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.9999,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
Infectivity[][in_atlantic_coast_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.9
Infectivity[][in_central_climate_zone|in_west_climate_zone]&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.85
Infectivity[][in_new_england_climate_zone|in_northwest_climate_zone]&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]=Constant Constant 0.95

[Infectivity8]
TimePeriodStart=640
TimePeriodStop=730
InfectivityRelativeTo=infection
MaximumTimeOfInfectiousness=BetaPert 30 34 42
ResetInfection=Y

```

```

ResetInfectionDelay=BetaPert 150 180 210
MaximumTimeOfInfectiousness[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine][]=BetaPer
t 7 10 14
MaximumTimeOfInfectiousness[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_c
alf_m|dairy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dai
ry|goat_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_fe
eder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nurs
ery_l|nursery_s|other_swine_l|other_swine_s|dealer_swine][]=BetaPert 30 34 42
ResetInfectionDelay[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|da
iry_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat_
other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|f
arrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nu
rsery_s|other_swine_l|other_swine_s|dealer_swine][]=BetaPert 150 180 210
ResetInfectionDelay[livestock_market_bison_cattle|livestock_market_goat_sheep|livestock_market_swine|processor_bison|pr
ocessor_cattle|processor_cattle_l|processor_goat|processor_sheep|processor_swine|processor_swine_l][]=Constant 1
TimeToClinicalSigns[bison]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[cattle]=Lookup 1,0.0014,0.0208,0.1257,0.4093,0.7927,1;0,0,1,2,3,4,5
TimeToClinicalSigns[goat]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sheep]=Lookup
1,0.0014,0.0104,0.0403,0.1058,0.2138,0.3561,0.5124,0.6596,0.7808,0.8695,0.9631,0.9921,0.9967,0.9987,0.9995,0.9998,0.999
9,1;0,0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
TimeToClinicalSigns[sow]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[piglet]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[nursery]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[finisher]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3
TimeToClinicalSigns[other_swine]=Lookup 1,0,0.7347,0.9959,1;0,0,1,2,3

```

```

Infectivity[[in_atlantic_coast_climate_zone|in_central_climate_zone|in_new_england_climate_zone|in_northwest_climate_
zone)&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swine_2|vaccimmune_swine)]] =Cons
tant Constant 1
Infectivity[[in_west_climate_zone&!(vaccinated_bison_cattle|vaccimmune_bison_cattle|vaccinated_swine_1|vaccinated_swin
e_2|vaccimmune_swine)]] =Constant Constant 0.95

```

```

[Depopulation1]
ControlName=depopulation_large_cattle
ActivationOption=detected_farm
FarmSelectionOption=detected_farm
FarmClasses=cow_calf_1 | dairy_heifer_calf_1|feedlot_cattle_s|stocker_1|sheep_1|processor_cattle_1
ActionResource=resource_depopulation_large_cattle
CompletedFarmState=depopulated

```

```

[Depopulation2]
ControlName=depopulation_small_cattle_other
ActivationOption=detected_farm
FarmSelectionOption=detected_farm
FarmClasses=bison | livestock_market_bison_cattle | dealer_bison | cow_calf_s | dairy_s | dairy_heifer_calf_m |
dairy_heifer_calf_s | stocker_s | dealer_cattle | goat_dairy | goat_other | livestock_market_goat_sheep | dealer_goat |
sheep_s | dealer_sheep | livestock_market_swine|processor_bison|processor_cattle|processor_goat|processor_sheep
ActionResource=resource_depopulation_small_cattle_other
CompletedFarmState=depopulated

```

```

[Depopulation3]
ControlName=depopulation_large_feedlots
ActivationOption=detected_farm
FarmSelectionOption=detected_farm

```

FarmClasses=feedlot_cattle_1
ActionResource=resource_depopulation_large_feedlots
CompletedFarmState=depopulated

[Depopulation4]
ControlName=depopulation_medium_feedlots
ActivationOption=detected_farm
FarmSelectionOption=detected_farm
FarmClasses=dairy_1|feedlot_cattle_m|feedlot_sheep
ActionResource=resource_depopulation_medium_feedlots
CompletedFarmState=depopulated

[Depopulation5]
ControlName=depopulation_large_swine
ActivationOption=detected_farm
FarmSelectionOption=detected_farm
FarmClasses=farrow_to_feeder_1 | farrow_to_finish_1 | farrow_to_wean_1 | grower_finisher_1 | nursery_1 |
other_swine_1|processor_swine_1
ActionResource=resource_depopulation_large_swine
CompletedFarmState=depopulated

[Depopulation6]
ControlName=depopulation_small_swine
ActivationOption=detected_farm
FarmSelectionOption=detected_farm
FarmClasses=transitional_swine | farrow_to_feeder_s | farrow_to_finish_s | farrow_to_wean_s | grower_finisher_s |
nursery_s | other_swine_s| dealer_swine|processor_swine
ActionResource=resource_depopulation_small_swine
CompletedFarmState=depopulated

```

[Depopulation7]
ControlName=post_depopulation_spread
ActivationOption=time_period
TimePeriodTrigger=first_detection
FarmSelectionOption=zone
SelectionZone=passive_surveillance_post_detection_zone
FarmStates=depopulated
ActionResource=resource_post_depopulation
DelayedFarmState=post_depopulation_spread_completed
TimePeriodToDelayedState=3
RemoveDetectedFarms=N

```

```

[Surveillance1]
ControlName=passive_surveillance_post_detection
ActivationOption=time_period
TimePeriodTrigger=first_detection
SelectionZone=passive_surveillance_post_detection_zone
SelectionProbability=1.0
VisitDelay=Constant 0
VisitFrequency=BetaPert 1 1 2
VisitDuration=Constant 730
DelayToDetection=BetaPert 2 2 3
DetectionRelativeTo=Clinical_signs
DetectionProbability[bison][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
1,0,1,2,3,4,14;0,0.164,0.223,0.282,0.341,0.4,0.4
DetectionProbability[dealer_bison|dealer_cattle][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
1,0,14;0,0.2,0.2

```


DetectionProbability[cow_calf_l|dairy_heifer_calf_l|dairy_heifer_calf_m][in_passive_surveillance_outbreak_phase&clinical
 l_signs][]=Table 1,0,1,2,3,4,5,6,7,8,14;0,0.024,0.1635,0.303,0.4425,0.582,0.5865,0.591,0.5955,0.6,0.6
 DetectionProbability[cow_calf_s|dairy_heifer_calf_s][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,14;0,0.246,0.3345,0.423,0.5115,0.6,0.6
 DetectionProbability[dairy_l][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,14;0,0.045,0.459,0.873,0.8865,0.9,0.9
 DetectionProbability[dairy_s][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,14;0,0.0063,0.4262,0.846,0.873,0.9,0.9
 DetectionProbability[feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s][in_passive_surveillance_outbreak_phase&clinical
 l_signs][]=Table 1,0,1,2,14;0,0.136,0.468,0.8,0.8
 DetectionProbability[stocker_l|stocker_s][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,14;0,0.08,0.185,0.29,0.395,0.5,0.5
 DetectionProbability[goat_dairy|goat_other|sheep_l|sheep_s][in_passive_surveillance_outbreak_phase&clinical_signs][]=Ta
 ble 1,0,1,2,3,4,5,6,7,8,9,10,11,12,14;0,0.015,0.087,0.159,0.174,0.189,0.177,0.165,0.1395,0.114,0.0885,0.063,0.0315,0,0
 DetectionProbability[feedlot_sheep][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,5,6,7,8,9,10,11,12,14;0,0.02,0.116,0.212,0.232,0.252,0.236,0.22,0.186,0.152,0.118,0.084,0.042,0,0
 DetectionProbability[dealer_goat|dealer_sheep][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,5,6,7,8,9,10,11,12,14;0,0.0125,0.0725,0.1325,0.145,0.1575,0.1475,0.1375,0.11625,0.095,0.07375,0.0525,0.0262
 5,0,0
 DetectionProbability[transitional_swine|farrow_to_feeder_s|farrow_to_wean_s|farrow_to_finish_s|grower_finisher_s|nurser
 y_s|other_swine_s][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table 1,0,14;0,0.9,0.9
 DetectionProbability[farrow_to_feeder_l|farrow_to_finish_l|farrow_to_wean_l|grower_finisher_l|nursery_l|other_swine_l][
 in_passive_surveillance_outbreak_phase&clinical_signs][]=Table 1,0,1,2,14;0,0.783,0.8415,0.9,0.9
 DetectionProbability[dealer_swine][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table 1,0,14;0,0.25,0.25
 DetectionProbability[livestock_market_bison_cattle][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,14;0,0.08,0.185,0.29,0.395,0.5,0.5
 DetectionProbability[livestock_market_goat_sheep][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,1,2,3,4,5,6,7,8,9,10,11,12,14;0,0.015,0.087,0.159,0.174,0.189,0.177,0.165,0.1395,0.114,0.0885,0.063,0.0315,0,0
 DetectionProbability[livestock_market_swine][in_passive_surveillance_outbreak_phase&clinical_signs][]=Table
 1,0,14;0,0.9,0.9

```

[Surveillance2]
ControlName=tracing_livestock_movements
ActivationOption=tracing
TimePeriodTrigger=first_detection
SurveillanceFarmState=direct_contact_tracing
SelectionProbability=1.0
VisitDelay=BetaPert 0 1 2
VisitFrequency=Constant 5
VisitDuration=Constant 28
DelayToDetection=BetaPert 0 1 2
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

```

```

[Surveillance3]
ControlName=tracing_indirect_contacts
ActivationOption=tracing
TimePeriodTrigger=first_detection
SurveillanceFarmState=indirect_contact_tracing
SelectionProbability=1.0
VisitDelay=BetaPert 0 2 6
VisitFrequency=Constant 5

```

```

VisitDuration=Constant 28
DelayToDetection=BetaPert 0 1 2
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

[Surveillance4]
ControlName=processors_detection_multiple_species
ActivationOption=detected_farm
TimePeriodTrigger=first_detection
SurveillanceFarmState=in_0m_to_5m_detection_zone
SelectionZone=0m_to_5m_detection_zone
SelectionProbability=1.0
VisitDelay=Constant 0
VisitFrequency=Constant 1
VisitDuration=Constant 1
DelayToDetection=Constant 0
DetectionRelativeTo=Infection
DetectionProbability[processor_bison|processor_cattle|processor_cattle_1|processor_goat|processor_sheep|processor_swine
|processor_swine_1][][]=Constant 1
DetectionProbability[bison|dealer_bison|livestock_market_bison_cattle|cow_calf_1|cow_calf_s|dairy_1|dairy_s|dairy_heife
r_calf_1|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_1|feedlot_cattle_m|feedlot_cattle_s|stocker_1|stocker_s
|dealer_cattle|goat_dairy|goat_other|livestock_market_goat_sheep|dealer_goat|sheep_1|sheep_s|feedlot_sheep|dealer_sheep

```

```
|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow
_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|livestock_market_swine|d
ealer_swine][[]]=Constant 0
```

```
[Surveillance5]
```

```
ControlName=active_surveillance_processors
```

```
ActivationOption=time_period
```

```
TimePeriodTrigger=first_detection
```

```
SelectionZone=passive_surveillance_post_detection_zone
```

```
SelectionProbability=1.0
```

```
VisitDelay=Constant 0
```

```
VisitFrequency=Constant 1
```

```
VisitDuration=Constant 730
```

```
DelayToDetection=Constant 0
```

```
DetectionRelativeTo=Clinical_signs
```

```
DetectionProbability[processor_bison][[]]=Constant BetaPert 0.25 0.5 0.75
```

```
DetectionProbability[processor_cattle|processor_cattle_l][[]]=Constant BetaPert 0.25 0.5 0.75
```

```
DetectionProbability[processor_goat|processor_sheep][[]]=Constant BetaPert 0.125 0.25 0.375
```

```
DetectionProbability[processor_swine|processor_swine_l][[]]=Constant BetaPert 0.25 0.5 0.75
```

```
DetectionProbability[bison|dealer_bison|livestock_market_bison_cattle|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heife
r_calf_l|dairy_heifer_calf_m|dairy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s
|dealer_cattle|goat_dairy|goat_other|livestock_market_goat_sheep|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep
|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow
_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|nursery_s|other_swine_l|other_swine_s|livestock_market_swine|d
ealer_swine][[]]=Constant 0
```

```
[Surveillance6]
```

```
ControlName=active_surveillance_livestock_markets
```

```
ActivationOption=time_period
```

```
TimePeriodTrigger=first_detection
```

```

SelectionZone=passive_surveillance_post_detection_zone
SelectionProbability=1.0
VisitDelay=Constant 0
VisitFrequency=Constant 7
VisitDuration=Constant 730
DelayToDetection=Constant 0
DetectionRelativeTo=Clinical_signs
DetectionProbability[livestock_market_bison_cattle][[]]=Constant BetaPert 0.12 0.24 0.36
DetectionProbability[livestock_market_goat_sheep][[]]=Constant BetaPert 0.04 0.08 0.12
DetectionProbability[livestock_market_swine][[]]=Constant BetaPert 0.08 0.16 0.24
DetectionProbability[bison|dealer_bison|cow_calf_l|cow_calf_s|dairy_l|dairy_s|dairy_heifer_calf_l|dairy_heifer_calf_m|d
airy_heifer_calf_s|feedlot_cattle_l|feedlot_cattle_m|feedlot_cattle_s|stocker_l|stocker_s|dealer_cattle|goat_dairy|goat
_other|dealer_goat|sheep_l|sheep_s|feedlot_sheep|dealer_sheep|transitional_swine|farrow_to_feeder_l|farrow_to_feeder_s|
farrow_to_finish_l|farrow_to_finish_s|farrow_to_wean_l|farrow_to_wean_s|grower_finisher_l|grower_finisher_s|nursery_l|n
ursery_s|other_swine_l|other_swine_s|dealer_swine|processor_bison|processor_cattle|processor_cattle_l|processor_goat|pr
ocessor_sheep|processor_swine|processor_swine_l][[]]=Constant 0

[Surveillance7]
ControlName=control_zone_0km_to_10km_early
ActivationOption=detected_farm
TimePeriodTrigger=first_detection
SurveillanceFarmState=in_0km_to_10km_surveillance_zone
SelectionZone=0km_to_10km_surveillance_zone
SelectionProbability=1.0
VisitDelay=BetaPert 0 8 21
VisitFrequency=Constant 5
VisitDuration=Constant 14
DelayToDetection=BetaPert 0 1 2
DetectionRelativeTo=Clinical_signs
DetectionProbability[][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97

```

```

DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

[Surveillance8]
ControlName=control_zone_0km_to_10km_late
ActivationOption=detected_farm
TimePeriodTrigger=first_detection
SurveillanceFarmState=in_0km_to_10km_surveillance_zone
SelectionZone=0km_to_10km_surveillance_zone
SelectionProbability=1.0
VisitDelay=Constant 15
VisitFrequency=Constant 10
VisitDuration=Constant 56
DelayToDetection=BetaPert 0 0 1
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

```

```

[Surveillance9]
ControlName=surveillance_zone_10km_to_20km
ActivationOption=detected_farm
TimePeriodTrigger=first_detection
SurveillanceFarmState=in_10km_to_20km_surveillance_zone
SelectionZone=10km_to_20km_surveillance_zone
SelectionProbability=0.65
VisitDelay=BetaPert 1 8 21
VisitFrequency=Constant 21
VisitDuration=Constant 56
DelayToDetection=BetaPert 0 1 2
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

```

```

[Surveillance10]
ControlName=tracing_livestock_movements1
ActivationOption=tracing
TimePeriodTrigger=first_detection
SurveillanceFarmState=direct_contact_tracing
SelectionProbability=1.0
VisitDelay=BetaPert 0 1 2

```

```

VisitFrequency=Constant 5
VisitDuration=Constant 28
DelayToDetection=BetaPert 0 1 2
DetectionRelativeTo=Clinical_signs
DetectionProbability[][][bison]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][cattle]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][goat]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sheep]=Table 1,0,1,43;-1,0.7275,0.97,0.97
DetectionProbability[][][sow]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][piglet]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][nursery]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][finisher]=Table 1,0,1,42;1,0.97,0.97,0.97
DetectionProbability[][][other_swine]=Table 1,0,1,42;1,0.97,0.97,0.97

```

