

ORIGINAL ARTICLE

Adaptive risk-based targeted surveillance for foreign animal diseases at the wildlife-livestock interface

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Abstract

Animal disease surveillance is an important component of the national veterinary infrastructure to protect animal agriculture and facilitates identification of foreign animal disease (FAD) introduction. Once introduced, pathogens shared among domestic and wild animals are especially challenging to manage due to the complex ecology of spillover and spillback. Thus, early identification of FAD in wildlife is critical to minimize outbreak severity and potential impacts on animal agriculture as well as potential impacts on wildlife and biodiversity. As a result, national surveillance and monitoring programs that include wildlife are becoming increasingly common. Designing surveillance systems in wildlife or, more importantly, at the interface of wildlife and domestic animals, is especially challenging because of the frequent lack of ecological and epidemiological data for wildlife species and technical challenges associated with a lack of non-invasive methodologies. To meet the increasing need for targeted FAD surveillance and to address gaps in existing wildlife surveillance systems, we developed an adaptive risk-based targeted surveillance approach that accounts for risks in source and recipient host populations. The approach is flexible, accounts for changing disease risks through time, can be scaled from local to national extents and permits the inclusion of quantitative data or when information is limited to expert opinion. We apply this adaptive risk-based surveillance framework to prioritize areas for surveillance in wild pigs in the United States with the objective of early detection of three diseases: classical swine fever, African swine fever and foot-and-mouth disease. We discuss our surveillance framework, its application to wild pigs and discuss the utility of this framework for surveillance of other host species and diseases.

KEYWORDS

African swine fever, classical swine fever, feral swine, foot-and-mouth disease, foreign animal diseases, risk, targeted surveillance, wild pig

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1 | INTRODUCTION

Animal disease surveillance systems are an essential component of the national veterinary infrastructure to protect animal agriculture. National surveillance programs serve an important role in identification of foreign animal disease (FAD) introduction and allow for disease freedom to be substantiated. Typically, national surveillance systems are solely focused on domestic animal populations. However, the role of wildlife in livestock diseases has increased globally in part due to spillover from livestock to wildlife resulting in some economically important animal diseases now involving wildlife (Miller et al., 2013; Siembieda et al., 2011). Once introduced, pathogens shared among domestic animals and wildlife are especially challenging to manage and can challenge determination of disease freedom (Arias et al., 2018; Gortazar et al., 2015; Wiethoelter et al., 2015). While the initial introduction of a pathogen into wildlife may be the result of spillover from domestic animals once a pathogen is established in wildlife it can be difficult to control resulting in disease persistence and re-emergence (Lloyd-Smith et al., 2009; VerCauteren et al., 2018). As a result national surveillance and monitoring programs that include wildlife are becoming increasingly common in part because substantiating national disease freedom and confirming the status of significant diseases in wildlife is increasingly important (Morner et al., 2002; Portier et al., 2019). Thus, early identification of FADs in wildlife is critical to minimize outbreak severity and potential impacts to wildlife, biodiversity and animal agriculture.

Important challenges for risk management of pathogen introduction include predictions of introduction risk, pathogen surveillance and risk mitigation strategies focused on minimizing potential for introduction. Routes of pathogen introduction are often poorly understood and can include trade in domestic animals and their products, air travellers, movement of goods and in some cases wildlife movement (Bevins et al., 2022; Herrera-Ibata et al., 2017; Jurado et al., 2019). Once a pathogen is introduced into wildlife species spillover and spillback dynamics between domestic animals and wildlife can introduce additional epidemiological cycles in host-pathogen systems (Chenais et al., 2019). Consequently, introduction pathways are difficult to understand and predict, since surveillance data for those pathways are frequently unavailable. When data are available, the relative risks associated among each pathway are typically unknown. These generally ill-understood pathways of introduction and how they relate to the likelihood of pathogen establishment complicate the development of surveillance systems that are sensitive and robust in the face of changing risks through time. Quantitative approaches can be the most effective method for defining surveillance priorities because of their capacity to assimilate and evaluate multiple, frequently complex processes simultaneously while accounting for potential uncertainties (Huyvaert et al., 2018; Manlove et al., 2019; Pepin et al., 2021, 2014).

