

Potential impact of introduction of foot-and-mouth disease from wild pigs into commercial livestock premises in California

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Objective—To estimate potential spread of foot-and-mouth disease (FMD) if introduced from wild pigs in California and to evaluate efficacies of various control strategies.

Design—Epidemiological model.

Procedures—A spatial, stochastic simulation model was used to simulate FMD epidemics that might occur if a dairy or beef herd were infected from contact with a wild pig. Index herd location and type were examined, in addition to different statewide movement ban (SWMB) durations, to determine their effect on extent of the epidemic.

Results—Duration, number of infected premises, size of simulated outbreak, number of culled animals, and spatial distribution of infected herds resulting from the simulated outbreaks varied considerably among geographic regions, depending on index case type and location. Outbreaks beginning in the southern region of California were consistently longest, whereas those beginning in the northern region were shortest. The largest outbreaks resulted from index cases located in the southern and valley regions, whereas outbreaks were smallest when originating in the Sonoma or northern regions. For all regions, when the index herd was a dairy herd, size and duration of the outbreak were consistently reduced with implementation of an SWMB ≥ 3 days.

Conclusions and Clinical Relevance—Introduction of FMDV from wild pigs into a dairy or beef herd could result in a large and rapidly spreading outbreak, potentially affecting large numbers of herds. Size and duration of the outbreak might be reduced with an SWMB; however, the impact is highly dependent on the index herd type and location. (*Am J Vet Res* 2010;71:xxx-xxx)

Pigs (*Sus scrofa*) are not native to the United States and were initially introduced to the mainland by European settlers hundreds of years ago. In California, the Spanish were the first to release domestic pigs in 1769, and a county landowner introduced the European wild boar onto his ranch in Monterey County in the 1920s for sport hunting.¹ Since then, there are believed to have been many illegal releases of boar within the state to create further hunting opportunities. Today, wild pigs are hybrid crosses of escaped feral domestic pigs and wild boar and are regulated as game animals by the state of California. Presently, wild pigs exist in 35 states and 56 of 58 California counties.²

Wild pigs are able to reproduce year-round, producing 10 to 12 piglets/y, which makes them difficult to eradicate once they are established.³ Because of their foraging behaviors, they are capable of destroying large

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ABBREVIATIONS

CDFCA	California Department of Food and Agriculture
CDFG	California Department of Fish and Game
FMD	Foot-and-mouth disease
FMDV	Foot-and-mouth disease virus
NAAS	National Agricultural Statistics Service
OIE	World Organisation for Animal Health
SWMB	Statewide movement ban
USGS	United States Geological Survey

areas of natural habitat. As California's rural-urban interface grows, wild pigs come into increased contact with agricultural systems. It is estimated that there are 4 million wild pigs nationally causing annual damage totaling \$1 billion.⁴ Damage to fences, trails, crops, and roads has been estimated to total \$1.7 million annually for 29 counties in California.¹ Although this is a small percentage of the state's direct farm sales (gross cash receipts) from agriculture (\$32 billion in 2005), there is potential for far greater economic losses.^{4,5} It is widely accepted that wild pigs are one of the possible sources for the *Escherichia coli* O157:H7 outbreak in September 2006, which was traced to the consumption of spinach grown in San Benito or Monterey counties.⁶

Wild pigs are susceptible to a variety of viral and bacterial diseases, including classical swine fever, ve-

sicular stomatitis, brucellosis, bovine tuberculosis, and FMD.⁷ Many of these diseases are transmissible to humans and livestock as well as other wildlife. Additionally, there is concern that should a disease such as FMD emerge in a wild pig population, it may become a disease reservoir resulting in the disease becoming endemic in wildlife.⁷⁻¹⁰ Foot-and-mouth disease is an economically important livestock disease that affects cloven-hoofed animals and is endemic to large parts of Asia, Africa, and South America.¹¹ Foot-and-mouth disease was eradicated in the United States in 1929, and the last large outbreak of FMD in California was in 1924, resulting in 109,759 livestock (cattle, swine, sheep, and goats) and 22,214 deer being slaughtered.¹² More recently, foreign animal diseases have spread from noncommercial sources into commercial livestock species.¹³ In 2002, exotic Newcastle disease was detected in noncommercial backyard flocks in the Los Angeles area. The disease quickly spread in this densely populated rural-urban area and eventually affected commercial poultry. By the time the outbreak ended, it had infected 22 commercial premises and hundreds of backyard flocks and spread to 2 other states at a cost of more than \$150 million in lost trade.¹³