```

[MovementRestriction1]
ControlName=Standstill_livestock_movements
TimePeriodTrigger=movement_standstill
MovementTypes=bison_&bison_dealer bison_movement_to_infect_market large_cow_calf_MW_PC large_cow_calf_GL_NE_SE
small_cow_calf_MW_PC small_cow_calf_GL_NE_SE large_dairy small_dairy large_dairy_heifer_calf medium_dairy_heifer_calf
small_dairy_heifer_calf large_medium_cattle_feedlot small_cattle_feedlot large_stocker_GL_MW_NE_PC large_stocker_SE
small_stocker_GL_MW_NE_PC small_stocker_SE cattle_movement_to_infect_market cattle_dealer dairy_goat fiber_meat_goat
goat_movement_to_infect_market goat_dealer large_sheep sheep_to_feedlot small_sheep sheep_feedlot
sheep_movement_to_infect_market sheep_dealer sheep_dealer_to_feedlot transitional_swine farrow nursery grower_finisher
other_swine sow_movement_from_large_units sow_movement_from_small_units transitional_swine_movement_to_infect_market
commercial_swine_movement_to_infect_market swine_dealer bison_cattle_through_market large_dairy_through_market
stocker_through_market goat_through_market sheep_through_market transitional_swine_through_market
commercial_swine_through_market bison_market cattle_market goat_market sheep_market swine_market
livestock_movement_to_infect_processor

```


SourceFarmStates=!detected

ProbMovementRestricted=0.5

[MovementRestriction2]

ControlName=Standstill_indirect_contacts

TimePeriodTrigger=movement_standstill

MovementTypes=indirect_bison_market indirect_cattle_market indirect_goat_market indirect_sheep_market
indirect_swine_market indirect_livestock_processor indirect_medium_risk_GL_MW_NE_SE indirect_medium_risk_PC
indirect_low_risk_GL_MW_NE_SE indirect_low_risk_PC indirect_detected_premises

SourceFarmStates=!detected

ProbMovementRestricted=0.25

[MovementRestriction3]

ControlName=post_standstill_livestock_movements

TimePeriodTrigger=post_movement_standstill

MovementTypes=bison_&_bison_dealer bison_movement_to_infect_market large_cow_calf_MW_PC large_cow_calf_GL_NE_SE
small_cow_calf_MW_PC small_cow_calf_GL_NE_SE large_dairy small_dairy large_dairy_heifer_calf medium_dairy_heifer_calf
small_dairy_heifer_calf large_medium_cattle_feedlot small_cattle_feedlot large_stocker_GL_MW_NE_PC large_stocker_SE
small_stocker_GL_MW_NE_PC small_stocker_SE cattle_movement_to_infect_market cattle_dealer dairy_goat fiber_meat_goat
goat_movement_to_infect_market goat_dealer large_sheep sheep_to_feedlot small_sheep sheep_feedlot
sheep_movement_to_infect_market sheep_dealer sheep_dealer_to_feedlot transitional_swine farrow nursery grower_finisher
other_swine sow_movement_from_large_units sow_movement_from_small_units transitional_swine_movement_to_infect_market
commercial_swine_movement_to_infect_market swine_dealer bison_cattle_through_market large_dairy_through_market
stocker_through_market goat_through_market sheep_through_market transitional_swine_through_market
commercial_swine_through_market bison_market cattle_market goat_market sheep_market swine_market
livestock_movement_to_infect_processor

SourceFarmStates=!detected & (in_0km_to_10km_surveillance_zone | direct_contact_tracing | indirect_contact_tracing)

SourceFarmClasses=bison | cow_calf_l | cow_calf_s | dairy_heifer_calf_l | dairy_heifer_calf_m | dairy_heifer_calf_s |
dairy_l | dairy_s | dealer_bison | dealer_cattle | dealer_goat | dealer_sheep | dealer_swine | farrow_to_finish_l |
farrow_to_finish_s | feedlot_cattle_l | feedlot_cattle_m | feedlot_cattle_s | feedlot_sheep | goat_dairy | goat_other |

```
grower_finisher_l | grower_finisher_s | livestock_market_bison_cattle | livestock_market_goat_sheep |  
livestock_market_swine | other_swine_l | other_swine_s | processor_bison | processor_cattle | processor_cattle_l |  
processor_goat | processor_sheep | processor_swine | sheep_l | sheep_s | stocker_l | stocker_s | transitional_swine |  
processor_swine_l  
ProbMovementRestricted=0.75
```

```
[MovementRestriction4]  
ControlName=post_standstill_indirect_contacts  
TimePeriodTrigger=post_movement_standstill  
MovementTypes=indirect_bison_market indirect_cattle_market indirect_goat_market indirect_sheep_market  
indirect_swine_market indirect_livestock_processor indirect_medium_risk_GL_MW_NE_SE indirect_medium_risk_PC  
indirect_low_risk_GL_MW_NE_SE indirect_low_risk_PC indirect_detected_premises  
SourceFarmStates=!detected & (in_0km_to_10km_surveillance_zone | direct_contact_tracing | indirect_contact_tracing)  
ProbMovementRestricted=0.25
```