These challenges are magnified for determining risks of FAD introduction into wildlife populations and the implementation of surveillance systems to mitigate these risks. In contrast to domestic animal populations, ecological and epidemiological data such as host abundance and host disease competence for wildlife species is frequently

unavailable (Stallknecht, 2007). This complicates multiple aspects of surveillance system design and implementation including difficulty in designing representative sampling strategies, a lack of diagnostic tests validated in wildlife, unknown disease prevalence in wildlife, difficulty interpreting surveillance data due to an absence of denominator or population data and the absent or insufficient wildlife surveillance infrastructure (Sleeman et al., 2012; Stallknecht, 2007). These challenges contribute to gaps in the development and implementation of rigorous surveillance in wildlife populations.

An important gap of disease surveillance systems is accounting for disease introduction risks arising from processes in source and recipient host populations (Lloyd-Smith et al., 2009; Pepin et al., 2021). Pathogen emergence and introduction risk can be altered through changes in source or recipient population ecology and should be accounted for when designing surveillance systems. Consequently, inference from a sole host population may produce flawed risk estimates, misallocating surveillance resources when conditions change. Similarly, surveillance systems based on static risk criteria can limit sensitivity of surveillance systems (Sleeman et al., 2012). This is especially important when developing surveillance systems at a national scale with potentially limited resources and fiscal constraints.

One of the most important wildlife species for FAD surveillance in the United States are wild pigs (*Sus scrofa*), commonly referred to as feral swine (Brown et al., 2020a). Wild pigs pose a significant disease risk to animal agriculture with the potential of 87% of World Organisation for Animal Health (OIE) listed swine pathogens potentially causing disease in livestock. In the United States, 57% of all farms and 77% of all domestic livestock are co-located within the invaded range of feral swine (Miller et al., 2017). In North America, wild pigs are considered an invasive species with populations distributed across large areas of the United States, Canada and Mexico causing significant ecological and agricultural damage as well as disease risks to wildlife, humans and domestic animals (Bevins et al., 2014; Lewis et al., 2017).

Wild pigs were first introduced into North America in the 16th century with continued introductions throughout the period of European colonization of North America (Mayer & Beasley, 2018; Mayer & Brisbin, 1991). Starting in the late 1800s wild boar were imported to the United States from Europe and introduced into established wild pig populations to improve hunting appeal of the species (Mayer & Brisbin, 1991). During the mid-20th century many states in the United States began managing wild pigs as game species with stocking of wild pigs into new areas becoming common (Keiter et al., 2016). The popularity of wild pigs as a recreational hunting species, their ability to rapidly establish populations and the legal and illegal introductions of wild pigs has resulted in their expansion throughout North America with free-ranging and breeding populations existing in the United States, Canada and Mexico (Tabak et al., 2018; VerCauteren et al., 2019). Genotypes of wild pig populations in the United States are most closely related to European wild boar and western heritage pig breeds with increased wild boar ancestry potentially having improved fitness and heightened invasive potential in some populations (Smyser et al., 2020). Despite the damage caused by wild pigs in North America they

remain an important wildlife species that is valued as a recreational hunting resource.