Although the United States has been FMD-free since 1929, the disease is still a major component of disaster planning because of the severe repercussions to domestic and export industries that would occur should it be introduced. Wild pigs are a potential host for the disease because they are highly susceptible, able to increase the amount of virus via shedding, and difficult to control. Predicting the potential effects of wild pig populations during an FMD outbreak is difficult because their numbers, locations, and interactions with livestock are not well understood. One study³ of California wild pig population sizes and locations used hunter surveys to estimate wild pig distributions. These surveys have been used for wild pigs since 1957, when they were designated a game species.² Successful hunters must fill out a tag with information including the location and county where they killed a pig and send it to the CDFG. Analysis of the tag data has revealed that wild pigs spread from 10 coastal counties in the early 1960s to 49 counties by 1996 and 56 counties by 2001.^{2,3}

Disease simulation models are a useful tool for improving our understanding of disease dynamics and the potential impact of control strategies. They have been commonly used to estimate disease spread associated with different control strategies.^{8,14-21} Simulation models have also been used to evaluate the risk and extent of disease spread within and among wildlife species and domestic livestock.^{8,17,22-23} The purpose of the study reported here was to estimate potential spread and control of FMD if introduced from wild pigs in California and to evaluate efficacies of various control strategies.

Materials and Methods

An individual-based, spatially explicit, stochastic disease transmission model was used to simulate the spread and control of FMD among livestock premises in California.^{14,16,24} The model mimics disease movement

through a livestock population by simulating direct contacts among individual animals within a herd and direct and indirect contacts among infected and susceptible animals located on premises over a geographic region. Thirty-two outbreak scenarios were defined to evaluate the potential impact of an FMD outbreak in the livestock population under various movement controls and for different index herd types and locations.

Data—The precise locations of domestic swine and dairy herds in California were obtained from the CDFG. Data on other herd types (beef, goat, sheep), including backyard herds and sales yards, were obtained from the NASS. Herd locations in the NASS dataset were only indicated by county, not by their precise location. Those herds were randomly assigned locations within the county. Data were obtained from 21,667 herds, including beef (35%), backyard (25%), sheep (19%), dairy (12%), goat (7%), and swine (3%; **Table 1**). With the exception of sales yards and backyard herds, it was assumed that all herds consisted of only a single species. Data from the hunter surveys on wild pigs were obtained from the CDFG where the tag returns were reported by use of the USGS topographical quadrangle map system (scale, 1:24,000; **Figure 1**).

Identification of high-risk areas—The high-risk areas for transmission of FMDV from the wild pig population into the livestock population were identified by use of the wild pig hunter tag return data and locations of dairy and beef herds. By use of the number of tag returns per quadrangle in the hunter tag return data as a proxy for wild pig population density, the location of dairy and beef herds was overlaid onto the tag return map. Areas with high wild pig density (ie, a large number of tag returns) overlapping with a high density of dairy or beef premises were defined as high-risk areas for transmission of FMDV from the wild pig population into the livestock population. Four high-risk areas were identified and delimited by county boundaries as north (Shasta, Tehama, Glenn, Butte, Colusa, Sutter, and Yuba counties), Sonoma (Sonoma County), valley (San Joaquin, Stanislaus, Merced, and Madera counties), and south (San Bernardino, Riverside, and San Diego counties [**Figure 1**]).