```
[MovementRestriction5]  
ControlName=post_standstill_livestock_movements_swine  
TimePeriodTrigger=post_movement_standstill  
MovementTypes=farrow_nursery  
SourceFarmStates=!detected & (in_0km_to_10km_surveillance_zone | direct_contact_tracing | indirect_contact_tracing)  
SourceFarmClasses=farrow_to_feeder_l | farrow_to_feeder_s | farrow_to_wean_l | farrow_to_wean_s | nursery_l | nursery_s  
ProbMovementRestricted=0.6
```

Supplement 2

Appendix B 1: Population File

Supplement 2: Population File			
Class	Count	Class	Count
Bison Dealer	5	Small Sheep	85,013
Bison	2547	Large Sheep	2,922
Small stocker	90,623	Goat Dealer	90
Large stocker	1,871	Sheep Dealer	182
Large cattle processor	39	Swine Dealer	1,702
Small cattle processor	625	Large Farrow to Feeder	124
Livestock Market: Cattle/Bison	1,098	Small Farrow to Feeder	353
Small cattle feedlot	26,126	Large Farrow to Finish	1,480
Medium cattle feedlot	416	Small Farrow to Finish	2,234
Large cattle feedlot	43	Large Farrow to Wean	862
Cattle Dealer	3,031	Small Farrow to Wean	322
Small dairy	32,523	Transitional Swine	47,062
Large dairy	3,451	Swine Market	876
Small dairy heifer calf	1,498	Large Nursery	1,030
Medium dairy heifer calf	1,373	Small Nursery	203
Large dairy heifer calf	474	Other Swine	969
Small cow calf	678,491	Other Swine Small	271
Large cow calf	48,144	Large Grow to Finish	6,126
Bison Processor	65	Small Grow to Finish	2,134
Goat Processor	208	Sheep Feedlot	23
Sheep Processor	347	Goat Dairy	29,456
Swine Processor	557	Other Goat	98,498
Large Swine Processor	40	Livestock Market Goat/Sheep	673

Supplement 3

Appendix B 2: Direct Farm to Farm Movements

Origin Farm Type	Number of Farms in Simulation	Poisson Rate/Day	Expected/day	Observed/day
Large Cow-Calf: Mtn West, Pacific Coast	34,247	0.06	2054.82	2067.3
Large Cow-Calf all other regions	13,897	0.05	694.85	691.9
Small Cow-Calf Mtn West, Pacific Coast	299,979	0.04	11999.16	1203.266667
Small Cow-Calf All other regions	378,512	0.02	7570.24	7592.866667

Large Dairy Heifer-Calf	474	0.3885	184.149	184.9
Med Dairy Heifer-Calf	1,373	0.0843	115.7439	116.4
Small Dairy Heifer-Calf	1,498	0.0313	46.8874	47.5
Large Dairy	3,480	0.1	348	342.5

Appendix B 3: Farm to Market Movements

Origin Farm Type	Number of farms in simulation	Poisson Rate/Day	Expected/day	Observed/Day
Large Cow-Calf	48144	0.012	577.728	536.8
Small Cow-Calf	678491	0.0078	5292.2298	5074.8
Large Dairy Heifer-Calf	474	0.013	6.162	5.4
Med Dairy Heifer-Calf	1373	0.0067	9.1991	7.6
Small Dairy Heifer-Calf	1498	0.0095	14.231	13.6
Large Dairy	3480	0.1216	423.168	301.8
Small Dairy	60577	0.0374	2265.5798	1994.2
Cattle Dealer	3031	0.3751	1136.9281	507.6
Large Feedlot	43	0.0206	0.8858	1.4
Medium Feedlot	416	0.0206	8.5696	8.2
Small Feedlot	26126	0.0298	778.5548	716.6
Large Stocker	1871	0.0169	31.6199	28
Small Stocker	90623	0.0096	869.9808	840.8

Supplement 4

Appendix B 4: Current Tracing Speed Parameters

Beef and Cattle Dealers	Traces Completed	0.01	0.03	0.1	0.23	0.41	0.62	0.8	0.93	0.98	0.99	1
	Day	0	1	2	3	4	5	6	7	10	14	21
Dairy	Traces Completed	0.01	0.11	0.29	0.54	0.77	0.9	0.94	0.96	0.98	0.99	1
	Day	0	1	2	3	4	5	6	7	10	14	21

Appendix B 5: Current Tracing Accuracy

Animal Type	Probability movement was forgotten
Beef	0.15
Dairies	0.125
Dairy Heifer/Calf	0.15

Appendix B 6: Partial Tracing Speed Parameters

All Beef and Dairy	Traces Completed	0.01	0.23	0.52	0.76	0.91	0.97	0.98	0.99	0.995	0.999	1
	Day	0	1	2	3	4	5	6	7	10	14	21

Appendix B 7: Partial Tracing Accuracy Parameter

Animal Type	Probability movement was forgotten
All Beef and Dairy	0.1

Appendix B 8: Ideal Tracing Parameters for all beef and dairy

Speed	Probability movement was forgotten
Beta 0 1 1	0.01

Supplement 5

Appendix B 9: Overflow tables from Chapter 4

**TABLE 1: INFECTED PREMISES CURRENT AND PARTIAL TRACING OUTBREAKS
DETECTED ON DAY 21**

INTRODUCTION SITE	Percentile	Partial	Current	Current vs Partial Difference	Current vs Partial Confidence Int.
NEBRASKA FEEDLOT	10th	46	47	-2	-22, 20
	50th	206	628	-422*	-669, -52
	90th	1,067	2,137	-1,070*	-1,854, -473
TEXAS FEEDLOT	10th	61	108	-46*	-93, -4
	50th	279	682	-403*	-715, -157
	90th	1,041	2,248	-1,206*	-1,770, -475
TENNESSEE DAIRY	10th	85	203	-118*	-206, -43
	50th	467	1,432	-965*	-1,368, -592
	90th	1,251	2,858	-1,607*	-2,006, -1,106
CALIFORNIA DAIRY	10th	164	212	-48	-88, 1
	50th	332	435	-103*	-211, -9
	90th	808	2,096	-1,288*	-1,961, -438
NEW YORK DAIRY	10th	131	231	-100*	-212, -14
	50th	454	1,019	-564*	-945, -307
	90th	949	2,683	-1,735*	-2,349, -1,288
NEBRASKA COW-CALF	10th	2	2	0	-1, 1
	50th	23	35	-12	-84, 30
	90th	779	1,679	-901*	-1,871, -112
TENNESSEE COW-CALF	10th	3	3	0	-2, 2
	50th	19	16	2	-17, 29
	90th	550	1,901	-1,351*	-1,875, -141
NEW MEXICO STOCKER	10th	2	3	0	-2, 1
	50th	42	58	-16	-155, 53
	90th	642	1,779	-1,137*	-2,525, -113

**TABLE 2: INFECTED PREMISES CURRENT AND IDEAL TRACING OUTBREAKS
DETECTED ON DAY 21**

INTRODUCTION SITE	Percentile	Ideal	Current	Current vs Ideal Difference	Current vs Ideal Confidence Int.
NEBRASKA FEEDLOT	10th	40	47	-7	-29, 7
	50th	128	628	-500*	-751, -156
	90th	414	2,137	-1,723*	-2,461, -1,205
TEXAS FEEDLOT	10th	57	108	-50*	-95, -14
	50th	153	682	-529*	-850, -305
	90th	367	2,248	-1,881*	-2,316, -1,423
TENNESSEE DAIRY	10th	67	203	-136*	-231, -70
	50th	217	1,432	-1,216*	-1,611, -824
	90th	592	2,858	-2,266*	-2,610, -1,870
CALIFORNIA DAIRY	10th	134	212	-79*	-123, -26
	50th	292	435	-144*	-255, -66
	90th	610	2,096	-1,486*	-2,183, -671
NEW YORK DAIRY	10th	81	231	-150*	-265, -65
	50th	264	1,019	-755*	-1,112, -485
	90th	533	2,683	-2,151*	-2,803, -1,769
NEBRASKA COW-CALF	10th	2	2	0	-1, 1
	50th	16	35	-19	-98, 9
	90th	346	1,679	-1,334*	-2,358, -686
TENNESSEE COW-CALF	10th	3	3	0	-2, 2
	50th	14	16	-2	-22, 6
	90th	135	1,901	-1,765*	-2,214, -641
NEW MEXICO STOCKER	10th	2	3	0	-2, 1
	50th	29	58	-29	-175, 21
	90th	323	1,779	-1,456*	-2,802, -529

**TABLE 3: DURATION OF PARTIAL AND CURRENT TRACING OUTBREAKS
DETECTED ON DAY 21**

INTRODUCTION SITE	Percentile	Partial	Current	Current vs Partial Difference	Current vs Partial Confidence Int.
NEBRASKA FEEDLOT	10th	56	56	0	-12, 11
	50th	108	170	-63*	-109, -13
	90th	233	311	-78*	-184, -24
TEXAS FEEDLOT	10th	64	86	-22*	-37, -5
	50th	115	210	-95*	-129, -51
	90th	238	347	-109*	-228, -32
TENNESSEE DAIRY	10th	65	95	-30*	-53, -11
	50th	132	234	-102*	-136, -60
	90th	246	380	-134*	-205, -70
CALIFORNIA DAIRY	10th	71	86	-15*	-26, -1
	50th	113	139	-26*	-50, -1
	90th	247	376	-130*	-235, -14
NEW YORK DAIRY	10th	75	98	-23*	-37, -9
	50th	116	199	-83*	-118, -37
	90th	212	328	-116*	-207, -76
NEBRASKA COW-CALF	10th	25	25	0	-2, 2
	50th	57	65	-8	-42, 20
	90th	206	270	-64	-193, 11
TENNESSEE COW-CALF	10th	30	30	0	-5, 5
	50th	53	47	6	-9, 22
	90th	183	272	-89	-146, 7
NEW MEXICO STOCKER	10th	26	26	0	-5, 5
	50th	68	76	-8	-56, 31
	90th	234	322	-87	-224, 43

**TABLE 4: DURATION OF IDEAL AND CURRENT TRACING OUTBREAKS DETECTED
ON DAY 21**

INTRODUCTION SITE	Percentile	Ideal	Current	Current vs Ideal Difference	Current vs Ideal Confidence Int.
NEBRASKA FEEDLOT	10th	52	56	-4	-15, 4
	50th	85	170	-86	-134, -38
	90th	163	311	-148	-261, -98
TEXAS FEEDLOT	10th	64	86	-22	-35, -9
	50th	85	210	-125	-158, -86
	90th	146	347	-201	-327, -133
TENNESSEE DAIRY	10th	60	95	-35	-56, -19
	50th	95	234	-139	-169, -106
	90th	167	380	-213	-274, -147
CALIFORNIA DAIRY	10th	68	86	-18	-28, -8
	50th	97	139	-41	-69, -16
	90th	223	376	-154	-275, -30
NEW YORK DAIRY	10th	60	98	-37	-53, -24
	50th	89	199	-109	-145, -65
	90th	147	328	-181	-256, -137
NEBRASKA COW-CALF	10th	25	25	-1	-3, 2
	50th	48	65	-17	-50, 5
	90th	135	270	-135	-243, -58
TENNESSEE COW-CALF	10th	29	30	0	-5, 5
	50th	44	47	-3	-15, 8
	90th	97	272	-175	-208, -84
NEW MEXICO STOCKER	10th	25	26	-1	-6, 4
	50th	56	76	-20	-64, 10
	90th	170	322	-152	-277, -8

**TABLE 5: NUMBER OF FARMS IN SURVEILLANCE ZONE CURRENT AND PARTIAL TRACING
OUBTREAKS DAY 21 DETECTION**

INTRODUCTION SITE	Percentile	Partial	Current	Current vs Partial Difference	Curr vs Part CI
NEBRASKA FEEDLOT	10th	5,158	5,576	-418	-3,332, 2,020
	50th	26,160	72,222	-46,062*	-76,221, -5,679
	90th	127,333	236,822	-109,489*	-195,437, -22,754
TEXAS FEEDLOT	10th	3,942	6,690	-2,748	-7,936, 539
	50th	26,057	74,696	-48,638*	-84,904, -16,078
	90th	127,276	231,935	-104,658*	-184,027, -27,132
TENNESSEE DAIRY	10th	19,381	42,038	-22,657*	-34,957, -8,459
	50th	79,117	183,964	-104,847*	-151,822, -66,925
	90th	179,522	342,900	-163,378*	-209,725, -115,540
CALIFORNIA DAIRY	10th	8,143	10,349	-2,206*	-4,311, -146
	50th	14,594	18,912	-4,318*	-9,845, -947
	90th	39,869	155,004	-115,135*	-206,041, -38,757
NEW YORK DAIRY	10th	16,903	25,678	-8,775*	-19,376, -729
	50th	50,353	115,682	-65,329*	-108,990, -28,529
	90th	113,641	329,053	-215,412*	-268,953, -135,672
NEBRASKA COW- CALF	10th	350	349	1	-92, 94
	50th	2,351	3,347	-996	-10,932, 3,320
	90th	82,615	187,236	-104,621*	-176,604, -7,878
TENNESSEE COW-CALF	10th	738	717	22	-374, 444
	50th	4,508	4,115	393	-4,247, 6,136
	90th	81,339	235,278	-153,939*	-217,411, -32,178
NEW MEXICO STOCKER	10th	95	95	0	-40, 40
	50th	3,556	4,419	-863	-12,554, 4,762
	90th	50,844	179,688	-128,844*	-265,764, -30,870

TABLE 6: NUMBER OF FARMS IN SURVEILLANCE ZONES CURRENT AND IDEAL OUTBREAKS DAY 21

INTRODUCTION SITE	DETECTION				
	Percentile	Ideal	Current	Current vs Ideal Difference	Curr vs Ideal CI
NEBRASKA FEEDLOT	10th	4,539	5,576	-1,037	-3,882, 783
	50th	14,651	72,222	-57,571*	-85,467, -18,903
	90th	46,116	236,822	-190,706*	-276,242, -127,384
TEXAS FEEDLOT	10th	2,905	6,690	-3,785*	-8,496, -1,127
	50th	12,183	74,696	-62,513*	-94,029, -33,413
	90th	34,998	231,935	-196,937*	-252,546, -145,844
TENNESSEE DAIRY	10th	15,333	42,038	-26,705*	-39,667, -14,559
	50th	42,173	183,964	-141,792*	-185,568, -104,216
	90th	93,715	342,900	-249,185*	-280,374, -206,514
CALIFORNIA DAIRY	10th	7,940	10,349	-2,409*	-4,633, -538
	50th	12,826	18,912	-6,085*	-10,903, -2,988
	90th	25,858	155,004	-129,146*	-215,010, -48,211
NEW YORK DAIRY	10th	10,605	25,678	-15,073*	-26,737, -6,141
	50th	29,775	115,682	-85,907*	-135,247, -50,100
	90th	57,177	329,053	-271,876*	-319,250, -204,562
NEBRASKA COW- CALF	10th	350	349	1	-92, 96
	50th	1,545	3,347	-1,802	-10,985, 1,125
	90th	37,833	187,236	-149,403*	-206,696, -64,473
TENNESSEE COW-CALF	10th	738	717	22	-421, 466
	50th	3,520	4,115	-595	-4,994, 2,089
	90th	27,304	235,278	-207,974*	-271,032, -98,471
NEW MEXICO STOCKER	10th	95	95	0	-40, 35
	50th	1,841	4,419	-2,578	-14,614, 1,687
	90th	29,808	179,688	-149,880*	-289,433, -64,343

**TABLE 7: NUMBER OF FARMS IN CONTROL AREAS CURRENT AND PARTIAL
TRACING OUTBREAKS DAY 21 DETECTION**

INTRODUCTION SITE	Percentile	Partial	Current	Current vs Partial Difference	Current vs Partial Confidence Int.
NEBRASKA FEEDLOT	10th	2,573	2,660	-86	-1,307, 995
	50th	13,055	40,562	-27,507*	-44,093, -3,343
	90th	71,241	142,602	-71,362*	-132,102, -22,086
TEXAS FEEDLOT	10th	2,045	3,530	-1,486	-4,236, 242
	50th	13,540	41,943	-28,403*	-47,059, -10,904
	90th	72,831	138,231	-65,400*	-112,302, -27,254
TENNESSEE DAIRY	10th	10,035	22,088	-12,053*	-19,742, -4,664
	50th	44,854	113,182	-68,327*	-96,796, -42,100
	90th	105,640	209,969	-104,329*	-132,264, -71,182
CALIFORNIA DAIRY	10th	6,646	9,213	-2,566*	-4,532, -229
	50th	13,204	16,639	-3,435*	-7,434, -542
	90th	32,987	101,302	-68,314*	-128,649, -23,487
NEW YORK DAIRY	10th	9,678	15,884	-6,206*	-13,555, -938
	50th	31,079	72,173	-41,094*	-68,977, -20,063
	90th	70,152	200,493	-130,340*	-167,435, -90,498
NEBRASKA COW-CALF	10th	134	134	0	-45, 43
	50th	1,101	1,597	-496	-4,751, 1,455
	90th	45,567	110,879	-65,312*	-112,382, -11,588
TENNESSEE COW-CALF	10th	311	307	4	-151, 153
	50th	2,069	1,867	202	-2,056, 3,432
	90th	46,805	144,764	-97,959*	-138,537, -26,154
NEW MEXICO STOCKER	10th	77	77	-1	-41, 31
	50th	2,219	2,622	-403	-9,457, 2,880
	90th	30,684	106,828	-76,144*	-155,902, -21,041

**TABLE 8: NUMBER OF FARMS IN CONTROL AREAS CURRENT AND IDEAL
TRACING OUTBREAKS DAY 21 DETECTION**

INTRODUCTION SITE	Percentile	Ideal	Current	Current vs Ideal Difference	Current vs Ideal Confidence Int.
NEBRASKA FEEDLOT	10th	2,269	2,660	-391	-1,546, 500
	50th	7,434	40,562	-33,128*	-49,632, -9,225
	90th	24,215	142,602	-118,387*	-164,827, -82,462
TEXAS FEEDLOT	10th	1,559	3,530	-1,972*	-4,398, -642
	50th	6,417	41,943	-35,526*	-54,561, -17,537
	90th	18,227	138,231	-120,003*	-151,853, -90,488
TENNESSEE DAIRY	10th	7,728	22,088	-14,360*	-22,041, -7,957
	50th	22,657	113,182	-90,524*	-116,063, -65,376
	90th	55,272	209,969	-154,697*	-179,603, -124,748
CALIFORNIA DAIRY	10th	6,044	9,213	-3,168*	-5,262, -1,137
	50th	11,388	16,639	-5,251*	-9,208, -2,542
	90th	21,589	101,302	-79,712*	-137,449, -36,501
NEW YORK DAIRY	10th	5,796	15,884	-10,088*	-16,851, -4,502
	50th	17,835	72,173	-54,338*	-80,922, -34,624
	90th	36,038	200,493	-164,455*	-199,737, -127,479
NEBRASKA COW-CALF	10th	134	134	0	-45, 45
	50th	732	1,597	-865	-5,082, 428
	90th	19,927	110,879	-90,952*	-128,694, -42,066
TENNESSEE COW-CALF	10th	311	307	4	-145, 156
	50th	1,611	1,867	-257	-2,616, 964
	90th	14,460	144,764	-130,304*	-164,753, -53,447
NEW MEXICO STOCKER	10th	77	77	-1	-41, 31
	50th	1,166	2,622	-1,456	-8,643, 1,124
	90th	17,752	106,828	-89,077*	-166,170, -40,117

Tables for Objective 2: Reduction of Control Areas and Surveillance Zones

**TABLE 9: NUMBER OF IPS IDEAL TRACING WITH STANDARD AND
REDUCED SURVEILLANCE AREAS**

INTRODUCTION SITE	Percentile	Reduced	Standard	Reduced vs Standard Difference	Reduced vs Standard Confidence Int.
NEBRASKA FEEDLOT	10th	43	40	3	-9, 14
	50th	161	128	33	-32, 92
	90th	513	414	100	-80, 274
TEXAS FEEDLOT	10th	62	57	5	-15, 30
	50th	180	153	27	-10, 82
	90th	656	367	289*	2, 536
TENNESSEE DAIRY	10th	71	67	4	-16, 35
	50th	238	217	22	-57, 97
	90th	774	592	182	-40, 363
CALIFORNIA DAIRY	10th	143	134	10	-34, 70
	50th	347	292	56	-12, 129
	90th	887	610	277	-114, 769
NEW YORK DAIRY	10th	107	81	25	-42, 93
	50th	314	264	51	-23, 122
	90th	683	533	150	-2, 362
NEBRASKA COW-CALF	10th	2	2	0	-1, 1
	50th	16	16	0	-15, 19
	90th	350	346	5	-213, 234
TENNESSEE COW-CALF	10th	4	3	0	-2, 3
	50th	15	14	1	-8, 9
	90th	297	135	161	-33, 347
NEW MEXICO STOCKER	10th	3	2	0	-1, 1
	50th	32	29	3	-38, 46
	90th	300	323	-23	-375, 408

**TABLE 10: DURATION OF OUTBREAKS IDEAL TRACING WITH STANDARD AND REDUCED
SURVEILLANCE AREAS**

INTRODUCTION SITE	Percentile	Reduced	Standard	Reduced vs Standard Difference	Reduced vs Standard CI
NEBRASKA FEEDLOT	10th	54	52	3	-5, 11
	50th	90	85	5	-11, 20
	90th	181	163	18	-33, 72
TEXAS FEEDLOT	10th	64	64	0	-9, 11
	50th	100	85	15*	1, 28
	90th	217	146	71*	19, 122
TENNESSEE DAIRY	10th	61	60	1	-8, 14
	50th	101	95	5	-7, 21
	90th	183	167	16	-25, 47
CALIFORNIA DAIRY	10th	77	68	9*	1, 18
	50th	123	97	26*	6, 49
	90th	271	223	48	-28, 202
NEW YORK DAIRY	10th	69	60	9	-2, 23
	50th	107	89	17*	5, 31
	90th	178	147	31	-5, 59
NEBRASKA COW- CALF	10th	25	25	0	-2, 2
	50th	46	48	-1	-13, 12
	90th	170	135	36	-55, 104
TENNESSEE COW-CALF	10th	29	29	-1	-6, 5
	50th	46	44	2	-9, 11
	90th	128	97	31	-11, 66
NEW MEXICO STOCKER	10th	25	25	0	-4, 5
	50th	59	56	2	-20, 24
	90th	184	170	14	-117, 91

TABLE 11: FARMS IN SURVEILLANCE ZONES IDEAL TRACING WITH STANDARD AND REDUCED SURVEILLANCE AREAS

INTRODUCTION SITE	Percentile	Reduced	Standard	Reduced vs Standard Difference	Reduced vs Standard CI
NEBRASKA FEEDLOT	10th	2,955	4,539	-1,584*	-3741, -166
	50th	11,226	14,651	-3,425	-8,061, 982
	90th	36,962	46,116	-9,154	-22,756, 3,958
TEXAS FEEDLOT	10th	2,375	2,905	-530	-2,229, 800
	50th	9,938	12,183	-2,245	-7,505, 2,790
	90th	43,628	34,998	8,630	-17,084, 24,821
TENNESSEE DAIRY	10th	10,353	15,333	-4,980*	-9,010, -139
	50th	28,761	42,173	-13,412*	-25,481, -3,907
	90th	75,571	93,715	-18,144*	-40,417, -2,324
CALIFORNIA DAIRY	10th	6,031	7,940	-1,909	-3,710, 893
	50th	12,148	12,826	-678	-3,018, 1,782
	90th	27,467	25,858	1,609	-8,658, 11,552
NEW YORK DAIRY	10th	8,125	10,605	-2,480	-8,603, 3,310
	50th	23,649	29,775	-6,126	-14,040, 257
	90th	51,950	57,177	-5,227	-20,848, 7,001
NEBRASKA COW-CALF	10th	191	350	-158*	-256, -60
	50th	927	1,545	-619	-1,990, 607
	90th	21,794	37,833	-16,039	-41,555, 5,151
TENNESSEE COW-CALF	10th	339	738	-399*	-895, -65
	50th	2,077	3,520	-1,443*	-3,701, -28
	90th	33,125	27,304	5,821	-12,598, 19,678
NEW MEXICO STOCKER	10th	72	95	-23	-71, 19
	50th	1,460	1,841	-381	-3,123, 1,354
	90th	19,836	29,808	-9,972	-28,286, 15,017

TABLE 12: FARMS IN CONTROL AREAS IDEAL TRACING WITH STANDARD AND REDUCED SURVEILLANCE AREAS

INTRODUCTION SITE	Percentile	Reduced	Standard	Reduced vs Standard Difference	Reduced vs Standard CI
NEBRASKA FEEDLOT	10th	1,363	2,269	-906*	-1,978, -335
	50th	5,238	7,434	-2,197	-4,736, 175
	90th	18,040	24,215	-6,174	-12,400, 8
TEXAS FEEDLOT	10th	1,094	1,559	-465	-1,255, 272
	50th	4,761	6,417	-1,657	-4,048, 928
	90th	21,049	18,227	2,821	-7,992, 12,005
TENNESSEE DAIRY	10th	4,723	7,728	-3,005*	-5,074, -399
	50th	14,170	22,657	-8,487*	-14,634, -2,162
	90th	40,104	55,272	-15,167*	-27,919, -4,877
CALIFORNIA DAIRY	10th	4,314	6,044	-1,730	-3,451, 570
	50th	9,755	11,388	-1,633	-3,792, 180
	90th	21,001	21,589	-588	-8,180, 5,055
NEW YORK DAIRY	10th	4,001	5,796	-1,796	-5,297, 1,389
	50th	12,881	17,835	-4,954*	-9,950, -697
	90th	29,747	36,038	-6,291	-15,502, 1,242
NEBRASKA COW-CALF	10th	63	134	-71*	-118, -32