The U.S. national disease surveillance in wild pigs started in 2006 and was primarily focused on classical swine fever (CSF) and various endemic diseases of interest (DeLiberto & Beach, 2006; Pedersen et al., 2012, 2013; Swafford et al., 2009). In 2014, the APHIS National Feral Swine Damage Management Program was created establishing an integrated approach to wild pig operational removal activities and disease surveillance (APHIS, 2015). Disease surveillance conducted in wild pigs from 2006 to 2017 was opportunistically collected with a focus on populations adjacent to landfills. Landfills have been proposed as a potential pathway of introduction and release of FADs including CSF and African swine fever (ASF), in wild pigs through discarded contaminated swine products that arrive in the country via international travellers (Herrera-Ibata et al., 2017; Jurado et al., 2019). Starting in 2017, a spatially targeted approach was developed that prioritized antibody surveillance in U.S. counties with landfills, ports of entry and livestock production (APHIS, 2017). Increasing concern over the potential role of wild pigs in the event of a FAD introduction, necessitated a revamping of wild pig surveillance to focus on FAD introduction risks (Brown et al., 2020a). Three pathogens were identified as a primary concern for introduction and surveillance in wild pigs—ASF, CSF and foot-and-mouth disease (FMD). These diseases cause significant economic burdens in countries where they are present (Brown et al., 2020b). In the United States, sympatric livestock and wild pig populations pose significant risks if one of these diseases were to be introduced into wild pigs.

To meet the increasing need for targeted FAD surveillance and address gaps and challenges in existing wildlife surveillance systems, we developed an adaptive risk-based targeted surveillance approach that prioritizes where to sample wild pigs and how many to sample. This approach accounts for risks in source and recipient host populations. The approach is flexible, accounts for changing disease risks through time, can be scaled from local to national extents, and permits the inclusion of quantitative data or expert opinion. This allows our surveillance framework to be rapidly implemented in any host species to address new emerging disease threats while also being useful for routine surveillance. We apply our adaptive risk-based surveillance framework to prioritize areas for surveillance in wild pigs in the United States with the objective of early detection for CSF, ASF and FMD. We evaluated the resulting surveillance prioritization using sensitivity and time series analyses to determine the influence of uncertainty in the risk factors used and the resulting risk rank. We present the results of our surveillance framework, its application to wild pigs, and discuss the utility of this framework for surveillance in other host species and diseases.

2 | MATERIALS AND METHODS

We apply a spillover framework first described by Plowright et al. (2017) and adopted to guide surveillance design at the wildlife–livestock–human interface by Pepin et al. (2021). We extended these frameworks by including directional risks associated with initial dis-

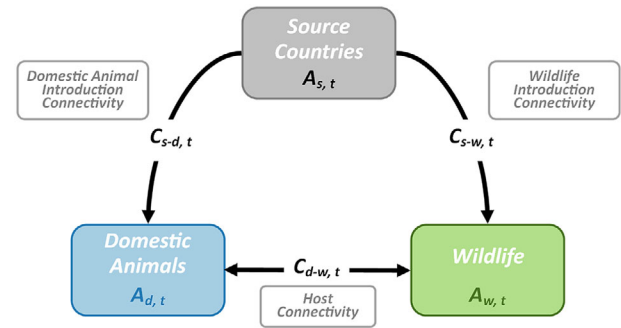


FIGURE 1 Conceptual framework and relationship among introduction and spillover-spillback processes. Colored boxes are risk factors for host pathogen availability within source countries ($A_{s,t}$), domestic ($A_{d,t}$), and wildlife ($A_{w,t}$) host populations in destination counties. These factors influence the dynamics of pathogen availability in source countries (s) and available hosts in at-risk counties. Risk factors that influence the contact and transmission (C) between host groups (introduction and interface connectivity) are shown in white boxes between the host groups that they connect. Arrows indicate assumed transmission direction. Note transmission among domestic and wildlife hosts is assumed to be bi-directional and transmission from source countries to domestic and wildlife host populations is unidirectional

ease introduction (Miller & Pepin, 2019), in our case, transboundary introduction, to further prioritize areas for surveillance with the objective of early detection. Thus, the process for risk ranking and prioritizing populations for surveillance first develops a risk ranking for introduction risks, host abundance risks and host connectivity risks. A final risk ranking is then created with these risks that can be weighted to prioritize introduction, host or between host risks depending on specific policy goals.