Control strategies—Consistent with USDA guidelines,²⁵ it was assumed that following diagnosis of at least 1 FMDV-infected animal in a herd, movement restrictions would be put in place and the entire herd would be slaughtered. Two movement restriction strategies were evaluated: circular movement restrictions surrounding herds with an FMDV diagnosis and an SWMB following identification of the first herd with that diag-

Table 1—Number of livestock herds of various types in 4 regions in California (Calif) and in the entire state.

Herd type	North	Sonoma	Valley	South	Calif
Backyard	900	186	843	293	5,521
Beef	1,060	245	1,160	200	7,528
Dairy	133	112	919	343	2,502
Goat	129	76	144	280	1,547
Sheep	526	379	381	300	4,009
Swine	67	19	87	58	560
All types	2,815	1,017	3,534	1,474	21,667

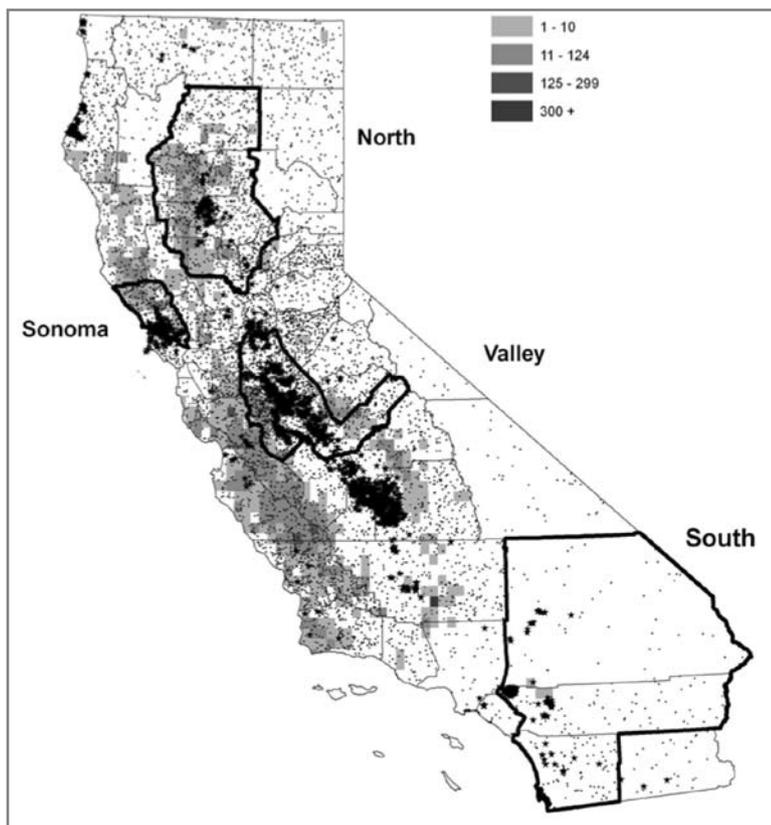


Figure 1—Schematic map of California illustrating number of wild pig hunter tags returned by hunters, 1992 to 2001 (shaded areas). Four geographic regions (northern, Sonoma, valley, and southern) from which index herds were selected in a model of an FMD outbreak are indicated by bold outlines enclosing counties. Point markers (stars and dots) represent the location of dairy and beef herds, respectively.

nosis. The circular movement control is divided into an inner infected area and an outer surveillance zone. The radii of the infected area and surveillance zone were 10 and 20 km, respectively, from an affected herd, and both were in place for the duration of the simulation following the diagnosis of the disease on that farm. The SWMB was in place for 0 (no SWMB), 3, 7, or 14 days.

Following diagnosis, herds were considered slaughtered. The delay between diagnosis and slaughter was drawn from a discrete random uniform distribution of 1 to 2 days,¹⁴ implying that typically half of affected herds would be slaughtered and disposed of in 1 day and the remainder in 2 days after diagnosis. There was no preemptive slaughter of noninfected herds determined to be either dangerous contacts or located on contiguous premises, and slaughtered herds were not restocked during the simulated period.