	50th	395	732	-337	-1,000, 220
	90th	11,361	19,927	-8,566	-22,510, 3,288
TENNESSEE COW-CALF	10th	176	311	-135*	-329, -10
	50th	954	1,611	-657	-1,822, 37
	90th	16,069	14,460	1,609	-82,88, 9,071
NEW MEXICO STOCKER	10th	53	77	-24	-62, 11
	50th	899	1,166	-268	-1,832, 713
	90th	10,902	17,752	-6,850	-18,737, 5,323

TABLE 11: FARMS IN SURVEILLANCE ZONES IDEAL TRACING WITH STANDARD AND REDUCED SURVEILLANCE AREAS

INTRODUCTION SITE	Percentile	Reduced	Standard	Reduced vs Standard Difference	Reduced vs Standard CI
NEBRASKA FEEDLOT	10th	2,955	4,539	-1,584*	-3741, -166
	50th	11,226	14,651	-3,425	-8,061, 982
	90th	36,962	46,116	-9,154	-22,756, 3,958
TEXAS FEEDLOT	10th	2,375	2,905	-530	-2,229, 800
	50th	9,938	12,183	-2,245	-7,505, 2,790
	90th	43,628	34,998	8,630	-17,084, 24,821
TENNESSEE DAIRY	10th	10,353	15,333	-4,980*	-9,010, -139
	50th	28,761	42,173	-13,412*	-25,481, -3,907
	90th	75,571	93,715	-18,144*	-40,417, -2,324
CALIFORNIA DAIRY	10th	6,031	7,940	-1,909	-3,710, 893
	50th	12,148	12,826	-678	-3,018, 1,782
	90th	27,467	25,858	1,609	-8,658, 11,552
NEW YORK DAIRY	10th	8,125	10,605	-2,480	-8,603, 3,310
	50th	23,649	29,775	-6,126	-14,040, 257
	90th	51,950	57,177	-5,227	-20,848, 7,001
NEBRASKA COW-CALF	10th	191	350	-158*	-256, -60
	50th	927	1,545	-619	-1,990, 607
	90th	21,794	37,833	-16,039	-41,555, 5,151
TENNESSEE COW-CALF	10th	339	738	-399*	-895, -65
	50th	2,077	3,520	-1,443*	-3,701, -28
	90th	33,125	27,304	5,821	-12,598, 19,678
NEW MEXICO STOCKER	10th	72	95	-23	-71, 19
	50th	1,460	1,841	-381	-3,123, 1,354
	90th	19,836	29,808	-9,972	-28,286, 15,017

Supplement 6

Appendix B 10 Tables for Outbreaks Detected on Day 8

Number of Infected Premises from outbreaks detected on Day 8

Nebraska Feedlot Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	3	3	0	-2	2
75	13	12	1	-29	18
90	86	147	-61	-648	396

Nebraska Feedlot Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	3	3	0	-2	2
75	9	12	-2	-31	8
90	28	147	-120	-718	10

Texas Feedlot Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	1
25	2	2	0	0	0
50	3	3	0	-1	1
75	10	11	-1	-32	17
90	68	234	-165	-887	140

Texas Feedlot Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	0
25	2	2	0	0	1
50	3	3	0	-1	1

75	9	11	-2	-29	8
90	49	234	-185	-1054	57
Tennessee Dairy Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	1
25	3	2	0	-1	1
50	7	8	0	-8	8
75	44	97	-52	-371	52
90	288	1306	-1019	-2250	130

Tennessee Dairy Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	1
25	2	2	0	-1	1
50	6	8	-2	-9	2
75	18	97	-79	-406	3
90	72	1306	-1234	-2383	-168

California Dairy Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2	2	0	-1	1
25	4	4	-1	-4	2
50	15	23	-9	-38	12
75	84	115	-31	-125	39
90	211	475	-264	-1656	88

California Dairy Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2	2	0	-1	1
25	4	4	0	-4	2
50	12	23	-12	-41	4

75	38	115	-76	-177	-15
90	101	475	-374	-1668	-35

Number of Infected Premises from outbreaks detected on Day 8

New York Dairy Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2	2	0	-1	1
25	3	4	0	-3	2
50	9	12	-3	-20	6
75	41	145	-104	-242	17
90	255	616	-360	-999	98

New York Dairy Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2	2	0	-1	1
25	4	4	0	-3	2
50	8	12	-4	-23	3
75	24	145	-121	-280	-21
90	78	616	-537	-1186	-146

Nebraska Cow-Calf Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	1	1	0	0	0
50	1	1	0	-1	1
75	3	3	0	-5	3
90	18	26	-8	-145	51

Nebraska Cow-Calf Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper

10	1	1	0	0	0
25	1	1	0	0	0
50	1	1	0	-1	1
75	3	3	0	-6	2
90	10	26	-16	-164	7

Number of Infected Premises from outbreaks detected on Day 8

Tennessee Cow-Calf Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	1	1	0	0	0
50	2	2	0	-1	1
75	4	4	0	-2	2
90	9	28	-19	-624	73

Tennessee Cow-Calf Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	1	1	0	0	0
50	2	2	0	-1	1
75	4	4	0	-2	2
90	10	28	-18	-528	31

New Mexico Stocker Detected Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	1	1	0	0	0
50	1	1	0	0	1
75	3	3	0	-4	3
90	11	21	-10	-602	15

New Mexico Stocker Detected Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	1	1	0	0	0
50	1	1	0	-1	1
75	3	3	0	-4	2
90	10	21	-11	-641	11

Duration (days) of outbreaks detected on Day 8

Nebraska Feedlot Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	13	12	1	-7	8
50	24	23	0	-7	7
75	39	39	0	-28	16
90	93	111	-18	-109	90

Nebraska Feedlot Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	12	12	0	-7	7
50	24	23	0	-6	7
75	35	39	-4	-37	8
90	52	111	-58	-126	6

Texas Feedlot Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-3	2
25	14	15	0	-4	4

50	18	18	0	-6	4
75	30	36	-5	-32	10
90	69	114	-45	-166	45

Texas Feedlot Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-3	2
25	14	15	0	-4	4
50	18	18	0	-6	4
75	30	36	-5	-32	10
90	69	114	-45	-166	45

Duration (days) of outbreaks detected on Day 8

Tennessee Dairy Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-3	3
25	13	14	0	-7	5
50	31	30	0	-11	12
75	63	85	-22	-92	27
90	122	231	-109	-239	16

Tennessee Dairy Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-3	2
25	13	14	-1	-6	3
50	23	30	-8	-19	4
75	45	85	-40	-114	3
90	76	231	-155	-281	-46

California Dairy Duration Day 8: Partial					

Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	11	11	0	-4	4
25	18	19	-1	-10	6
50	40	48	-9	-29	16
75	87	104	-18	-61	22
90	133	187	-54	-290	29

California Dairy Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	11	11	-1	-4	3
25	18	19	-1	-9	4
50	33	48	-16	-35	4
75	59	104	-45	-88	-2
90	99	187	-88	-321	14

Duration (days) of outbreaks detected on Day 8

New York Dairy Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	10	10	0	-4	4
25	16	19	-2	-8	4
50	30	36	-7	-33	8
75	60	105	-45	-81	-3
90	129	194	-65	-160	24

New York Dairy Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	10	10	0	-4	3
25	16	19	-2	-9	5
50	28	36	-8	-35	4
75	50	105	-56	-92	-19

90	81	194	-113	-186	-44

Nebraska Cow Calf Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	8	8	0	0	0
50	9	10	0	-6	5
75	19	20	-1	-14	8
90	44	47	-3	-52	32

Nebraska Cow Calf Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	8	8	0	0	0
50	9	10	-1	-5	4
75	17	20	-3	-14	6
90	35	47	-11	-60	15

Duration (days) of outbreaks detected on Day 8

Tennessee Cow Calf Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	8	8	0	-1	0
50	14	14	0	-5	5
75	22	23	-1	-8	6
90	37	47	-10	-124	42

Tennessee Cow Calf Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0

25	8	8	0	-1	0
50	14	14	0	-6	5
75	23	23	0	-6	7
90	37	47	-11	-128	26

New Mexico Stocker Duration Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	8	8	0	0	0
50	8	8	0	-2	2
75	17	19	-2	-15	10
90	37	48	-11	-132	21

New Mexico Stocker Duration Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	0	0
25	8	8	0	0	0
50	8	8	0	-3	3
75	17	19	-2	-15	7
90	33	48	-15	-118	9

Number of Farms in Control Areas from Outbreaks Detected on Day 8

Nebraska Feedlot Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	134	134	0	0	0
25	142	142	0	-49	51
50	290	276	14	-146	159
75	822	767	55	-1,774	1,241
90	5,585	10,842	-5,257	-46,624	27,888

Nebraska Feedlot Control Area Day 8: Ideal					

Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	134	134	0	0	0
25	142	142	0	-40	43
50	277	276	0	-126	127
75	656	767	-110	-2,586	487
90	1,918	10,842	-8,924	-48,188	746

Texas Feedlot Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	7	7	0	-5	5
25	18	18	0	-8	8
50	46	47	-2	-49	44
75	275	250	25	-935	585
90	3,082	13,223	-10,141	-65,992	7,101

Texas Feedlot Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	7	7	0	-5	5
25	18	18	0	-8	8
50	45	47	-2	-43	36
75	200	250	-50	-1,599	324
90	1,960	13,223	-11,263	-67,700	3,908

Number of Farms in Control Areas from Outbreaks Detected on Day 8

Tennessee Dairy Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	87	87	0	-77	79
25	282	279	3	-198	206
50	974	988	-14	-1,051	937
75	5,400	11,440	-6,040	-31,346	5,473

90	27,174	99,066	-71,892	-150,895	10,519

Tennessee Dairy Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	87	87	0	-85	81
25	272	279	-7	-183	155
50	720	988	-268	-1,378	271
75	2,291	11,440	-9,149	-35,843	-103
90	8,323	99,066	-90,743	-169,969	-16,497

California Dairy Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	92	93	0	-66	63
25	229	243	-15	-246	186
50	851	1,408	-557	-2,155	640
75	4,547	6,019	-1,472	-6,118	2,276
90	10,640	20,343	-9,703	-71,507	4,403

California Dairy Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	92	93	0	-68	64
25	221	243	-22	-271	149
50	635	1,408	-773	-2,159	115
75	2,267	6,019	-3,752	-7,976	-393
90	5,224	20,343	-15,118	-75,020	-2,979

Number of Farms in Control Areas from Outbreaks Detected on Day 8

New York Dairy Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	113	113	0	-70	70

25	252	272	-20	-227	169
50	729	1,027	-298	-1,855	370
75	3,550	11,397	-7,847	-18,833	1,350
90	19,955	46,967	-27,013	-76,720	6,031

New York Dairy Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	113	113	-1	-70	67
25	275	272	3	-197	164
50	659	1,027	-368	-1,701	201
75	1,841	11,397	-9,556	-21,045	-1,447
90	6,969	46,967	-39,998	-89,733	-9,257

Nebraska Cow Calf Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	91	91	0	0	0
25	91	91	0	0	0
50	94	95	-1	-32	28
75	203	212	-9	-316	162
90	933	1,452	-519	-8,596	3,303

Nebraska Cow Calf Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	91	91	0	0	0
25	91	91	0	0	0
50	94	95	-1	-33	30
75	186	212	-25	-325	115
90	554	1,452	-897	-9,071	446

Number of Farms in Control Areas from Outbreaks Detected on Day 8

Tennessee Cow Calf Control Area Day 8: Partial

Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	248	248	0	0	0
25	248	248	0	-1	1
50	266	266	0	-54	46
75	525	532	-7	-382	318
90	1,375	3,297	-1,922	-42,992	5,264

Tennessee Cow Calf Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	248	248	0	0	0
25	248	248	0	-1	1
50	266	266	0	-29	27
75	520	532	-13	-411	318
90	1,436	3,297	-1,862	-47,569	3,678

New Mexico Stocker Control Area Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	68	68	0	0	0
25	68	68	0	0	0
50	68	68	0	-1	1
75	94	97	-2	-209	84
90	392	1,453	-1,062	-31,234	1,299

New Mexico Stocker Control Area Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	68	68	0	0	0
25	68	68	0	0	0
50	68	68	0	-2	1
75	89	97	-7	-183	66
90	392	1,453	-1,062	-28,028	557

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 8

Nebraska Feedlot Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	380	380	0	0	0
25	392	392	0	-95	96
50	703	680	23	-195	242
75	1,791	1,708	83	-3,863	2,759
90	11,815	22,397	-10,582	-84,380	42,252

Nebraska Feedlot Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	380	380	0	0	0
25	392	392	0	-94	87
50	680	680	0	-205	195
75	1,471	1,708	-237	-5,755	1,109
90	4,244	22,397	-18,153	-83,935	1,628

Texas Feedlot Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	33	33	0	-9	9
25	63	63	0	-28	26
50	117	117	0	-94	94
75	552	569	-17	-1,607	942
90	5,952	25,021	-19,069	-105,546	13,808

Texas Feedlot Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	33	33	0	-12	14
25	63	63	0	-22	20
50	116	117	0	-98	83

75	440	569	-129	-2,303	615
90	3,247	25,021	-21,775	-118,206	5,039

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 8

Tennessee Dairy Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	564	564	0	-260	255
25	1,042	1,050	-8	-340	350
50	2,510	2,624	-113	-2,284	1,959
75	11,620	22,057	-10,437	-54,196	11,023
90	50,190	165,677	-115,487	-251,877	11,617

Tennessee Dairy Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	564	564	0	-219	226
25	1,025	1,050	-25	-432	326
50	1,951	2,624	-673	-2,928	664
75	5,159	22,057	-16,898	-70,746	-230
90	16,542	165,677	-149,135	-274,297	-31,523

California Dairy Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	283	288	-5	-199	150
25	643	701	-58	-398	283
50	1,661	2,333	-672	-2,871	1,040
75	6,310	7,912	-1,602	-7,059	2,018
90	13,094	24,132	-11,038	-102,246	7,040

California Dairy Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper

10	283	288	-5	-211	174
25	633	701	-68	-443	203
50	1,349	2,333	-983	-2,866	336
75	3,482	7,912	-4,430	-9,632	-872
90	7,212	24,132	-16,920	-103,779	-2,732

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 8

New York Dairy Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	325	325	0	-174	154
25	631	676	-44	-491	298
50	1,731	2,378	-647	-3,162	997
75	7,260	19,892	-12,631	-31,924	3,663
90	32,563	78,601	-46,038	-132,618	9,092

New York Dairy Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	325	325	0	-165	179
25	652	676	-24	-488	275
50	1,599	2,378	-779	-3,050	355
75	4,088	19,892	-15,803	-33,607	-1,773
90	13,444	78,601	-65,157	-143,386	-18,659

Nebraska Cow Calf Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	241	241	0	0	0
25	241	241	0	0	0
50	248	249	-1	-84	76
75	504	527	-23	-567	349
90	1,890	3,041	-1,151	-19,668	7,572

Nebraska Cow Calf Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	241	241	0	0	0
25	241	241	0	0	0
50	248	249	-1	-90	83
75	460	527	-67	-587	284
90	1,219	3,041	-1,822	-18,749	1,402

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 8

Tennessee Cow Calf Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	562	562	0	0	0
25	562	562	0	-3	4
50	605	605	0	-61	57
75	1,165	1,192	-27	-927	673
90	3,073	6,925	-3,852	-81,960	12,508

Tennessee Cow Calf Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	562	562	0	0	0
25	562	562	0	-1	1
50	605	605	0	-108	82
75	1,160	1,192	-32	-985	735
90	3,290	6,925	-3,635	-78,586	6,326

New Mexico Stocker Surveillance Zone Day 8: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	82	82	0	0	0
25	82	82	0	0	0
50	82	82	0	-2	3

75	136	139	-3	-264	135
90	631	2,275	-1,644	-35,915	3,282

New Mexico Stocker Surveillance Zone Day 8: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	82	82	0	0	0
25	82	82	0	0	0
50	82	82	0	-3	2
75	131	139	-7	-237	110
90	500	2,275	-1,775	-41,751	1,072

Appendix B 11 Tables for Day 14 Outbreaks

Nebraska Feedlot Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	5	5	0	-2	2
25	10	10	-1	-5	5
50	27	33	-6	-32	24
75	134	400	-266	-893	117
90	541	1558	-1017	-1670	-148

Nebraska Feedlot Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	5	5	0	-2	2
25	10	10	-1	-5	4
50	23	33	-10	-34	10
75	56	400	-344	-905	-13
90	110	1558	-1447	-1990	-670
Texas Feedlot Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-5	4
25	17	20	-3	-14	6

50	43	65	-21	-75	16
75	138	310	-172	-589	15
90	385	1635	-1250	-2301	-48

Texas Feedlot Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	8	8	0	-6	3
25	15	20	-5	-15	5
50	35	65	-30	-84	2
75	86	310	-224	-628	-51
90	161	1635	-1474	-2519	-402

Tennessee Dairy Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	12	12	0	-8	7
25	25	29	-4	-23	10
50	70	142	-73	-407	20
75	221	1202	-981	-1653	-298
90	596	2374	-1778	-2429	-918

Tennessee Dairy Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	12	12	0	-8	7
25	24	29	-5	-24	8
50	52	142	-91	-398	-6
75	122	1202	-1080	-1684	-446
90	277	2374	-2098	-2792	-1323

California Dairy Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper

10	35	44	-9	-33	10
25	68	89	-20	-58	11
50	123	183	-60	-119	3
75	224	433	-209	-607	-20
90	582	1124	-542	-1198	75

California Dairy Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	31	44	-13	-35	2
25	52	89	-36	-71	-10
50	86	183	-97	-150	-44
75	153	433	-280	-632	-94
90	243	1124	-881	-1509	-462

New York Dairy Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	11	14	-3	-14	7
25	42	57	-15	-109	36
50	138	366	-228	-571	-40
75	422	1220	-798	-1307	-384
90	839	2162	-1323	-2092	-554

New York Dairy Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	11	14	-3	-14	6
25	28	57	-30	-111	6
50	62	366	-304	-659	-125
75	128	1220	-1092	-1568	-695
90	210	2162	-1952	-2663	-1249

Nebraska Cow-Calf Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	3	4	0	-4	2
75	13	20	-6	-143	24
90	115	711	-596	-1203	138

Nebraska Cow-Calf Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	3	4	0	-4	2
75	13	20	-7	-138	12
90	80	711	-630	-1354	46

Tennessee Cow-Calf Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	5	5	0	-2	3
75	19	20	-1	-40	38
90	161	190	-29	-584	397

Tennessee Cow-Calf Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	0	0
25	2	2	0	-1	1
50	5	5	0	-2	2
75	14	20	-5	-45	15

90	56	190	-134	-715	20

New Mexico Stocker Detected Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	1
25	2	2	0	0	0
50	5	5	0	-5	3
75	27	39	-12	-191	60
90	253	901	-648	-2001	323

New Mexico Stocker Detected Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1	1	0	-1	1
25	2	2	0	0	0
50	5	5	0	-6	3
75	16	39	-23	-211	10
90	77	901	-823	-2246	-32

Nebraska Feedlot Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	26	26	0	-5	5
25	32	35	-3	-11	6
50	54	54	0	-18	17
75	99	152	-53	-149	27
90	180	285	-105	-190	-33

Nebraska Feedlot Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	26	26	0	-5	4

25	31	35	-4	-11	4
50	47	54	-7	-25	6
75	69	152	-83	-173	-9
90	96	285	-189	-247	-122

Texas Feedlot Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	28	28	-1	-5	4
25	36	42	-6	-18	6
50	64	80	-17	-42	10
75	105	157	-51	-123	5
90	167	261	-95	-179	-5

Texas Feedlot Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	27	28	-2	-6	2
25	36	42	-7	-19	6
50	56	80	-24	-47	-1
75	83	157	-74	-142	-21
90	121	261	-141	-206	-84

Tennessee Dairy Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	33	35	-1	-9	6