Applying the frameworks of Plowright et al. (2017) and Pepin et al. (2021), we expect the risk of FAD introduction into the United States during a time interval t is highest for wild (w) and domestic (d) populations ($A_{w,t}$ and $A_{d,t}$) that have contact ($C_{s-w,t}$ and $C_{s-d,t}$) with populations ($A_{s,t}$) in source countries (s) where the FAD of interest is present (Figure 1). Further, that potential transmission among domestic and wild populations ($C_{d-w,t}$) is of greater importance for surveillance to mitigate spread and establishment of the disease in either. This framework differs from that of Pepin et al. (2021) in that host pathogen availability is only initially important in the source country. Additionally, each component risk factor is time varying, representing the state of the risk factor for a specified time interval (t).

The simplest proxy for risk can be defined as the multiplicative process using $A_{w,t} \cdot A_{d,t} \cdot C_{d-w,t}$. Component risk factors within A and C , if present, are also multiplicative (Table 1). The relative risk of each geographic area, counties in our case, can be represented as,

$$\prod_{r=1}^R \omega_{r,t} \theta_{j,r,t}$$

where ω is the weight for risk factor r during time interval t and $\theta_{j,r,t}$ is the relative risk score for risk factor r in county j during the same time

TABLE 1 Risk factors used for triaging and targeting surveillance for FADs

Risk factor	Component	Description	Scale and units	Source
Pathogen availability in hosts (A)				
FAD Presence	$A_{c,t}$	Pathogen availability in source countries represented as a binary variable (1 = present and 0 = not present).	Country, binary by year	(WAHIS, 2021)
Livestock host density ^a	$A_{d,t}$	Livestock host density measured as operation density by operation size for domestic swine, cattle, sheep, goats, cervids.	County, operations per km ² by year	(USDA, 2020)
Wild pigs host density	$A_{w,t}$	Wild pig host presence and density.	County, wild pigs per km ² by year	Miller et al. Unpublished data.
Connectivity (C)				
Agricultural Quarantine Inspection Monitoring (QMI)	C_{c-d}, C_{c-w}	Movements of agricultural products by air passengers and foreign mail from source country to counties within the United States.	County, QMI per km ² by year	(USDA, 2021a, 2021b)
Landfills	$C_{w-d}, C_{c-d}, C_{c-w}$	Landfills have been identified as an important risk factor for FAD introduction into wildlife host populations.	County, landfills per km ²	infoUSA, Inc.
Seaports	C_{c-d}, C_{c-w}	Seaports provide a potential source of introduction via smuggled or legally imported products.	County, seaports per km ²	(BTS, 2020)
Airports	C_{c-d}, C_{c-w}	Airports provide a potential source of introduction via smuggled or legally imported products.	County, airports per km ²	(BTS, 2020)

Note: The scale and source columns describe the data sources used in our map examples. This is not an exhaustive list of possibilities, rather it represents risk factors for which there are already available data and additional risk factors can be included as new evidence for additional risk factors arises.

^aLivestock density is weighted by operation size to arrive at a final livestock density. Size categories by commodity are described in Table S1.

interval t . To consider risk factors equally each risk factor, θ_r , is normalized using ordered quantile normalization transformation and then placed on 0 to 1 scale using minimum–maximum scaling (Beasley et al., 2009; Peterson & Peterson, 2020). This ensures that county values are relative to one another such that the highest risk is represented by a value of 1 (see). The weights, ω_r , determine the importance of each risk factor relative to the other risk factors. Weights can be defined by data (e.g., probability of transmission), based on expert opinion, or reflect policy objectives (e.g., to maximize early detection an higher weight would be placed on introduction risks, $C_{s-d,t}$ or $C_{s-w,t}$). Here, we weight each risk factor equally ($\omega_r = 1$; Figure 1) and conduct sensitivity analysis (see section below on sensitivity analysis) over a range of weights to determine the importance of the county for surveillance. In practice the relationships among component risk processes are likely hierarchical and many are potentially non-linear (e.g., Cross et al., 2019; Plowright et al., 2017). However, in the case of FADs which may not have ever been present in the at-risk populations there is frequently limited (or no) information that allows for these relationships to be parameterized appropriately. We implemented our risk ranking algorithm using custom code in R (R-project, 2020).