Simulations—For each high-risk region (north, Sonoma, valley, and south), 2 index herd types (beef or dairy) and 4 SWMBs (0, 3, 7, and 14 days after initial FMD diagnosis) were examined, for a total of 32 scenarios. For each scenario, the outbreak was initiated with a single latently infected animal in either a beef or dairy herd (index herd), which was presumed infected from contact with an FMDV-infectious wild pig. The index herd was selected randomly from among all of the beef and dairy premises in a given geographic region that were located in a quadrangle where wild pig

hunting tag returns were reported (Table 1). The number of potential index herds in each region (ie, the subset of beef and dairy herds located in a quadrangle having reported tag returns) was as follows: north, 609 beef and 82 dairy; Sonoma, 200 beef and 45 dairy; valley, 574 beef and 278 dairy; and south, 5 beef and 146 dairy. Epidemics were simulated for 90 days following incursion in 1-day time steps. Infected animals were assumed to be latently infected, subclinically infected, clinically infectious, or immune. Mean values and statistical distributions of duration for each of these disease states were based on results of published reports^{14,26} that analyzed data from previous studies.^{27,28} Briefly, mean estimated times that an individual animal would be latently infected, subclinically infected, clinically infectious, or immune were 3.7, 2.6, 18.4, and 20.0 days, respectively. The delay between the first latent case and diagnosis of FMD was 21 days. Implementation of control measures occurred 1 day after diagnosis in the index herd. Diagnosis in secondary case herds occurred 2 days after at least 1 animal in that herd had clinical signs. Five hundred iterations (simulated epidemics) were run for each scenario and were summarized by outbreak duration, number of infected herds, and number of culled animals, which were categorized by herd type and region.

Statistical analysis—Statistical analyses were performed by use of the statistical computing and graphics language R.²⁹ A series of box plots illustrates medians and 25% to 75% and 5% to 95% probability intervals for each of the 32 scenarios (Figures 2–4). Fixed-effect ANOVAs were used to analyze differences among scenarios in each of 3 metrics of outbreak severity (duration, total number of infected herds, and total number of animals in infected herds). Each ANOVA included 3 independent variables, along with all 2- and 3-way interactions among them, which included region (north, south, valley, and Sonoma), index herd type (beef and dairy), and SWMB (0, 3, 7, and 14 days). To reduce heterogeneity of variance in the response variables, each was transformed by use of a Box-Cox power transformation prior to model fitting.³⁰ In all 3 instances, profile likelihoods for the parameter of the transformation indicated that a log transformation was most appropriate. Accordingly, ANOVAs were performed on the log-transformed response variables. A value of $P = 0.05$ was considered significant for all hypothesis tests.

Results

Outbreak duration—Mean duration of simulated outbreaks varied significantly ($P < 0.001$) among outbreaks with different index cases in different geographic regions. Outbreaks beginning in the southern region were typically longer and had greater variability than those beginning in other regions of the state (Figure 2).