25	44	50	-6	-22	8
50	74	98	-25	-66	4
75	109	217	-107	-144	-38
90	195	262	-67	-137	-20

Tennessee Dairy Duration Day 14: Ideal					

Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	33	35	-2	-9	5
25	43	50	-7	-22	4
50	65	98	-34	-77	-8
75	84	217	-133	-163	-70
90	117	262	-145	-175	-109

California Dairy Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	48	54	-6	-19	6
25	64	74	-11	-25	2
50	88	101	-14	-37	4
75	126	183	-57	-123	17
90	214	294	-80	-218	35

California Dairy Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	44	54	-10	-23	2
25	58	74	-16	-29	-6
50	74	101	-27	-47	-12
75	104	183	-79	-145	-15
90	156	294	-138	-291	-59

New York Dairy Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	32	35	-3	-15	7
25	51	62	-10	-37	11
50	91	130	-39	-102	-7
75	132	251	-119	-155	-52

90	226	309	-83	-187	-37

New York Dairy Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	31	35	-4	-17	6
25	48	62	-14	-40	4
50	66	130	-64	-121	-32
75	90	251	-161	-191	-112
90	120	309	-190	-283	-146

Nebraska Cow Calf Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	0	0
25	16	16	0	-3	3
50	22	23	-2	-9	4
75	44	49	-5	-49	21
90	87	177	-90	-174	38

Nebraska Cow Calf Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	0	0
25	16	16	0	-4	3
50	21	23	-2	-9	4
75	40	49	-9	-48	16
90	76	177	-101	-190	18

Tennessee Cow Calf Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	-1	1
25	18	18	0	-5	5

50	27	27	0	-7	6
75	44	47	-2	-32	23
90	111	114	-3	-112	75

Tennessee Cow Calf Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	-1	1
25	18	18	0	-4	4
50	27	27	0	-8	6
75	39	47	-7	-34	9
90	64	114	-50	-132	13

New Mexico Stocker Duration Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	-2	2
25	18	18	0	-3	3
50	27	28	-1	-12	9
75	60	78	-19	-81	23
90	137	244	-108	-303	71

New Mexico Stocker Duration Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	14	14	0	-2	2
25	18	18	0	-3	3
50	28	28	0	-11	9
75	49	78	-30	-90	6
90	82	244	-163	-315	-19

Number of Farms in Control Areas from Outbreaks Detected on Day 14

Nebraska Feedlot Control Area Day 14: Partial

Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	420	435	-15	-172	113
25	675	716	-41	-302	250
50	1,723	1,982	-258	-1,878	1,436
75	8,293	24,213	-15,920	-53,330	8,333
90	35,492	100,486	-64,994	-123,629	-3,923

Nebraska Feedlot Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	420	435	-15	-166	118
25	681	716	-35	-304	256
50	1,535	1,982	-446	-1,931	665
75	3,618	24,213	-20,595	-61,794	-467
90	7,395	100,486	-93,091	-142,692	-43,042

Texas Feedlot Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	146	157	-11	-129	97
25	378	509	-130	-565	224
50	1,374	2,410	-1,036	-4,050	827
75	7,300	20,405	-13,105	-39,454	1,238
90	23,802	108,406	-84,604	-152,685	-8,740

Texas Feedlot Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	130	157	-27	-138	78
25	339	509	-170	-604	134
50	1,037	2,410	-1,374	-4,206	63
75	3,681	20,405	-16,724	-42,621	-2,883
90	6,777	108,406	-101,628	-162,044	-27,584

Number of Farms in Control Areas from Outbreaks Detected on Day 14

Tennessee Dairy Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,433	1,524	-91	-1,138	920
25	3,274	3,952	-678	-2,936	1,337
50	7,792	16,381	-8,589	-34,459	1,820
75	23,915	93,846	-69,931	-121,088	-25,592
90	52,792	178,086	-125,294	-174,552	-64,905

Tennessee Dairy Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,391	1,524	-133	-1,199	1,391
25	2,554	3,952	-1,398	-3,587	2,554
50	6,678	16,381	-9,703	-38,418	6,678
75	14,644	93,846	-79,202	-127,888	14,644
90	28,986	178,086	-149,100	-193,530	28,986

California Dairy Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,673	2,368	-695	-1,854	591
25	3,758	4,642	-884	-2,943	777
50	6,388	8,414	-2,026	-4,524	-3
75	10,694	21,180	-10,486	-25,202	-843
90	20,174	49,309	-29,135	-50,500	2,776

California Dairy Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,605	2,368	-763	-1,994	405
25	3,029	4,642	-1,613	-3,380	-252

50	4,869	8,414	-3,545	-6,498	-1,696
75	7,302	21,180	-13,878	-28,760	-4,434
90	11,581	49,309	-37,728	-58,098	-19,774

Number of Farms in Control Areas from Outbreaks Detected on Day 14

New York Dairy Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	809	1,064	-255	-1,017	617
25	3,304	4,459	-1,155	-7,454	2,399
50	10,648	26,225	-15,578	-41,149	-1,444
75	31,794	84,197	-52,404	-85,559	-24,496
90	61,938	149,558	-87,621	-151,934	-31,302

New York Dairy Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	826	1,064	-238	-1,041	424
25	2,174	4,459	-2,285	-7,951	456
50	5,107	26,225	-21,119	-47,109	-7,920
75	10,019	84,197	-74,179	-104,579	-50,258
90	16,091	149,558	-133,467	-192,398	-86,613

Nebraska Cow Calf Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	91	91	0	0	0
25	99	99	0	-35	34
50	201	216	-16	-174	105
75	647	1,008	-361	-10,569	1,266
90	6,908	47,138	-40,230	-83,993	9,766

Nebraska Cow Calf Control Area Day 14: Ideal					

Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	91	91	0	0	0
25	99	99	0	-33	31
50	196	216	-21	-166	85
75	588	1,008	-420	-11,867	992
90	4,979	47,138	-42,159	-85,535	2,054

Number of Farms in Control Areas from Outbreaks Detected on Day 14

Tennessee Cow Calf Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	248	248	0	-2	2
25	259	259	0	-19	21
50	570	581	-11	-466	419
75	2,610	2,537	73	-5,940	5,122
90	15,535	19,482	-3,947	-47,230	30,848

Tennessee Cow Calf Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	248	248	0	-2	2
25	259	259	0	-30	29
50	550	581	-31	-429	343
75	1,879	2,537	-658	-5,731	2,041
90	6,673	19,482	-12,809	-54,510	2,802

New Mexico Stocker Control Area Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	68	68	0	-1	1
25	75	75	0	-25	30
50	172	182	-9	-229	131

75	1,199	1,913	-714	-12,644	3,325
90	12,029	54,634	-42,606	-102,854	12,556

New Mexico Stocker Control Area Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	68	68	0	-2	2
25	75	75	0	-22	26
50	174	182	-8	-228	128
75	780	1,913	-1,133	-13,612	582
90	3,798	54,634	-50,836	-115,229	-3,218

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 14

Nebraska Feedlot Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	853	866	-13	-277	269
25	1,357	1,388	-31	-509	486
50	3,493	4,012	-519	-4,338	2,904
75	17,361	44,968	-27,607	-93,807	16,075
90	65,638	168,095	-102,457	-199,131	-20,023

Nebraska Feedlot Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	853	866	-13	-266	213
25	1,315	1,388	-73	-619	516
50	3,200	4,012	-812	-4,558	1,338
75	7,846	44,968	-37,122	-103,040	-903
90	15,897	168,095	-152,198	-244,634	-82,113

Texas Feedlot Surveillance Zone Day 14: Partial					

Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	295	327	-31	-279	175
25	749	1,060	-311	-1,215	458
50	2,772	4,556	-1,784	-6,719	1,676
75	14,508	39,488	-24,979	-75,224	2,623
90	46,829	183,917	-137,088	-244,204	-4,716

Texas Feedlot Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	253	327	-74	-298	128
25	700	1,060	-360	-1,248	349
50	2,097	4,556	-2,459	-8,010	174
75	6,840	39,488	-32,647	-83,136	-6,989
90	14,400	183,917	-169,517	-268,642	-51,091

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 14

Tennessee Dairy Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	3,290	3,335	-45	-2,279	2,039
25	7,235	8,737	-1,503	-6,097	3,061
50	15,701	32,107	-16,406	-59,668	3,234
75	44,943	156,527	-111,584	-201,817	-44,070
90	91,733	297,061	-205,328	-270,601	-110,890

Tennessee Dairy Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	3,157	3,335	-178	-2,264	1,236
25	5,721	8,737	-3,016	-7,823	1,067
50	13,983	32,107	-18,123	-60,660	-1,184
75	28,115	156,527	-128,412	-214,067	-63,534

90	54,265	297,061	-242,795	-305,381	-157,455

California Dairy Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2,750	3,643	-893	-2,582	872
25	5,476	6,386	-910	-2,802	663
50	7,923	9,889	-1,966	-5,143	202
75	12,599	25,657	-13,058	-34,321	-211
90	26,129	70,543	-44,414	-80,641	3,455

California Dairy Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	2,583	3,643	-1,060	-2,943	763
25	4,544	6,386	-1,842	-3,598	-570
50	6,574	9,889	-3,315	-6,372	-1,541
75	9,204	25,657	-16,453	-37,105	-4,968
90	15,071	70,543	-55,472	-91,606	-24,087

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 14

New York Dairy Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,939	2,294	-356	-2,030	1,241
25	6,771	8,963	-2,192	-11,573	4,503
50	18,971	42,926	-23,955	-66,924	-1,653
75	51,696	138,680	-86,983	-144,293	-40,057
90	105,912	240,582	-134,669	-240,663	-48,372

New York Dairy Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	1,918	2,294	-376	-1,867	1,134
25	4,693	8,963	-4,270	-13,057	1,064
50	9,975	42,926	-32,951	-75,413	-11,882
75	18,199	138,680	-120,481	-171,959	-81,439
90	28,027	240,582	-212,555	-313,284	-140,274

Nebraska Cow Calf Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	241	241	0	0	0
25	259	259	0	-75	76
50	489	543	-55	-416	289
75	1,508	2,350	-843	-19,314	2,767
90	13,068	83,865	-70,797	-149,365	16,328

Nebraska Cow Calf Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	241	241	0	-1	1
25	259	259	0	-69	66
50	467	543	-76	-439	237
75	1,356	2,350	-994	-17,153	1,551
90	10,042	83,865	-73,824	-151,284	3,075

Number of Farms in Surveillance Zones from Outbreaks Detected on Day 14

Tennessee Cow Calf Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	562	562	0	-3	3
25	583	583	0	-64	59
50	1,243	1,265	-23	-968	945
75	5,574	5,267	307	-10,175	11,552
90	31,294	36,932	-5,638	-79,929	48,317

Tennessee Cow Calf Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	562	562	0	-3	3
25	583	583	0	-70	58
50	1,181	1,265	-85	-984	888
75	3,987	5,267	-1,280	-11,198	4,095
90	13,932	36,932	-23,000	-89,067	6,862

New Mexico Stocker Surveillance Zone Day 14: Partial					
Percentile	Partial Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	82	82	0	-1	1
25	91	91	0	-28	31
50	211	223	-12	-356	222
75	1,915	2,828	-913	-17,751	5,694
90	20,674	93,007	-72,333	-168,033	17,165

New Mexico Stocker Surveillance Zone Day 14: Ideal					
Percentile	Ideal Tracing	Current Tracing	Estimated Difference	ci_lower	ci_upper
10	82	82	0	-2	1
25	91	91	0	-31	31
50	217	223	-7	-359	200
75	1,236	2,828	-1,592	-20,595	1,228
90	5,972	93,007	-87,035	-187,614	-3,758

Appendix C - Chapter 5 Supplementary Materials

Supplement 1

Appendix C 1: Sample Movement Parameters

Regions defined in ISP

Great Lakes	Mountain West	Northeast	Pacific Coast	Southeast
Minnesota	Montana	Maine	California	Arkansas
Iowa	North Dakota	New Hampshire	Oregon	Louisiana
Missouri	South Dakota	Vermont	Washington	Mississippi
Illinois	Idaho	Massachusetts		Tennessee
Indiana	Utah	Rhode Island		Alabama
Ohio	Nevada	Connecticut		Georgia
Wisconsin	Colorado	New Jersey		Florida
Michigan	Arizona	Delaware		North Carolina
Kentucky	New Mexico	Maryland		South Carolina
	Texas	West Virginia		
	Nebraska	Virginia		
	Oklahoma	New York		
	Kansas	Pennsylvania		
	Wyoming			

Direct Farm to Farm Movements Sample:

Origin Farm Type	Number of Farms in Simulation	Poisson Rate/Day	Expected/day	Observed/day
Large Cow-Calf: Mtn West, Pacific Coast	34,247	0.06	2054	2067
Large Cow-Calf all other regions	13,897	0.05	695	692
Small Cow-Calf Mtn West, Pacific Coast	299,979	0.04	1200	1203
Small Cow-Calf All other regions	378,512	0.02	7570	7593
Large Dairy Heifer-Calf	474	0.3885	184	185
Med Dairy Heifer-Calf	1,373	0.0843	116	116
Small Dairy Heifer-Calf	1,498	0.0313	47	47
Large Dairy	3,480	0.1	348	343

Farm to Market Movements:

Origin Farm Type	Number of farms in simulation	Poisson Rate/Day	Expected/day	Observed/Day
Large Cow-Calf	48144	0.012	578	537
Small Cow-Calf	678491	0.0078	5292	5075
Large Dairy Heifer-Calf	474	0.013	6	5
Med Dairy Heifer-Calf	1373	0.0067	9	8
Small Dairy Heifer-Calf	1498	0.0095	14	14
Large Dairy	3480	0.1216	423	302
Small Dairy	60577	0.0374	2266	1994
Large Feedlot	43	0.0206	1	1
Medium Feedlot	416	0.0206	9	8
Small Feedlot	26126	0.0298	779	717
Large Stocker	1871	0.0169	32	28
Small Stocker	90623	0.0096	870	841

Origin Farm Type	Probability	Distance (meters)	Probability	Destination
Large Cow-Calf: Mtn West, Pacific Coast	0	0	0.0044	bison
	0.03	10000	0.0996	cow_calf_l
	0.22	50000	0.0996	cow_calf_s
	0.12	100000	0.0632	feedlot_cattle_l
	0.5	250000	0.1585	feedlot_cattle_m
	0.09	500000	0.1565	feedlot_cattle_s
	0.04	1000000	0.0998	stocker_l
			0.0794	stocker_s
			0.239	dealer_cattle

Large Cow-Calf all other regions	0 0.1 0.66 0.18 0.06	0 10000 50000 100000 500000	0.008 bison 0.0992 cow_calf_l 0.0992 cow_calf_s 0.063 feedlot_cattle_l 0.158 feedlot_cattle_m 0.156 feedlot_cattle_s 0.0994 stocker_l 0.0792 stocker_s 0.238 dealer_cattle
Small Cow-Calf Mtn West, Pacific Coast	0 0.1 0.28 0.17 0.45	0 10000 50000 100000 500000	0.01 bison 0.0495 cow_calf_l 0.0495 cow_calf_s 0.0215 feedlot_cattle_l 0.0539 feedlot_cattle_m 0.0533 feedlot_cattle_s 0.0827 stocker_l 0.0658 stocker_s 0.6138 dealer_cattle
Small Cow-Calf All other regions	0 0.1 0.58 0.17 0.15	0 10000 50000 100000 500000	0.02 bison 0.049 cow_calf_l 0.049 cow_calf_s 0.0213 feedlot_cattle_l 0.0534 feedlot_cattle_m 0.0527 feedlot_cattle_s 0.0818 stocker_l 0.0652 stocker_s 0.6076 dealer_cattle

Origin Farm Type	Probability	Distance (meters)	Probability	Destination
Large Dairy Heifer-Calf	0 0 0.15 0.133 0.183 0.534	0 8047 32026 80306 160774 321869	0.001 bison 0.0147 cow_calf_l 0.0249 cow_calf_s 0.3131 dairy_l 0.2081 dairy_s 0.0228 dairy_heifer_calf_l 0.0031 dairy_heifer_calf_m 0.0006 dairy_heifer_calf_s 0.0043 feedlot_cattle_l 0.0148 feedlot_cattle_m	

			0.1197 feedlot_cattle_s 0.0009 stocker_l 0.019 stocker_s 0.25 dealer_cattle 0.001 goat_other 0.0002 sheep_l 0.0008 sheep_s 0.001 transitional_swine
Med Dairy Heifer-Calf	0 0 0.094 8047 0.229 32026 0.271 80306 0.146 160774 0.26 321869		0.0096 cow_calf_l 0.0162 cow_calf_s 0.422 dairy_l 0.2806 dairy_s 0.0126 dairy_heifer_calf_l 0.0017 dairy_heifer_calf_m 0.0003 dairy_heifer_calf_s 0.0028 feedlot_cattle_l 0.0096 feedlot_cattle_m 0.0777 feedlot_cattle_s 0.0006 stocker_l 0.0123 stocker_s 0.15 dealer_cattle 0.001 goat_other 0.0002 sheep_l 0.0008 sheep_s 0.002 transitional_swine

Origin Farm Type	Probability	Distance (meters)	Probability	Destination
Small Dairy Heifer-Calf	0 0 0.196 8047 0.283 32026 0.304 80306 0.087 160774 0.13 321869		0.0099 cow_calf_l 0.0168 cow_calf_s 0.2594 dairy_l 0.1724 dairy_s 0.3262 dairy_heifer_calf_l 0.0446 dairy_heifer_calf_m 0.008 dairy_heifer_calf_s 0.0029 feedlot_cattle_l 0.01 feedlot_cattle_m 0.0805 feedlot_cattle_s 0.0006 stocker_l	

		0.0127 stocker_s 0.05 dealer_cattle 0.002 goat_other 0.0004 sheep_l 0.0016 sheep_s 0.002 transitional_swine
Large Dairy	0 0 0 10000 0.0005 50000 0.062 100000 0.2475 200000 0.69 500000	0.005 cow_calf_l 0.003 cow_calf_s 0.14 dairy_l 0.047 dairy_s 0.335 dairy_heifer_calf_l 0.167 dairy_heifer_calf_m 0.056 dairy_heifer_calf_s 0.002 feedlot_cattle_l 0.002 feedlot_cattle_m 0.001 feedlot_cattle_s 0.036 stocker_l 0.024 stocker_s 0.179 dealer_cattle 0.001 goat_other 0.001 sheep_s 0.001 transitional_swine

Origin Farm Type	Probability	Distance (meters)	Probability	Destination
Small Dairy	0 0 0 10000 0.0005 50000 0.062 100000 0.2475 200000 0.69 500000		0.007 cow_calf_l 0.01 cow_calf_s 0.065 dairy_l 0.196 dairy_s 0.019 dairy_heifer_calf_l 0.058 dairy_heifer_calf_m 0.31 dairy_heifer_calf_s 0.001 feedlot_cattle_l 0.002 feedlot_cattle_m 0.003 feedlot_cattle_s 0.053 stocker_l 0.08 stocker_s	

		0.184 dealer_cattle 0.004 goat_other 0.004 sheep_s 0.004 transitional_swine

Rate of Movements of cattle to Processors

Origin Farm Type	% to Large Processor	% to Small Processor
Large Cow Calf	20	80
Small Cow Calf	10	90
Large Dairy	20	80
Small Dairy and all Dairy Heifer/Calf	10	90
All Feedlots	70	30
All Stockers	10	90

☒	NumberPerTimePeriod[livestock_market_bison_cattle]	Poisson 7.9261
☒	NumberPerTimePeriod[cow_calf_l]	Poisson 0.0018
☒	NumberPerTimePeriod[cow_calf_s]	Poisson 0.0003
☒	NumberPerTimePeriod[dairy_l]	Poisson 0.063
☒	NumberPerTimePeriod[dairy_s]	Poisson 0.0046
☒	NumberPerTimePeriod[dairy_heifer_calf_l]	Poisson 0.0082
☒	NumberPerTimePeriod[dairy_heifer_calf_m]	Poisson 0.0055
☒	NumberPerTimePeriod[dairy_heifer_calf_s]	Poisson 0.0027
☒	NumberPerTimePeriod[feedlot_cattle_l]	Poisson 2.4751
☒	NumberPerTimePeriod[feedlot_cattle_m]	Poisson 1.2714
☒	NumberPerTimePeriod[feedlot_cattle_s]	Poisson 0.0635
☒	NumberPerTimePeriod[stocker_l]	Poisson 0.0024
☒	NumberPerTimePeriod[stocker_s]	Poisson 0.0004
☒	NumberPerTimePeriod[processor_cattle]	Constant 0
☒	NumberPerTimePeriod[processor_cattle_l]	Constant 0
☒	NumberPerTimePeriod[dealer_cattle]	Poisson 0.1429

Supplement 2

Appendix C 2: Post Processing of Movement Network R Code

Definitions:

Movement File: The output from ISP

Irrelevant species: non-cattle source or destination farms

Easting/Northing: The X and Y coordinate system used by ISP for farm geolocation

The purpose of this code is to generate the movement networks that can be assessed for traceability.

Step 1: Remove all non-cattle and indirect movements from the ISP output.

Step 2: Assign the movements that passed through a market a specific market location

Step 3: Recover the movements that failed from the warning file and assign them a destination.

The original simulation was for 60 days of movements throughout this code, the movements will be filtered to 30 days.