We implemented our risk ranking using the risk factors from Table 1. To generate measures of host density, data describing the nationwide distribution (presence/absence) of wild pigs at the county level were

compiled from APHIS-Wildlife Services and the Southeastern Cooperative Wildlife Disease Study (SCWDS) (Corn & Jordan, 2017). These data represent the known nationwide county-level distribution of wild pigs over the past 38 years and have been used to forecast the spread of wild pigs (Snow et al., 2017), estimate occurrence (McClure et al., 2015), estimate effects of management on spatial spread (Pepin et al., 2019), determine wild pig risks posed to agriculture (Miller et al., 2017) and predict corresponding policy activity (Miller et al., 2018). These occurrence data were used with management removal data using a Bayesian catch-effort model implemented on the scale of management units (Davis et al., 2021) and scaled up to the county-level using spatial statistics and environmental covariates (Miller et al., Unpublished data). The catch effort model generates predictions of wild pig density for each county at a monthly scale while accounting for differing removal methods, habitat, climate and other factors affecting either population growth or probability of capture.

Livestock host densities were estimated using National Agricultural Statistics Service (NASS) data (USDA, 2020). Because introduction risk is at the operation level, we used the density of production weighted by operation size in each county to represent livestock host density. Operation size category definitions are provided in Table S1. Our interest is potential introduction of risks associated with livestock FADs, specifically ASF, CSF and FMD. To account for the broad host range of FMD we

included all cattle, sheep, goat, cervid and domestic swine operations. Counties that had years with missing data were imputed assuming a linear change in number of operations by inventory size among years.

Agricultural Quarantine Inspection Monitoring (AQIM) and Mail287 data were used to represent connectivity among counties and foreign countries with FADs of interest (i.e., introduction risk pathway) (USDA, 2021a, 2021b). These data represent air passenger and international mail inspections and interceptions for agricultural quarantine materials (QM). AQIM data covers randomized inspection data for air passenger and international mail and the Mail287 database covers targeted inspection data for the international mail pathway. These data include the country of origin and the destination address for the material. While there is targeted inspection data available for the air passenger pathway, it does not include origin-destination data needed for this analysis. The collected data were used with OIE data (WAHIS, 2021) describing, by year, those countries known to have the FAD of interest resulting in the number of observed QM events by county, by year and by FAD.

In addition to these time varying risk factors, three static risk factors were included to inform introduction risks and connectivity among domestic swine and wild pigs. Landfills have been proposed as a potential pathway of introduction and release of FADs into wild pigs through discarded contaminated products from international travellers (Herrera-Ibata et al., 2017; Jurado et al., 2019). Landfills are known to serve as a potential forage resource for wild pigs (Mayer et al., 2021). While no empirical studies are available to substantiate this proposed risk pathway, it may be an important route of introduction. To account for this pathway, we used landfill locations obtained from InfoUSA, Inc. (Omaha, Nebraska).

Ports of entry can also serve as an important route of introduction via passengers, baggage or legal and illegally imported products (Jurado et al., 2019). To represent these potential pathways, we used airport and seaport location data (BTS, 2020). We assume that an increasing number of ports in a county increases risks of introduction and potential release into wild pigs or domestic swine. We assumed that the size of the port is proportional to the volume of passengers, baggage and products. We scaled each port by the number of docks or runways as a proxy for total volume.

2.1 | Sensitivity analyses

Sensitivity analyses were run to quantify the impact of the model inputs on the relative risk ranking of counties, specifically changes in risk factor weights, ω . Parameter sets for the sensitivity analyses were created using Latin hypercube (LHC) sampling, selecting 100 values across the ranges of all risk factor weights allowing weights to range from 0.1 to 10. Each of the 100 parameter sets were used to calculate relative risk rankings within each year from 2010 to 2020 for each county resulting in 110,000 realizations of relative risk ranking for each of the 3072 counties for a total of 337,920,000 realizations.