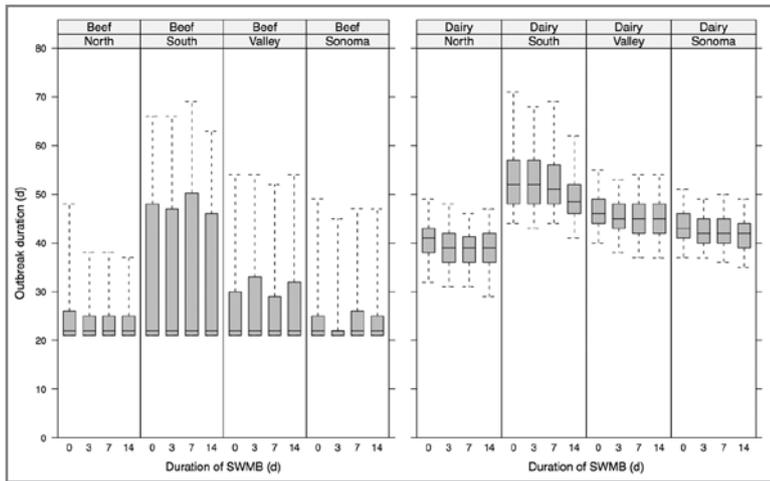


Figure 2—Box plots of estimated duration of an FMD outbreak in beef or dairy herds in 4 regions of California associated with SWMBs of various durations. Horizontal lines in the box plots represent median outbreak duration, boxes represent the 25% to 75% percentiles, upper and lower ends of whiskers represent 5% and 95% percentiles, and the interval between the end of the whiskers represents the 90% probability interval. Each scenario is based on 500 iterations of the model.

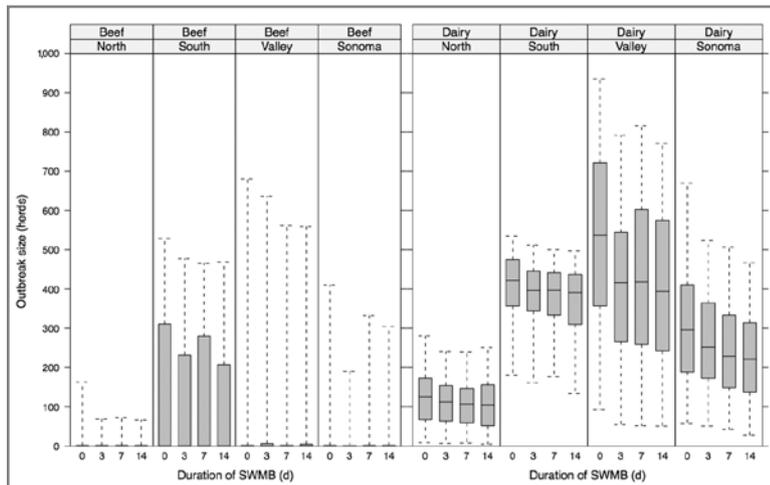


Figure 3—Box plots of estimated number of herds infected during an FMD outbreak in beef or dairy herds in 4 regions of California associated with SWMBs of various durations. Horizontal lines in the box plots represent median outbreak duration, boxes represent the 25% to 75% percentiles, upper and lower ends of whiskers represent 5% and 95% percentiles, and the interval between the end of the whiskers represents the 90% probability interval. Each scenario is based on 500 iterations of the model.

Median durations for outbreaks beginning in beef herds were identical (22 days) in all regions. However, the 90% probability interval for outbreaks beginning in the southern region when there was no SWMB was 45 days (range, 21 to 66 days), compared with 27 days (range, 21 to 48) in the northern, 33 days (range, 21 to 54) in the valley, and 28 days (range, 21 to 49) in the Sonoma regions.

Across scenarios, the mean duration of outbreaks beginning in dairy herds was significantly ($P < 0.001$) longer than for outbreaks beginning in beef herds. In addition, there was a significant ($P < 0.001$) interaction between index herd type and region because 32% of outbreaks beginning in beef herds did not spread beyond the index herd. Thus, although worst-case scenarios (as measured by the 95% probability limit) for each re-

gion were similar among index herd types, the best-case scenarios (as measured by 5% probability limit) were consistently shorter when the index case was in a beef versus dairy herd. For example, in the southern region with no SWMB, more than half of outbreaks beginning in beef herds lasted < 21 days, whereas only 5% of outbreaks in dairy index herds lasted < 44 days.

Across regions, mean outbreak duration was reduced significantly ($P < 0.001$) by the imposition of an SWMB (Figure 2). A 3-day movement ban shortened median epidemic duration in dairy index herds by 0 to 2 days for different regions, whereas 7- and 14-day movement bans did not further decrease the median duration, except for a small decrease in the southern region when the index herd was a dairy herd. In outbreaks with beef index herds, movement bans of any length had no effect on the median outbreak duration, which was 21 days. There was, however, a significant ($P = 0.002$) interaction between SWMB and region.