```
library(dplyr)
library(tidyverse)

FarmFile<-read_csv("C:/Users/marykasmith/Desktop/New FF and Markets/FarmFileStates2024.csv")

FarmFile<-FarmFile%>%select(-...1)

Movements<-read.table("C:/Users/marykasmith/Desktop/60d Run 2/Movements60d.2.txt")
```

Begin by adding the farm types back into the source and destination farms

```
colnames(Movements)<-c("Iteration","DayMov","Source","EastingS","NorthingS", "Destination", "EastingD", "NorthingD", "Type")

Movements<-Movements%>%filter(DayMov<31)

FarmFile_Source<-FarmFile%>%select(FarmID, Class, State)

FarmFile_Source<-FarmFile_Source%>%rename(Source=FarmID, S.FarmType=Class, S.State=State)

MovementSources<-left_join(Movements, FarmFile_Source, by="Source")

FarmFile_Dest<-FarmFile%>%rename(Destination=FarmID, D.FarmType=Class, D.State=State)

MovementsComplete<-left_join(MovementSources, FarmFile_Dest, by="Destination")

MovementTable<-table(MovementsComplete$Type) #Optional to see movement Types
print(MovementTable)
```

```
table(MovementsComplete$DayMov) #optional to confirm all days present
```

Remove movement types that are indirect movements that are in the model parameters for capturing the contamination of markets or other locations

```
ReMoveIndirect<-MovementsComplete%>%filter (Type!="MovementType60"&
      Type!="MovementType61"&
      Type!="MovementType62"&
      Type!="MovementType63"&
      Type!="MovementType64"&
      Type!="MovementType54"&
      Type!="MovementType55"&
      Type!="MovementType56"&
      Type!="MovementType57"&
      Type!="MovementType58"&
      Type!="MovementType59")
#table(ReMoveIndirect$S.FarmType) #optional to see farm types represented
```

Remove all sources that are not cattle and the odd cattle farm that ships to bison processors

```
OnlyCattle<-ReMoveIndirect%>%filter (S.FarmType!="bison"&
      S.FarmType!="dealer_bison"&
      S.FarmType!="transitional_swine"&
      S.FarmType!="sheep_s"&
      S.FarmType!="sheep_l"&
      S.FarmType!="other_swine_s"&
      S.FarmType!="other_swine_l"&
      S.FarmType!="nursery_s"&
      S.FarmType!="nursery_l"&
      S.FarmType!="grower_finisher_l"&
      S.FarmType!="grower_finisher_s"&
      S.FarmType!="livestock_market_goat_sheep"&
      S.FarmType!="livestock_market_swine"&
      S.FarmType!="dealer_goat"&
      S.FarmType!="dealer_sheep"&
      S.FarmType!="dealer_swine"&
      S.FarmType!="farrow_to_feeder_l"&
      S.FarmType!="farrow_to_feeder_s"&
      S.FarmType!="farrow_to_finish_l"&
```

```

S.FarmType!="farrow_to_finish_s"&
S.FarmType!="farrow_to_wean_l"&
S.FarmType!="farrow_to_wean_s"&
S.FarmType!="goat_dairy"&
S.FarmType!="feedlot_sheep"&
S.FarmType!="goat_other"&
D.FarmType!="processor_bison")

head(OnlyCattle)#optional to confirm only cattle are present

CattleSource<-as.data.frame(table(OnlyCattle$S.FarmType)) #optional to see all sources
of cattle

CattleDestinations<-as.data.frame(table(OnlyCattle$D.FarmType)) #optional to see all d
estinations cattle shipped to

```

This completes the removal of indirect movements and irrelevant species.

Currently, MovementType42 does not have a specific market node that they are passing through. This will be remedied at the end of the clean up after the movements that were in the warning file as “can not find destination farm” are re-incorporated into the movement file. These failed movements are typically the result of the inability to find a farm of the desired type in the distance band that ISP selected. In reality, a producer would just ship farther.

At this time, there are several dataframes created that are not needed anymore and can be removed for space

```

rm(FarmFile_Dest, FarmFile_Source, ReMoveIndirect, Movements, MovementsComplete, Movem
entSources, MovementTable); gc()

```

Bringing in the movements from the warning file - The warning file has been pre-edited in Notepad++ to “mark” all of the lines that had “can not find destination farm” and those were copied to a new text file. Then all lines that included “indirect” were marked and removed.

The following code could likely be simplified by more pre-editing of columns in the plain-text files

```

DestinationWarning<-read.table("C:/Users/marykasmith/Desktop/60d Run 2/Cannot find des
tination farm 60d2.txt", sep="\t")

head(DestinationWarning)

DestinationWarning<-DestinationWarning%>%select(V5,V9,V11) #Day, MovementType, column
with destination information

DestinationWarning<-DestinationWarning%>%separate(V11, into = c("A", "B", "C", "D"), sep
= "=") #Placeholders to separate out the line lines of text

DestinationWarning<-DestinationWarning%>%select(-A, -D)

DestinationWarning<-DestinationWarning%>%separate(B, into = c("Nada", "FarmID", "5", "6"
, "7", "8", "9"), sep = " ")

DestinationWarning<-DestinationWarning%>%separate(C, into = c("DestClass", "Other"), s
ep = ",")

DestinationWarning<-DestinationWarning%>%select(V5, FarmID, DestClass, V9)

```

```
DestinationWarning<-DestinationWarning%>%rename (DayMov=V5)
```

```
DestinationWarning <- transform(DestinationWarning,  
                                FarmID = as.numeric(FarmID))
```

Assess what movement types are present and change them to the same system as the original output file

```
DestWarnSource<-left_join(DestinationWarning, FarmFile, by="FarmID")  
DestWarnSource<-DestWarnSource%>%rename (S.FarmType=Class, EastingS=Easting, NorthingS=Northing)  
DestWarningOnlyCattle<-DestWarnSource%>%filter (S.FarmType!="bison"&  
                                                S.FarmType!="dealer_bison"&  
                                                S.FarmType!="transitional_swine"&  
                                                S.FarmType!="sheep_s"&  
                                                S.FarmType!="sheep_l"&  
                                                S.FarmType!="other_swine_s"&  
                                                S.FarmType!="other_swine_l"&  
                                                S.FarmType!="nursery_s"&  
                                                S.FarmType!="nursery_l"&  
                                                S.FarmType!="grower_finisher_l"&  
                                                S.FarmType!="grower_finisher_s"&  
                                                S.FarmType!="livestock_market_goat_sheep"&  
                                                S.FarmType!="livestock_market_swine"&  
                                                S.FarmType!="dealer_goat"&  
                                                S.FarmType!="dealer_sheep"&  
                                                S.FarmType!="dealer_swine"&  
                                                S.FarmType!="farrow_to_feeder_l"&  
                                                S.FarmType!="farrow_to_feeder_s"&  
                                                S.FarmType!="farrow_to_finish_l"&  
                                                S.FarmType!="farrow_to_finish_s"&  
                                                S.FarmType!="farrow_to_wean_l"&  
                                                S.FarmType!="farrow_to_wean_s"&  
                                                S.FarmType!="goat_dairy"&  
                                                S.FarmType!="feedlot_sheep"&  
                                                S.FarmType!="goat_other"&  
                                                S.FarmType!="processor_swine")
```



```

DestWarningOnlyCattle<-DestWarningOnlyCattle%>%mutate(Type = case_when(
  V9 == "cattle_dealer" ~ "MovementType19",
  V9 == "cattle_market" ~ "MovementType42",
  V9 == "small_cattle_feedlot" ~ "MovementType13",
  V9 == "large_medium_cattle_feedlot" ~ "MovementType12",
  V9 == "large_cow_calf_MW_PC" ~ "MovementType3",
  V9 == "large_cow_calf_GL_NE_SE" ~ "MovementType4",
  V9 == "small_cow_calf_MW_PC" ~ "MovementType5",
  V9 == "small_cow_calf_GL_NE_SE" ~ "MovementType6",
  V9 == "large_dairy" ~ "MovementType7",
  V9 == "small_dairy" ~ "MovementType8",
  V9 == "large_dairy_heifer_calf" ~ "MovementType9",
  V9 == "medium_dairy_heifer_calf" ~ "MovementType10",
  V9 == "small_dairy_heifer_calf" ~ "MovementType11",
  V9 == "large_stocker_GL_MW_NE_PC" ~ "MovementType14",
  V9 == "large_stocker_SE" ~ "MovementType15",
  V9 == "small_stocker_GL_MW_NE_PC" ~ "MovementType16",
  V9 == "small_stocker_SE" ~ "MovementType17",
  TRUE ~ NA_character_
))
table(DestWarningOnlyCattle$Type)

table(DestWarningOnlyCattle$S.FarmType)

```

There are many NA types in the dataframe at this point. They are all indirect or other movement types we don't care about. They'll be removed now.

```

DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("farrow", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("sheep", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("swine", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("goat", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("finish", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%

```

```

  filter(if_all(everything(), ~ !str_detect(., regex("bison", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("nursery", ignore_case = TRUE))))
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("indirect", ignore_case = TRUE)))
)
DestWarningOnlyCattle <- DestWarningOnlyCattle %>%
  filter(if_all(everything(), ~ !str_detect(., regex("infect", ignore_case = TRUE))))

table(DestWarningOnlyCattle$S.FarmType) #optional to confirm only cattle
table(DestWarningOnlyCattle$DestClass) #to see where they are trying to go

```

All the farms now need to be matched to a destination farm. The feedlots will be in KS, TX, or CO. All others will just be randomly assigned to a destination in their region.

```

DestWarningOnlyCattle<-DestWarningOnlyCattle%>%rename(S.State=State)
DestWarningOnlyCattle<-DestWarningOnlyCattle%>%filter(DayMov<31)
FarmFileDest<-FarmFile%>%rename(
  Destination=FarmID,
  D.FarmType=Class,
  EastingD=Easting,
  NorthingD=Northing,
  D.State=State
)

```

Create the regions

```

GreatLakes<-c("Minnesota", "Iowa", "Missouri", "Indiana", "Ohio", "Wisconsin", "Michigan", "Kentucky", "Illinois")

MountainWest<-c("Montana", "North Dakota", "South Dakota", "Idaho", "Utah", "Nevada", "Colorado", "Arizona", "New Mexico", "Texas", "Nebraska", "Oklahoma", "Kansas", "Wyoming")

Northeast<-c("Maine", "New Hampshire", "Vermont", "Massachusetts", "Rhode Island", "Connecticut", "New Jersey", "Delaware", "Maryland", "West Virginia", "Virginia", "New York", "Pennsylvania")

Pacific<-c("California", "Oregon", "Washington")

Southeast<-c("Arkansas", "Louisiana", "Mississippi", "Tennessee", "Alabama", "Georgia", "Florida", "North Carolina", "South Carolina")

```

```
Feedlot<-c("Kansas","Texas","Colorado","Iowa","Nebraska","Oklahoma")
```

Assign the movements to a region based on the source state and the farm file

```
DestWarningOnlyCattle<-DestWarningOnlyCattle%>%mutate(Region = case_when(
  S.State %in% GreatLakes ~ "GreatLakes",
  S.State %in% MountainWest ~ "MountainWest",
  S.State %in% Northeast ~ "Northeast",
  S.State %in% Pacific ~ "Pacific",
  S.State %in% Southeast ~ "Southeast"))

FarmFileDest<-FarmFileDest%>%mutate(Region = case_when(
  D.State %in% GreatLakes ~ "GreatLakes",
  D.State %in% MountainWest ~ "MountainWest",
  D.State %in% Northeast ~ "Northeast",
  D.State %in% Pacific ~ "Pacific",
  D.State %in% Southeast ~ "Southeast"))

FarmFileDest<-FarmFileDest%>%mutate(RegionB = case_when(
  D.State %in% Feedlot ~ "Feedlot"))

Feedlot_s<-FarmFileDest%>%filter(D.FarmType=="feedlot_cattle_s")
Feedlot_m<-FarmFileDest%>%filter(D.FarmType=="feedlot_cattle_m")
Feedlot_l<-FarmFileDest%>%filter(D.FarmType=="feedlot_cattle_l")
FailedFeeder_s<-DestWarningOnlyCattle%>%filter(DestClass==" feedlot_cattle_s")
FailedFeeder_m<-DestWarningOnlyCattle%>%filter(DestClass==" feedlot_cattle_m")
FailedFeeder_l<-DestWarningOnlyCattle%>%filter(DestClass==" feedlot_cattle_l")
assign_Feeder1 <- function(Failed, Destinations) {
  Failed$Destination <- rep(NA_real_, nrow(Failed)) # Ensure numeric NA

  for (i in 1:nrow(Failed)) {
    src_region <- Failed$Region[i]

    eligible_dests <- Destinations %>% filter(Region == src_region|RegionB=="Feedlot")

    if (nrow(eligible_dests) > 0) {
      eligible_dests$Destination <- as.numeric(as.character(eligible_dests$Destination
    ))
  }
```

```

        selected <- sample(eligible_dests$Destination, 1)
        Failed$Destination[i] <- selected

    }
}

return(Failed)
}

Feedlots_s_merge<-assign_Feeder1(FailedFeeder_s, Feedlot_s)
Feedlots_s_merge<-left_join(Feedlots_s_merge, FarmFileDest, by="Destination")
Feedlots_s_merge<-Feedlots_s_merge%>%rename(Source=FarmID)
Feedlots_s_merge<-Feedlots_s_merge%>%select(DayMov, Source, Destination, S.FarmType, D
.FarmType, EastingS, NorthingS, EastingD, NorthingD, S.State, D.State)
Feedlots_m_merge<-assign_Feeder1(FailedFeeder_m, Feedlot_m)

Feedlots_m_merge<-left_join(Feedlots_m_merge, FarmFileDest, by="Destination")
Feedlots_m_merge<-Feedlots_m_merge%>%rename(Source=FarmID)

Feedlots_m_merge<-Feedlots_m_merge%>%select(DayMov, Source, Destination, S.FarmType, D
.FarmType, EastingS, NorthingS, EastingD, NorthingD, S.State, D.State)
Feedlots_l_merge<-assign_Feeder1(FailedFeeder_l, Feedlot_l)
Feedlots_l_merge<-left_join(Feedlots_l_merge, FarmFileDest, by="Destination")
Feedlots_l_merge<-Feedlots_l_merge%>%rename(Source=FarmID)
Feedlots_l_merge<-Feedlots_l_merge%>%select(DayMov, Source, Destination, S.FarmType, D
.FarmType, EastingS, NorthingS, EastingD, NorthingD, S.State, D.State)
AllFeeders<-bind_rows(Feedlots_s_merge, Feedlots_m_merge, Feedlots_l_merge)

AllFeeders<-AllFeeders%>%mutate(Distance=(sqrt((EastingS-EastingD)^2+(NorthingS-Northi
ngD)^2)))

AllFeedersTab<-AllFeeders%>%group_by(S.FarmType)%>%
  summarise(mean(Distance),
             median(Distance),
             min(Distance),
             max(Distance))

REgionalDistribution<-FarmFileDest %>%
  group_by(Region, D.FarmType) %>%

```

```

summarise(count = n()) %>%
  arrange(Region)
`summarise()` has grouped output by 'Region'. You can override using the ` .groups ` argument.
print(REgionalDistribution)

```

There are multiple of each farm type within the regions - the destinations will be assigned within region The non-cattle species will be omitted