To estimate the effect and relative importance of each model attribute, partial-rank correlation coefficients (PRCC) between the

county-level relative risk rank and the model attributes (both parameters and year) were used (Blower & Dowlatabadi, 1994). Prior to running the PRCC analysis, we checked the relationships between model attributes and county level relative risk rank to ensure that monotonicity assumptions were met. The PRCC estimates the effect of each model attribute on county-level relative risk rank, but we are also interested in the interactions between attributes (Buhnerkempe et al., 2014). To explore the effect of these interactions, we estimated sensitivities from regression coefficients. We checked the results from regressions without interaction terms to ensure results were similar to the PRCC, since the former includes an assumption of linearity. We then proceeded with the regression analyses that included the interaction terms between model attributes.

2.2 | Temporal change in risk

A primary advantage of our surveillance framework is the capacity to adapt surveillance in response to changes in the global distribution of disease through time as well as changes in host densities and connectivity. To investigate changes in surveillance prioritization through time, relative risk rankings were generated annually from 2010 to 2020. Four metrics were used to evaluate changes in relative risk ranking through time. First, to investigate the importance of a single county for surveillance through time the probability a county was ranked in the upper and lower 5-percentile, upper and lower 25-percentile and upper and lower 50-percentile in any given year was calculated. Additionally, the annual change in a county's risk rank percentile was evaluated. Two autocorrelation metrics were used to investigate county ranking variability through time. The autocorrelation function (ACF) was used to determine the correlation in ranking across different time lags and the partial autocorrelation function (PACF) was used to measure the linear correlation of each county time series with the lagged version of itself with the linear dependence of removed.

3 | RESULTS

3.1 | Sensitivity analyses

In the PRCC analyses, the attributes that were consistently important for determining relative risk rank were related to connectivity among wild pigs and domestic animals (Figure 2). Attributes important for determining relative risk rank were not associated with the variation in the risk factors (see Table S1). Changes in metrics for domestic animal host density had the least impact on relative risk ranking. Similarly, in the regression analyses, connectivity among wild pigs and domestic animals had large impacts on relative risk ranking (Figure 3). With the interactions included, some attributes became more important than they were in the PRCC analysis. Specifically, the interaction between domestic animal host density and introduction risks for domestic animals had the second largest impact on relative risk ranking. Most interactions had effects close to zero indicating little to no impact on

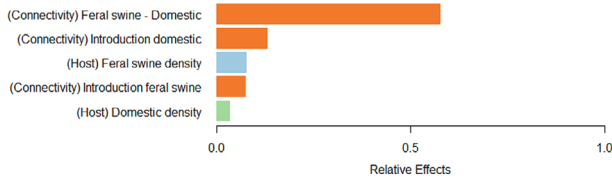


FIGURE 2 Results from partial-rank correlation coefficients (PRCC) sensitivity analysis for attributes used to determine targeted surveillance priorities. Connectivity among wild pigs and domestic animals had the largest impact on relative risk ranking

relative risk ranking. The adjusted r^2 value for the regression model was moderate ($r^2 = 0.51$), so the results and estimated magnitude of impact for each of the attributes should be considered cautiously.

3.2 | Relative risk ranking and temporal change in risk

The relative risk ranking of counties changed through time with an average $17.7\% \pm 0.018\%$ of counties having their risk rank change annually (Figures 4 and 5). The mean number of counties with an increase ($9.1\% \pm 0.013\%$) or decrease ($8.5\% \pm 0.016\%$) in risk ranking was similar but varied among years with the largest changes in risk ranking occurring in 2012 and 2017. Counties with a high probability of being in the upper 5-percentile and upper 25-percentile demonstrated spatial clustering (Figure 6). Those counties with the highest probability of being in the upper quartiles for risk were frequently in regions with high wild pig densities or areas with higher likelihood for introduction or potential contact among wild pigs and domestic animals. A