Number of infected herds—Mean number of infected herds varied significantly ($P < 0.001$) among outbreaks with different index herds and among outbreaks in different geographic regions. Outbreaks starting in dairy index herds infected more herds (median, 289 infected herds), whereas outbreaks starting in beef index herds affected a median of 1 herd (ie, rarely spreading beyond the index herd [Figure 3]). For outbreaks that spread beyond the beef index herd, the median number of herds infected was 51. The difference in the median number of herds infected in dairy index versus beef index outbreaks was largest in the valley region and smallest in the northern region.

Among the outbreaks starting in beef index herds, 75% infected 1 or 2 herds in all regions except the southern region, where 75% of the outbreaks infected from 1 to 311 herds (Figure 3). Across both index species, outbreaks starting in index herds located in the valley region had the greatest variability, with 90% of outbreaks (with no SWMB) infecting from 1 to 680 herds when starting in a beef index herd and from 93 to 935 herds when starting in a dairy index herd. Outbreaks starting in the northern region had the lowest variability in the number of infected herds, with 90% of outbreaks infecting from 1 to 163 herds and from 9 to 280 herds for beef and dairy index herds, respectively.

As with epidemic duration, both the main effect of SWMB and its interaction with region on the number of infected herds were significant. Although there was a significant decrease in the number of infected herds not associated with an SWMB (ie, 0 day's duration), there was no significant difference associated with SWMBs of 3, 7, or 14 days. Imposition of an SWMB reduced

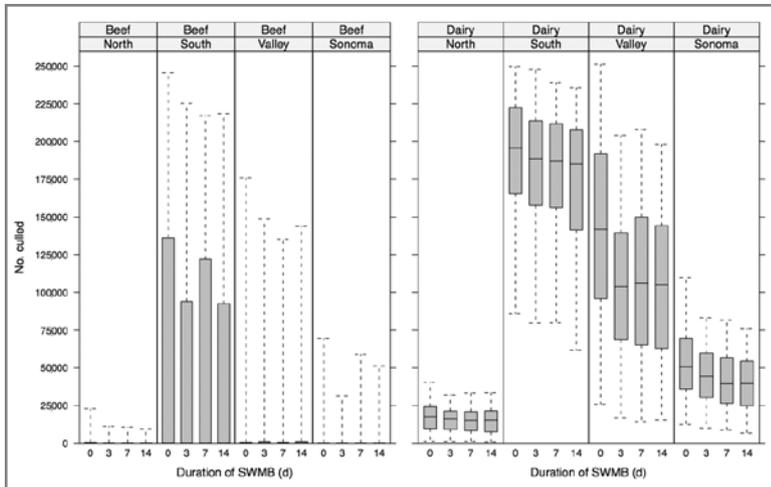


Figure 4—Box plots of estimated number of animals culled during an FMD outbreak in beef or dairy herds in 4 regions of California associated with SWMBs of various durations. Horizontal lines in the box plots represent median outbreak duration, boxes represent the 25% to 75% percentiles, upper and lower ends of whiskers represent 5% and 95% percentiles, and the interval between the end of the whiskers represents the 90% probability interval. Each scenario is based on 500 iterations of the model.

the median number of herds infected by up to 162, depending on the length of the ban. The positive effect of an SWMB (especially in dairy-index outbreaks) was strongest for outbreaks starting in the valley and Sonoma regions.

Number of culled animals—Mean number of culled animals varied significantly ($P < 0.001$) among outbreaks with different index herds and among outbreaks in different geographic regions. If the index herd was beef, the median number of culled animals was < 51 (Figure 4). Conversely, if the index herd was dairy, the median number of culled animals ranged from approximately 20,000 to 200,000 for the northern and southern regions, respectively.