```

assign_withinregion <- function(Failed, Destinations) {
  Failed$Destination <- NA # Add a destination column

  for (i in 1:nrow(Failed)) {
    src_region <- Failed$Region[i]

    # Filter destinations that match region or are in MountainWest
    eligible_dests <- Destinations%>%filter(Region==src_region)

    # Assign destination
    if (nrow(eligible_dests) > 0) {
      selected <- sample(eligible_dests$Destination, 1)
      Failed$Destination[i] <- selected
    }
  }

  return(Failed)
}

table(DestWarningOnlyCattle$DestClass)

FailedCC_l<-DestWarningOnlyCattle%>%filter(DestClass==" cow_calf_l")
FailedCC_s<-DestWarningOnlyCattle%>%filter(DestClass==" cow_calf_s")
FailedDHC_l<-DestWarningOnlyCattle%>%filter(DestClass==" dairy_heifer_calf_l")
FailedDHC_m<-DestWarningOnlyCattle%>%filter(DestClass==" dairy_heifer_calf_m")
FailedDHC_s<-DestWarningOnlyCattle%>%filter(DestClass==" dairy_heifer_calf_s")
FailedDairy_l<-DestWarningOnlyCattle%>%filter(DestClass==" dairy_l")
FailedDairy_s<-DestWarningOnlyCattle%>%filter(DestClass==" dairy_s")
FailedProc_l<-DestWarningOnlyCattle%>%filter(DestClass==" processor_cattle_l")
FailedProc_s<-DestWarningOnlyCattle%>%filter(DestClass==" processor_cattle")

```

```
FailedDealer<-DestWarningOnlyCattle%>%filter(DestClass==" dealer_cattle")
FailedStocker<-DestWarningOnlyCattle%>%filter(DestClass==" stocker_l")
FailedStocker_s<-DestWarningOnlyCattle%>%filter(DestClass==" stocker_s")
```

There were no failed shipments for the following types in this iteration so they are omitted below - Small or Large CC - Small Stocker - Processors of any size - Small Dairies and small dairy heifer calf ranches

```
Dairy_l<-FarmFileDest%>%filter(D.FarmType=="dairy_l")

Dairy_L_merge<-assign_withinregion(FailedDairy_l, Dairy_l)

Dealer<-FarmFileDest%>%filter(D.FarmType=="dealer_cattle")
Dealer_merge<-assign_withinregion(FailedDealer, Dealer)

DHC_L<-FarmFileDest%>%filter(D.FarmType=="dairy_heifer_calf_l")
DHC_M<-FarmFileDest%>%filter(D.FarmType=="dairy_heifer_calf_m")

DHC_L_merge<-assign_withinregion(FailedDHC_l, DHC_L)
DHC_m_merge<-assign_withinregion(FailedDHC_m, DHC_M)

Stocker_L<-FarmFileDest%>%filter(D.FarmType=="stocker_l")
Stocker_L_merge<-assign_withinregion(FailedStocker, Stocker_L)
DestFailsA<-bind_rows(Stocker_L_merge,
                      Dealer_merge,
                      DHC_L_merge,
                      DHC_m_merge,
                      Dairy_L_merge)
DestFails1<-left_join(DestFailsA,FarmFileDest, by="Destination")
DestFails1<-DestFails1%>%rename(Source=FarmID)

DestFails<-bind_rows(DestFails1, Feedlots_l_merge, Feedlots_m_merge, Feedlots_s_merge)
```

Remove the dataframes created that are not needed anymore to prevent mess

```
rm(FailedCC_l, FailedCC_s, FailedDairy_l, FailedDairy_s, FailedDealer, FailedDHC_l, FailedDHC_m, FailedDHC_s, FailedFeeder_l, FailedFeeder_m, FailedFeeder_s, FailedProc_l, FailedProc_s, FailedStocker, FailedStocker_s);gc()
```

```
rm(Dairy_l, Dairy_L_merge, Dealer, Dealer_merge, Feedlot_l, Feedlot_m, Feedlot_s, Feedlots_s_merge, Feedlots_m_merge, Feedlots_l_merge, Stocker_L, Stocker_L_merge); gc()

rm(DHC_L, DHC_L_merge, DHC_M, DHC_m_merge, DHC_S, DHC_s_merge); gc()
```

The two files are ready to be merged and the markets as nodes added back in

```
DestFails<-DestFails%>%select(DayMov, Source, EastingS, NorthingS, Destination, EastingD, NorthingD, Type, S.FarmType, S.State, D.FarmType, D.State)

OnlyCattle<-OnlyCattle%>%select(DayMov, Source, EastingS, NorthingS, Destination, EastingD, NorthingD, Type, S.FarmType, S.State, D.FarmType, D.State)

AllMovements<-bind_rows(DestFails, OnlyCattle)
```

Sort out the movements from farms to a market that happened in Movement Type 18 (to infect market) and movement 42 (those that passed thru somewhere)

```
MarketFarm<-AllMovements%>%filter(Type=="MovementType18")

MarketThru<-AllMovements%>%filter(Type=="MovementType42") #339,410

Michigan<-MarketThru%>%filter(S.State=="Michigan")

#write.csv(Michigan, "Michigan Movement 42s 60d.2.csv")
```

Select the UP farms in QGIS then reimport – QGIS is a software that can plot the farm locations on the US map built for the farm file.

```
UpperPenn<-read_csv("C:/Users/marykasmith/Desktop/60d Run 2/UP 60.2.csv")
UpperPenn<-UpperPenn%>%filter(DayMov<31)

MarketThru2<-MarketThru%>%filter(!(Source %in% UpperPenn$Source))
```

Did all the farms that made a 42 make a 18?

```
all(MarketThru2$Source %in% MarketFarm$Source) #determines if all Movement 42 Sources are in 18, usually false

[1] FALSE
```

Some sources that had a movement 18 had multiple markets they contacted, sort those out and select the closest one to use as the selected market that movement 42s go to

```
# Find sources with multiple destinations
```

```
multiple_dest_sources <- MarketFarm %>%
  group_by(Source) %>%
  summarize(unique_dest = n_distinct(Destination)) %>%
  filter(unique_dest > 1)
```

Find the distance to the multiple markets contacted in Movement 18

```
MultipleDests<-MarketFarm%>%mutate(Distance=(sqrt((EastingS-EastingD)^2+(NorthingS-NorthingD)^2)))
```

Select the closest one to be the favorite market

```
ClosestMarket<-MultipleDests %>%
  group_by(Source) %>%
  filter(Distance == min(Distance)) %>%
  ungroup()

ClosestMarket<-ClosestMarket%>%select(Source,EastingS,NorthingS,Type, Destination, EastingD,NorthingD,D.State)

ClosestMarket<-ClosestMarket%>%rename(MarketDest=Destination)
```

Remove duplicate shipments to the same market - this is to make the merge to a movement 42 cleaner

```
ClosestMarket <- ClosestMarket %>% distinct(Source, .keep_all = TRUE)

ClosestMarket<-ClosestMarket%>%mutate(D.FarmType="livestock_market_bison_cattle")

MarketThruSource<-MarketThru2%>%select(DayMov,Source,EastingS,NorthingS,S.FarmType, S.State)

AssignMarket<-left_join(MarketThruSource,ClosestMarket,by=c("Source","EastingS","NorthingS")) #needs to equal the number of MarketThru
```

The NA's in the assign market are from farms that did not have a number 18, they will get a random market within their state.

```
NADest<- AssignMarket %>% filter(is.na(MarketDest))

Taggedto18<-AssignMarket%>%filter(!is.na(MarketDest))

Taggedto18<-Taggedto18%>%select(DayMov,Source,EastingS,NorthingS,MarketDest,EastingD,NorthingD,S.FarmType, D.FarmType, S.State, D.State)

Taggedto18<-Taggedto18%>%rename(Destination=MarketDest)

FarmFileSource<-FarmFile%>%select(FarmID, State, Class,Easting,Northing)
```



```

FarmFileSource<-FarmFileSource%>%rename(Source=FarmID)
NeedMarket<-left_join(NADest, FarmFileSource, by="Source")
NeedMarket<-NeedMarket%>%select(DayMov, Source, EastingS, NorthingS, S.FarmType, State
)
NeedMarket<-NeedMarket%>%rename(S.State=State)

NeedMarketSources<-NeedMarket %>% distinct(Source, .keep_all = TRUE)
MarketStates<-FarmFileSource%>%filter(Class=="livestock_market_bison_cattle")
MarketStates<-MarketStates%>%rename(MarketDest=Source,D.State=State)
MatchMarket<-left_join(NeedMarketSources, MarketStates, by=c("S.State"="D.State"))%>%g
roup_by(Source)%>%
  slice_sample%>%ungroup()
Warning: Detected an unexpected many-to-many relationship between `x` and `y`.
MatchMarket<-MatchMarket%>%rename(EastingD=Easting, NorthingD=Northing, D.FarmType=Cla
ss)
MatchMarket<-MatchMarket%>%select(Source, MarketDest, EastingD, NorthingD,D.FarmType)

AssignedStateMarket<-left_join(NeedMarket, MatchMarket, by=c("Source"))
AssignedStateMarket$D.State=AssignedStateMarket$S.State

AssignedWithin1<-AssignedStateMarket%>%filter(!is.na(MarketDest))
AssignedWithin1<-AssignedWithin1%>%rename(Destination=MarketDest)

```

There are states that do not have a market in them in the New England area. They will be assigned to one of the markets that is in that area.

```

Assigned_NA<-AssignedStateMarket%>%filter(is.na(MarketDest))
table(Assigned_NA$S.State)

New Hampshire
      227

Assigned_NA<-Assigned_NA%>%select(-EastingD, -NorthingD, -D.FarmType, -D.State)
assigned_state2 <- Assigned_NA %>%
  rowwise() %>%
  mutate(MarketDest = ifelse(
    any(MarketStates$D.State %in% c("Maine", "New Hampshire", "Vermont","Massachusetts
")), # Check if states exist
    sample(MarketStates$MarketDest[MarketStates$D.State %in% c("Maine", "New Hampshire
", "Vermont","Massachusetts")], 1),
    NA_real_ # Assign NA if no match found

```

```

)) %>%
  ungroup()

NewEnglandMarket<-left_join(assigned_state2, MarketStates, by="MarketDest")
NewEnglandMarket<-NewEnglandMarket%>%rename(EastingD=Easting, NorthingD=Northing, D.FarmType=Class, Destination=MarketDest)

wi_markets <- MarketStates %>%
  filter(D.State == "Wisconsin") %>%
  pull(MarketDest)

# Randomly assign one Wisconsin market to each row
UPtoWI <- UpperPenn %>%
  rowwise() %>%
  mutate(MarketDest = sample(wi_markets, 1)) %>%
  ungroup()

UPtoWI<-UPtoWI%>%select(DayMov, Source, EastingS, NorthingS, S.FarmType, S.State, MarketDest)

UPMarket<-left_join(UPtoWI, MarketStates, by="MarketDest")
UPMarket<-UPMarket%>%rename(EastingD=Easting, NorthingD=Northing, D.FarmType=Class, Destination=MarketDest)

```

Add all the lines back together now with markets assigned - these are the movements to market

```

ReassignedMarketState<-bind_rows(NewEnglandMarket, AssignedWithin1, Taggedto18, UPMarket) #again should equal the movement 42 from above

```

The other half of the movement from movement 42 (to the final farm destination) need to be relinked

```

FirstHalf<-ReassignedMarketState%>%rename(Market=Destination, Sourcecx=Source) #source x to be the linking piece for ascending order to match the second half
FirstHalf<-FirstHalf%>%select(Sourcecx, Market, EastingD, NorthingD)
FirstHalf<-FirstHalf%>%rename(EastingM=EastingD, NorthingM=NorthingD) #M to indicate is the market
FirstHalf <- FirstHalf %>%
  arrange(Sourcecx) #this is the to market side

SecondHalf <- MarketThru %>%
  arrange(Source) #this has the final destination
setdiff(FirstHalf$Sourcecx, SecondHalf$Source)

```

```

numeric(0)

ToDest<-bind_cols(FirstHalf,SecondHalf) #should equal the market thru
ToDest<-ToDest%>%select(-Source,-SourceX, -EastingS, -NorthingS, -S.FarmType,-Type)
ToDest<-ToDest%>%rename(Source=Market, EastingS=EastingM, NorthingS=NorthingM)
ToDest<-ToDest%>%mutate(S.FarmType="livestock_market_bison_cattle", Type="FromMarket")

```

Remove the Movement 42s and 18 from the list so they are not duplicated

```

Movementsno42<-AllMovements%>%filter(Type!="MovementType42")
Movementsno42<-Movementsno42%>%filter(Type!="MovementType18")

```

Add all of the movements back together - the original list (Movements no 42), the to market (Reassigned Market) and the second half (ToDest)

```

FinalMovements<-bind_rows(Movementsno42, ReassignedMarketState, ToDest)

```

Write the final movements dataframe to a file as needed for the further analysis.

```

write.csv(FinalMovements,"30DaysNetwork2.csv")

```

Supplement 3

Appendix C 3: Example Creation of Traceable Network: Ideal 75/90

```
library(dplyr)
library(tidyverse)

set.seed(0502)#to ensure that all traceable networks use the same random number sequence
```

Load in the full network movement file

```
edges<-read_csv("C:/Users/marykasmith/Desktop/60d Run 2/30DaysNetwork2.csv")

farmfile<-read.table("C:/Users/marykasmith/Desktop/New FF and Markets/FarmFile2024MarketsDairies.txt")

farmfiledest<-farmfile%>%rename(D.type=V2)%>%mutate(destination=as.integer(V1))%>%select(destination,D.type)

ffsource<-farmfiledest%>%rename(source=destination, S.type=D.type)
```

Convert the shape of the movement file to match how EpiContactTrace wants it. The date is arbitrary just started at 01-01-01 for simplicity

```
edges$Date <- as.Date("2001-01-01") + edges$time - 1
edges<-edges%>%select(from, to, Date)

edges <- edges %>%
  rename(
    source = from,
    destination = to,
    t=Date
  )

edges$source<-as.integer(edges$source)
edges$destination<-as.integer(edges$destination)

edges<-as.data.frame(edges)
edges_dest<-left_join(edges, farmfiledest, by="destination")
edges_type<-left_join(edges_dest, ffsource, by="source")
sources <- edges_type %>%
  distinct(source, S.type)
```

```
dests <- edges_type %>%
  distinct(destination,D.type)
```

This defines the types of farms that are receiving the tagging information. The two .csv files have the full names of the farm types and what tag/reporting value they use for the list below

```
S.Rates<-read.csv("tag_table.csv")
D.Rates<-read.csv("report_table.csv")

tag_cc_s<-0.75
tag_cc_l<-0.75
tag_dairy<-0.95
tag_stocker.dealer<-0.75
tag_feeder_s.m<-0.75
tag_feeder_l<-0.75
tag_market<-0.75

report_cc.stocker<-0.9
report_dairy<-0.9
report_feeder<-0.9
report_feeder_l<-0.9
report_dealer<-0.9
report_market<-0.9
report_processor<-0.9
```

Assignment of source farms to tag outgoing movements or not

```
SourcesTag <- sources %>%
  left_join(S.Rates, by = "S.type") %>%
  # Convert rate variable name to actual numeric value
  mutate(rate = sapply(rate, get),
         tagfarm = rbinom(n(), size = 1, prob = rate))
SourcesTag<-SourcesTag%>%select(source,tagfarm)
```

Assignment of destination farms to report incoming movements

```
DestReport <- dests %>%
  left_join(D.Rates, by = "D.type") %>%
  # Convert rate variable name to actual numeric value
```

```

mutate(rate = sapply(rate, get),
       repfarm = rbinom(n(), size = 1, prob = rate))
DestReport<-DestReport%>%select(destination,repfarm)

```

merge back together with movements

```

Taggedmoves <- edges_type %>%
  right_join(SourcesTag, by = "source") %>%
  right_join(DestReport, by = "destination") %>%
  mutate(
    tagged = as.integer(tagfarm == 1),
    reported = as.integer(repfarm == 1)
  )

```

This is the initial tagging from a farm to an intermediate farm that may not tag

```

pct_table <- Taggedmoves %>%
  group_by(destination) %>%
  summarise(
    total = n(),
    tagged1 = sum(tagged == 1),
    outgolikely = tagged1 / total
  )

```

Merging the percent of incoming tagged movements to the intermediate farm and applying the rbinom to the outgoing movements of that farm

```

Taggedmoves2 <- Taggedmoves %>%
  left_join(pct_table %>% select(destination, outgolikely),
           by = "destination") %>%
  mutate(
    tagged2 = case_when(
      tagged == 1 ~ 1, # always keep 1's as 1
      tagged == 0 & tagfarm == 0 ~ rbinom(n(), 1, outgolikely), # simulate new tag
      TRUE ~ 0 # all others remain 0
    )
  )

```

Showing that the number of tagged movements increased after the intermediate tagging steps

```

table(Taggedmoves2$tagged)

```

```
      0      1
414769 1324954
table(Taggedmoves2$tagged2)
```

```
      0      1
133973 1605750
```

Filter for only the traceable movements and write the CSV that contains them