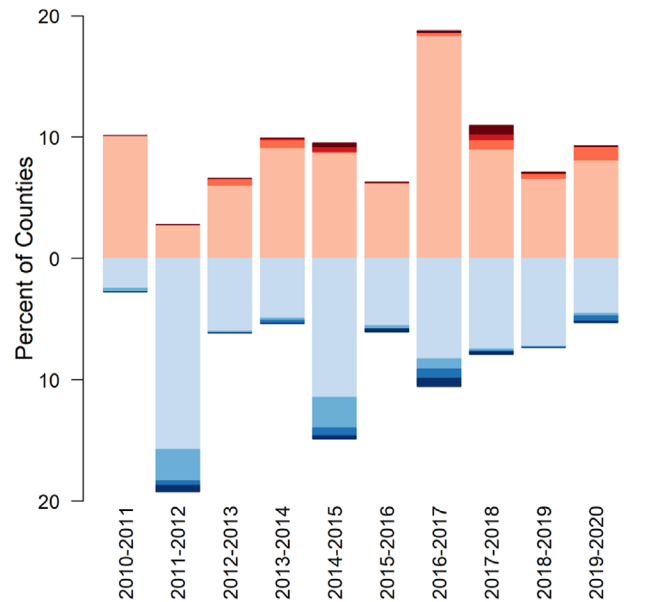


FIGURE 4 Percentage of counties that had a change in relative risk ranking quartile assignment from 2010 to 2020. On average 17.7% of counties change relative risk ranking annually. Most (15.9%) only change one quartile (light red and light blue) while a small percentage (1.8%) change more than one quartile (darker red and blue colours) when compared to the previous year ranking

small number of counties ($n = 36$, 1.2%) had a high probability (>0.90) of being included in the upper 5-percentile of risk ranking (Figure 6). Similarly, 552 (18%) of counties had a high probability (>0.90) of being ranking in the upper 25-percentile. Autocorrelation and partial autocorrelation in each counties risk ranking from 2010 to 2011 indicates large variation in the temporal autocorrelation (Figure S2). Most

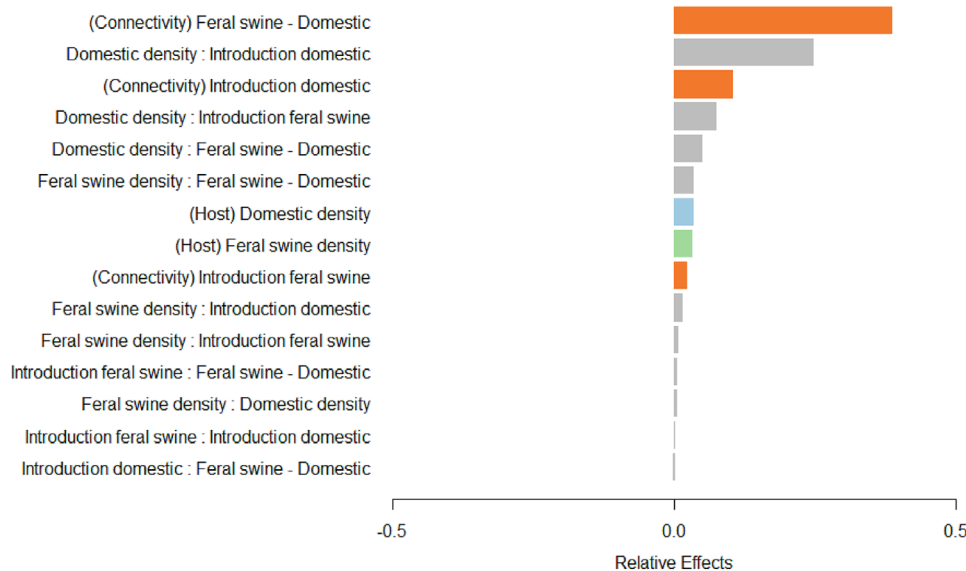


FIGURE 3 Sensitivity analysis showing relative effects (x-axis) of attributes used to generate relative risk ranking of counties to determine targeted surveillance priorities. The relative effect (x-axis) was estimated as linear model coefficients for the county level risk rank. Connectivity among wild pigs and domestic animals had the largest impact on risk ranking. Most interactions had little influence on relative risk ranking except for the interaction between domestic animal density and introduction risk into domestic animals that had the second largest impact on risk ranking