The variability in the number of culled animals followed a pattern similar to that seen for the number of infected herds (Figures 3 and 4). Both index herd type and its interaction with region were significantly ($P < 0.001$) associated with the number of animals culled in an outbreak. Variability in number of culled animals was higher for outbreaks starting in dairy herds than for outbreaks starting in beef herds for all regions except the southern region, where the pattern was reversed. The 90% probability intervals for outbreaks in the northern region spanned 35,142 (range, 1,045 to 36,187) and 22,813 animals (range, 51 to 22,864) for dairy and beef index herds, respectively. For outbreaks starting in the Sonoma region, the interval spanned 103,117 animals (range, 6,725 to 109,842) and 69,362 animals (range, 51 to 69,413) for dairy and beef index herds, respectively. For outbreaks starting in the valley region, the interval spanned 225,345 animals (range, 25,875 to 251,219) and 175,988 animals (range, 51 to 176,039) for dairy and beef index herds, respectively. In contrast, for outbreaks starting in the southern region, the interval spanned 167,909 animals (range, 81,824 to 249,733) and 245,536 animals (range, 51 to 245,587) for dairy and beef index herds, respectively.

The effect of an SWMB on the mean number of culled animals was less clear than its effect on the number of culled herds. Across regions, there was no significant effect of SWMB, but there was a significant ($P = 0.033$) interaction between SWMB and region, indicating that regions differed in their apparent response to an SWMB. Imposition of an SWMB yielded the greatest reduction in the median number of culled animals for outbreaks beginning in dairies located in the southern region and had the least effect on outbreaks starting in dairy index herds in the northern region (Figure 4). For all regions, an SWMB had no effect on reducing the number of culled animals for outbreaks starting in beef index herds.

Discussion

The livestock industry in California is dynamic and important to the state's economy, totaling \$7.6 billion in 2006 and ranking the state fourth nationally in livestock cash receipts, with beef accounting for \$1.7 billion and dairy more than \$5 billion/y. As the largest milk-producing state, it accounts for more than 21% of the total US production.⁵

The impact of an exotic disease on agriculture could be very disruptive. In livestock industries that are in decline, restocking of farms after a major disease outbreak might not occur, as in the 2001 FMD outbreak in the United Kingdom. In a survey of 160 farms that culled animals during the 2001 FMD outbreak, only 29% of beef farms in England and 23% in Wales had restocked by the end of the accounting year.³¹ This was despite the fact that the compensation (mean compensation equivalent to US \$350,000) received was substantially higher than the mean net livestock revenue before the outbreak (equivalent to US \$120,000). If an FMD outbreak were to occur in California, it would likely further damage the already declining livestock industry³² in the state and negatively impact the state's already fragile economy.³³ The livestock industry and state economy would be affected directly in the short term by the implemented control strategies (movement restrictions and culling) as well as long term by trade restrictions resulting from the OIE-based standards used by FMD-free importing countries. The United States has held an FMD-free status without vaccination since 1929, following the eradication of the disease from California. The status of being FMD-free without vaccination is defined by OIE as there having been no FMD outbreaks or FMD vaccination in the past 12 months and no importation of FMD-vaccinated animals since the cessation of vaccination.³⁴ This status is lost when an outbreak of the disease occurs, and a free status without vaccination may only be regained after the following conditions apply: 3 months after the last case, where depopulation and serologic surveillance are applied; 3 months after the slaughter of the last vaccinated animal, where depopulation, serologic surveillance, and emergency vaccination are applied; or 12 months after the last case