```
Traceable<-Taggedmoves2 %>%
  mutate(Traced = if_else(tagged2 == 1 & reported == 1, 1, 0)) %>%
  filter(Traced == 1)

write.csv(Traceable,"Ideal7590.csv")
```

Supplement 4

Appendix C 4: Example Tracing Protocol: 100 Cow Calf FOI in All 75/90 Scenario

Definition:

FOI: the farmID for a farm of interest that is “infected” and being traced

1. Find all movements that have the FOI as the destination
2. Search the entire 28 days without markets
3. Filter only the markets that made direct movements

```
library(dplyr)
library(tidyverse)
library(EpiContactTrace)
library(readr)
library(lubridate)
library(purrr)
```

Load in the network, farmfile, and farms to sample

```
edges<-read_csv("Ideal7590.csv")

farmfile<-read.table("C:/Users/marykasmith/Desktop/New FF and Markets/FarmFile2024MarketsDairies.txt")

ccsample<-read_csv("CowCalfSampleN2D30_100.csv")

farmfiledest<-farmfile%>%rename(D.type=V2)%>%mutate(destination=as.integer(V1))%>%select(destination,D.type)

ffsource<-farmfiledest%>%rename(source=destination, S.type=D.type)
```

Convert the time stamp to a date because that's how EpiContactTrace wants it

```
edges<-edges%>%select(source, destination, t)
edges$source<-as.integer(edges$source)
edges$destination<-as.integer(edges$destination)
edges<-as.data.frame(edges)
Dailycount<-edges%>%count(t)
summary(Dailycount$n)#optional to see network metrics
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  41414   47870   49293   48518   50125   51327
edges_dest<-left_join(edges, farmfiledest, by="destination")
```



```
edges_type<-left_join(edges_dest, ffsource, by="source")
```

Remove all markets - to have the direct farm to farm shipments only

```
edges_filtered<-edges_type%>%filter(D.type!="livestock_market_bison_cattle")
edges_filtered<-edges_filtered%>%filter(S.type!="livestock_market_bison_cattle")
ccsample2<-data.frame(node=c("15991","44509"))
df_market_destination <- edges_type %>%
  filter(destination %in% ccsample$node,
         S.type == "livestock_market_bison_cattle") %>%
  select(destination, source, D.type, S.type, t) %>%
  mutate(unique_id = row_number())

# Herd destinations
df_herd_destination <- edges_type %>%
  filter(destination %in% ccsample$node,
         S.type != "livestock_market_bison_cattle") %>%
  select(destination, source, D.type, S.type, t) %>%
  mutate(unique_id = row_number())

# Peek at the results
head(df_market_destination)
head(df_herd_destination)

# initialize an empty tibble
filtered_edges <- tibble::tibble(FOI = integer(), edges = character(), unique_id = integer())

for (i in seq_len(nrow(df_market_destination))) {
  unique_id <- df_market_destination$unique_id[i]
  market    <- df_market_destination$source[i]
  dest      <- df_market_destination$destination[i]

  result <- edges_type %>%
    mutate(cut = case_when(
      destination == market ~ 0,
      D.type == "livestock_market_bison_cattle" ~ 1,
      TRUE ~ 0
    )) %>%
```

```

    filter(cut == 0) %>%
    mutate(unique_id = unique_id)

# Build object name
obj_name <- paste0("edges_", dest, "_", unique_id)

# Save dataframe in global environment
assign(obj_name, result, envir = .GlobalEnv)

# Append new row to the accumulator
filtered_edges <- dplyr::bind_rows(
  filtered_edges,
  tibble::tibble(FOI = dest, edges = obj_name, unique_id = unique_id)
)
}

```

FIX THIS DF TO MERGE

```

matchedFOItime<-right_join(filtered_edges,df_market_destination, by="unique_id")%>%sel
ect(FOI, edges, unique_id, t)

print(matchedFOItime)

pwalk(
  list(matchedFOItime$edges,
        matchedFOItime$FOI,
        matchedFOItime$unique_id,
        matchedFOItime$t),
  function(df_edges_name, FOI, uid, t) {
    # get the correct edges object
    df_edges_obj <- get(df_edges_name, envir = .GlobalEnv)

    # run Trace
    Farm_FOI <- Trace(
      df_edges_obj,
      FOI,
      tEnd = t + 1,    # adjust as needed
      days = 6
    )
  }
)

```

```

# build output dataframe from incomingContacts
contact_df <- data.frame(
  source      = Farm_FOI@incomingContacts@source,
  destination = Farm_FOI@incomingContacts@destination,
  time        = Farm_FOI@incomingContacts@t,
  stringsAsFactors = FALSE
)

# build the object name
obj_name <- paste0("contact_df_in_", FOI, "_", uid)

# assign it to global env
assign(obj_name, contact_df, envir = .GlobalEnv)
}
)
pwalk(
  list(ccsample$node),
  function(node) {
    # run Trace
    Farm_FOI <- Trace(
      edges_filtered,
      node,
      tEnd = "2001-01-30",
      days = 28
    )

    # build output dataframe from incomingContacts
    contact_df <- data.frame(
      source      = Farm_FOI@incomingContacts@source,
      destination = Farm_FOI@incomingContacts@destination,
      time        = Farm_FOI@incomingContacts@t,
      stringsAsFactors = FALSE
    )

    # build the object name
    obj_name <- paste0("contact_df_direct_", node)

```

```

    # assign it to global env
    assign(obj_name, contact_df, envir = .GlobalEnv)
  }
)

```

TEST- Confirmed working same count.

```

Farm_FOI <- Trace(
  edges_filtered,
  33338,
  tEnd = "2001-01-30",
  days = 28
)

```

contact_herd <- data.frame(source = Farm_FOI@incomingContacts@source, destination = Farm_FOI@incomingContacts@destination, time = Farm_FOI@incomingContacts@t) #131 contacts

Now add them all together

```

rm(list = ls(pattern = "edges", envir = .GlobalEnv), envir = .GlobalEnv)

# run garbage collection
gc()

      used   (Mb) gc trigger   (Mb)    max used   (Mb)
Ncells 3495039 186.7  11389096 608.3   22537390 1203.7
Vcells 28852102 220.2  230289503 1757.0 3934688851 30019.3

walk(ccsample$node, function(n) {
  # find objects with this node in their name
  obj_names <- ls(pattern = n, envir = .GlobalEnv)

  # filter objects that are dataframes and have the expected columns
  obj_names <- keep(obj_names, ~ {
    obj <- get(.x, envir = .GlobalEnv)
    is.data.frame(obj) && all(c("source", "destination", "time") %in% names(obj))
  })

  # pull them into a named list
  dfs <- map(set_names(obj_names), ~ get(.x, envir = .GlobalEnv))

```

```

# bind them together
final_df <- bind_rows(dfs, .id = "source_df")

# assign into global env with name like "final_48992"
assign(paste0("final_", n), final_df, envir = .GlobalEnv)
})

```

Find the unique ID count

```

node_summary <- map_dfr(ccsample$node, function(n) {
  df_name <- paste0("final_", n)

  # Check if the dataframe exists
  if (!exists(df_name, envir = .GlobalEnv)) {
    return(tibble(node = n, n_rows = NA_integer_, unique_farmids = NA_integer_))
  }

  df <- get(df_name, envir = .GlobalEnv)

  # Validate columns
  if (!all(c("source", "destination") %in% names(df))) {
    return(tibble(node = n, n_rows = NA_integer_, unique_farmids = NA_integer_))
  }

  # Handle empty dataframes gracefully
  if (nrow(df) == 0) {
    return(tibble(node = n, n_rows = 0, unique_farmids = 0))
  }

  # Count rows
  n_rows <- nrow(df)

  # Count unique farm IDs across both columns, excluding the node itself
  unique_count <- df %>%
    select(source, destination) %>%
    unlist(use.names = FALSE) %>%
    unique() %>%
    setdiff(n) %>% # exclude the node itself if it appears

```

```

length()

tibble(node = n, n_rows = n_rows, unique_farmids = unique_count)
})

node_summary<-node_summary%>%rename(FOI=node)

print(node_summary)

write.csv(node_summary, "100CCAll7590_standard.csv")

rm(list = setdiff(ls(), "node_summary")) #cleanup all intermediate files
gc()

```

Reload in the edges and sample files for 1 phone call tracing

```

edges<-read_csv("Ideal7590.csv")

farmfile<-read.table("C:/Users/marykasmith/Desktop/New FF and Markets/FarmFile2024MarketsDairies.txt")

ccsample<-read_csv("CowCalfSampleN2D30_100.csv")

farmfiledest<-farmfile%>%rename(D.type=V2)%>%mutate(destination=as.integer(V1))%>%select(destination,D.type)

ffsource<-farmfiledest%>%rename(source=destination, S.type=D.type)

```

Convert the time stamp to a date because that's how EpiContactTrace wants it

```

edges<-edges%>%select(source, destination, t)

edges$source<-as.integer(edges$source)
edges$destination<-as.integer(edges$destination)

edges<-as.data.frame(edges)
edges_dest<-left_join(edges, farmfiledest, by="destination")
edges_type<-left_join(edges_dest, ffsource, by="source")

```

Remove all markets - to have the direct farm to farm shipments only

```

edges_filtered<-edges_type%>%filter(D.type!="livestock_market_bison_cattle")
edges_filtered<-edges_filtered%>%filter(S.type!="livestock_market_bison_cattle")

```

```

directcontacts<-read.csv("100_CC_directcontacts.csv")
marketcontacts<-read.csv("100_CC_marketcontacts.csv")
sampledirect<-data.frame(node = directcontacts$source)
samplemarket<-data.frame(node = marketcontacts$source, t=marketcontacts$t)
samplemarket$t<-as.Date(samplemarket$t)

df_market_destination_market <- edges_type %>%
  filter(destination %in% samplemarket$node,
          S.type == "livestock_market_bison_cattle") %>%
  select(destination, source, D.type, S.type, t) %>%
  mutate(unique_id = row_number())

# Herd destinations
df_herd_destination_market <- edges_type %>%
  filter(destination %in% samplemarket$node,
          S.type != "livestock_market_bison_cattle") %>%
  select(destination, source, D.type, S.type, t) %>%
  mutate(unique_id = row_number())

# Peek at the results
head(df_market_destination_market)
head(df_herd_destination_market)
for (i in seq_len(nrow(samplemarket))) {

  node <- samplemarket$node[i]    # FOI
  t<-samplemarket$t[i]

  filtered <- edges_type %>%
  filter(
    !(S.type == "livestock_market_bison_cattle" & source != node),
    !(D.type == "livestock_market_bison_cattle" & destination != node)
  )

  # Run trace
  Farm_FOI <- Trace(
    filtered,
    node,
    tEnd = t+1,

```

```

    days = 6
  )

  # Extract incoming contacts
  contact_df <- data.frame(
    source      = Farm_FOI@incomingContacts@source,
    destination = Farm_FOI@incomingContacts@destination,
    time        = Farm_FOI@incomingContacts@t,
    stringsAsFactors = FALSE
  )

  # Name the output object
  obj_name <- paste0("contact_df_in_", node)

  # Save to global environment
  assign(obj_name, contact_df, envir = .GlobalEnv)
}

walk(samplemarket$node, function(n) {
  # find objects with this node in their name
  obj_names <- ls(pattern = n, envir = .GlobalEnv)

  # filter objects that are dataframes and have the expected columns
  obj_names <- keep(obj_names, ~ {
    obj <- get(.x, envir = .GlobalEnv)
    is.data.frame(obj) && all(c("source", "destination", "time") %in% names(obj))
  })

  # pull them into a named list
  dfs <- map(set_names(obj_names), ~ get(.x, envir = .GlobalEnv))

  # bind them together
  final_df <- bind_rows(dfs, .id = "source_df")

  # assign into global env with name like "final_48992"
  assign(paste0("final_", n), final_df, envir = .GlobalEnv)
})

node_summary2 <- map_dfr(samplemarket$node, function(n) {

```



```

df_name <- paste0("contact_df_in_", n)

# Check if the dataframe exists
if (!exists(df_name, envir = .GlobalEnv)) {
  return(tibble(node = n, n_rows = NA_integer_, unique_farmids = NA_integer_))
}

df <- get(df_name, envir = .GlobalEnv)

# Validate columns
if (!all(c("source", "destination") %in% names(df))) {
  return(tibble(node = n, n_rows = NA_integer_, unique_farmids = NA_integer_))
}

# Handle empty dataframes gracefully
if (nrow(df) == 0) {
  return(tibble(node = n, n_rows = 0, unique_farmids = 0))
}

# Count rows
n_rows <- nrow(df)

# Count unique farm IDs across both columns, excluding the node itself
unique_count <- df %>%
  select(source, destination) %>%
  unlist(use.names = FALSE) %>%
  unique() %>%
  setdiff(n) %>% # exclude the node itself if it appears
  length()

tibble(node = n, n_rows = n_rows, unique_farmids = unique_count)
}))

print(node_summary2)

mergeback<-data.frame(FOI=marketcontacts$destination, node= marketcontacts$source)
FOINodeSummary<-left_join(mergeback, node_summary2, by="node")
Warning: Detected an unexpected many-to-many relationship between `x` and `y`.

```

```

print(FOINodeSummary)
result <- FOINodeSummary %>%
  group_by(FOI, node) %>%
  slice(1) %>%          # keep first occurrence per FOI-Node
  ungroup() %>%
  group_by(FOI) %>%
  summarise(
    n_rows = sum(n_rows),
    unique_farmids = sum(unique_farmids),
    .groups = "drop"
  )

print(result)
ccsample<-ccsample%>%rename(FOI=node)

final_df <- result %>%
  full_join(ccsample, result, by = "FOI") %>%
  mutate(
    n_rows = coalesce(n_rows, 0),
    unique_farmids = coalesce(unique_farmids, 0)
  )
print(final_df)
completenode_summary <- node_summary %>%
  left_join(final_df, by = "FOI", suffix = c("", "_final")) %>%
  mutate(
    n_rows = ifelse(n_rows == 0, n_rows + n_rows_final, n_rows),
    unique_farmids = ifelse(unique_farmids == 0, unique_farmids + unique_farmids_final
, unique_farmids)
  ) %>%
  select(FOI, n_rows, unique_farmids)
print(completenode_summary)

```

Save the 1 phone call node summary

```
write.csv(completenode_summary, "100CCAl17590_1phonecall.csv")
```

Supplement 5

Appendix C 5: Additional Network Metrics

Out Degree by Farm Type		
farm type	Mean Out Degree	Median Out degree
cow calf l	2.248	2.0
cow calf s	1.725	1.0
dairy heifer calf l	12.240	12.0
dairy heifer calf m	2.931	3.0
dairy heifer calf s	1.352	1.0
dairy l	8.620	8.0
dairy s	2.770	2.0
dealer cattle	23.584	23.0
feedlot cattle l	66.534	67.0
feedlot cattle m	33.913	33.0
feedlot cattle s	3.547	3.0
Market	468.122	428.5
processor cattle	0	0.0
processor cattle l	0	0.0
stocker l	1.849	2.0
stocker s	0.929	1.0

In Degree by Farm Type		
farm type	Mean In degree	Median in degree
cow calf l	1.483	1
cow calf s	0.112	0
dairy heifer calf l	43.120	30.5
dairy heifer calf m	5.287	4
dairy heifer calf s	8.959	9
dairy l	14.145	6
dairy s	0.486	0
dealer cattle	156.407	115
feedlot cattle l	160.139	116
feedlot cattle m	157.409	68
feedlot cattle s	9.711	5
Market	309.116	264
processor cattle	328.94	257
processor cattle l	1,505.564	1234
stocker l	29.304	20
stocker s	0.981	1

Movement Matrix: Destinations are the Columns, Sources are the Rows

values are the number of shipments made between the farm types

	Cow calf l	Cow calf s	Dairy heifer calf l	Dairy heifer calf m	Dairy heifer calf s	dairy l	dairy s	Dealer cattle	Feedlot l	Feedlot m	Feedlot s	market	Processor cattle	Processor cattle l	Stocker l	Stocker s
cow calf l	10409	10686	0	0	0	0	0	22499	742	7181	13955	18839	2049	148	8448	8303
cow calf s	34642	35373	0	0	0	0	0	371958	2069	13641	31611	173024	5262	128	42791	46787
dairy heifer calf l	75	135	131	12	6	1739	1243	1363	5	26	624	221	101	6	4	111
dairy heifer calf m	32	62	37	8	0	1374	1122	542	0	4	279	316	190	11	2	40
dairy heifer calf s	16	36	345	70	13	376	333	85	0	1	142	461	122	1	4	21
dairy l	54	29	3417	1698	607	1525	509	1865	4	12	9	13624	5195	546	387	267
dairy s	266	367	728	2215	12181	2510	7843	7191	1	23	138	40109	3821	123	2094	3056
dealer cattle	1796	164	413	71	17	1194	885	0	239	3340	13151	37665	11335	94	611	510
feedlot cattle l	0	3	0	0	0	0	0	0	6	14	15	27	1066	1728	2	0
feedlot cattle m	7	12	0	0	0	0	0	0	54	135	158	285	5820	7615	7	15
feedlot cattle s	180	192	0	0	0	0	0	0	9	1793	21456	25389	26285	16973	180	165
market	20674	2058	15368	3175	597	40097	2556	62496	1715	31334	158803	0	143280	31309	270	267
stocker l	0	0	0	0	0	0	0	961	111	496	702	1070	117	2	0	0
stocker s	0	0	0	0	0	0	0	5111	1931	7482	12501	28380	945	33	0	0