and last vaccination, where depopulation in outbreaks, emergency vaccination not followed by depopulation of all vaccinated animals, and serologic surveillance are applied.³⁴ When an outbreak of FMD is declared, other FMD-free trading partners may put in place import restrictions resulting in large economic losses for the FMD-affected country or region. These trade restrictions are typically lifted only after FMD-free status is reinstated. Therefore, anything that acts to delay a return to FMD-free status increases the economic impact of the outbreak. Preemptive actions or control strategies during an outbreak that can be taken to shorten outbreak duration and initiate the 3- or 12-month wait period necessary to regain free status are therefore of particular interest. A key result of the present study was that the duration and size of the outbreak were strongly influenced by the herd type and geographic location in which an outbreak originated. Correlating these herd-type and regional differences with the increased transmission risk of high-density wild pig areas is of utmost importance to reduce the risk of transmission between livestock and wild pig populations as well as limiting the duration and size of an outbreak should transmission occur. Although further work is necessary to determine the causal basis of these differences, these results provide important information for the planning of management strategies and control measures in the event of an actual FMD outbreak in California. Results suggested that the most efficient preemptive action to reduce the duration of an outbreak originating from an infected wild pig population is to minimize the opportunity for a transmission event to take place between wild pigs and dairy herds, particularly in the southern region. This could be achieved by reducing the exposure and transmission risk for animals coming into contact with wild pigs; for example, by implementing more rigorous biosecurity practices and reducing wild pig population numbers in the area, the opportunity for livestock to come into contact with wild pigs could be reduced. This assumes, however, that only the wild pig population is infected. Because FMD is highly contagious among livestock, the extent and rate of spread when a livestock herd has been infected are principally determined by factors intrinsic to the livestock industry (eg, direct and indirect contacts), not the exposure rate of wild pigs.

One common control strategy used to reduce epidemic duration is to restrict animal movement. In our simulations, we considered 2 levels of movement restriction: local (within 20 km of infected premises) and statewide. The SWMB was evaluated by varying the duration of the movement ban from 0 days (ie, no SWMB) to 14 days. Clearly, implementing an SWMB is an extreme control measure that could encounter major difficulties associated with man power constraints and compliance, which were not considered in this study; the effects on commerce were also not considered. The simulation results indicated that effective implementation of an SWMB is dependent on several factors, such as location and livestock type of the index herd. Simulation revealed that a 3-day SWMB was an effective control measure and that in most situations, a 7- or 14-day SWMB might have only marginal additional

benefits. In the simulations, 100% compliance with the imposed SWMB was assumed. If less compliance occurred (which is likely in a real outbreak), benefits of an SWMB would be diminished. A 1- to 2-day lag between diagnosis and slaughter was also assumed.^{14,35} If the lag were longer, which would be likely in a large outbreak with limited resources for depopulation and disposal of carcasses, the present results would underestimate the extent and duration of the outbreak and, likely, the effectiveness of movement bans. With an increased lag between diagnosis and slaughter, the effectiveness of movement bans, particularly the SWMB, may increase. Further studies are required to fully explore the role of the duration of the diagnosis-slaughter lag. Because of the high cost associated with a prolonged SWMB, the duration of this type of movement control should be minimized. Although our results suggest that an SWMB longer than 3 days confers little added benefits, further studies are needed to evaluate the benefit of even shorter movement restrictions. Furthermore, depending on the type and location of the index herd, a herd-type-specific SWMB may be recommended.

Although the present study indirectly addressed the effect of wild pig population density in the risk of FMDV transmission from wild pig populations to commercial premises, more information about wild pig populations would be beneficial, such as the distribution, density, and connectivity of pig populations⁹; the interaction between wild pig and livestock populations; and the epidemic dynamics of the virus in the wild pig population. This might aid in evaluating issues such as the risk of multiple transmissions of FMDV into livestock populations and the risk of transmission taking place in the opposite direction (ie, from livestock to the wild pigs). During an FMD outbreak, control strategies would likely also be put in place for wild animal populations within an infected area as happened during the 1929 outbreak when many deer were culled.¹²

Results of the present study indicated that introduction of FMDV from wild pigs into dairy or beef herds in high-risk areas could result in large and rapidly spreading outbreaks, especially when the index herd was in the southern and valley regions. Although the size and duration of the outbreak could be reduced with an SWMB, its effect would be highly dependent on the index herd type and location. In general, however, a longer SWMB would have a greater impact on larger outbreaks than smaller outbreaks. Predicting the potential effect of wild pig populations is difficult because population numbers, locations, and interactions with livestock are not well understood. Outbreaks starting in the southern and valley regions were more likely to give rise to larger and longer outbreaks. Outbreaks starting in the northern and Sonoma regions were more likely to give rise to opportunities for transmission back into the wild pig population.

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