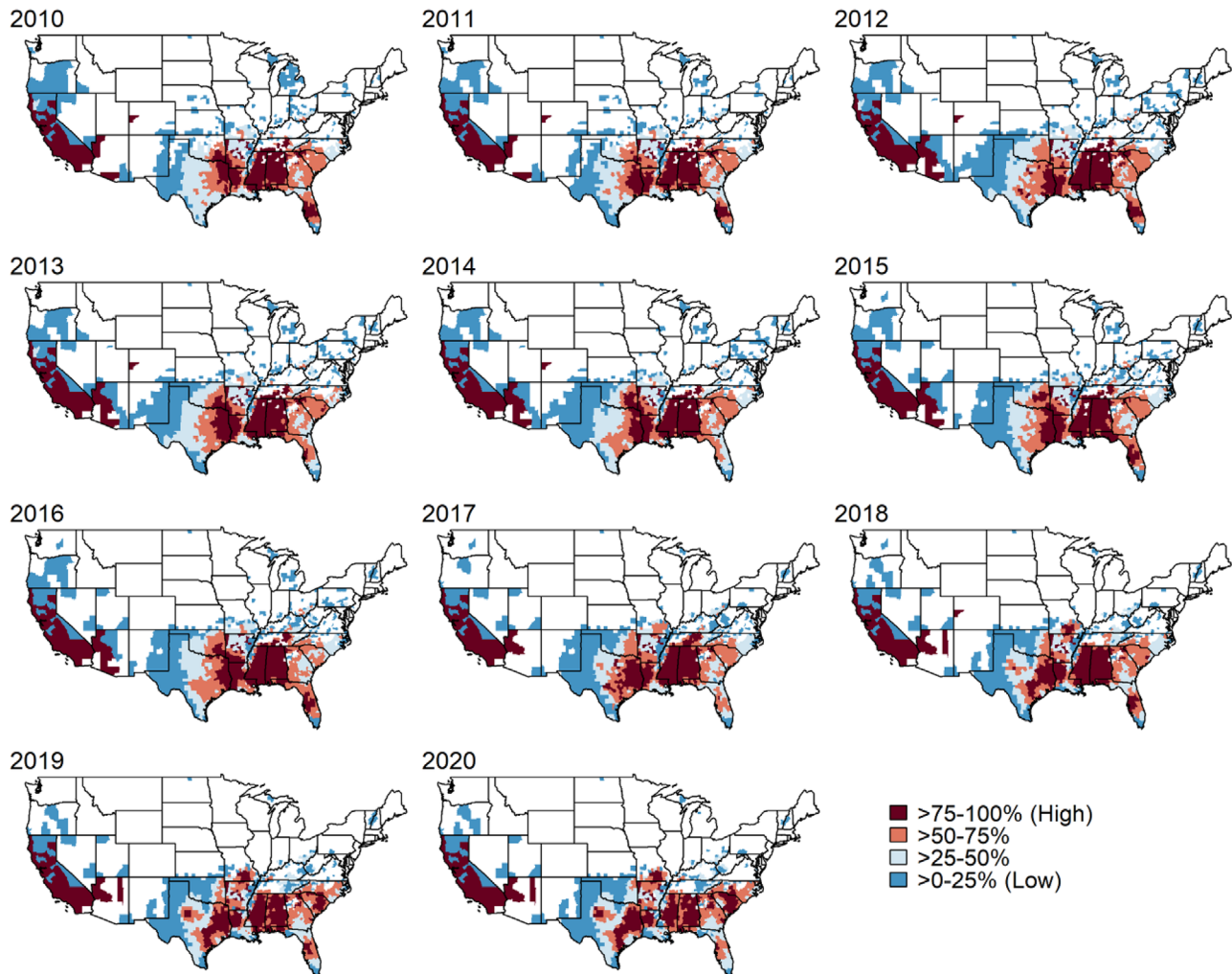


FIGURE 5 Annual relative risk ranking from 2010 to 2020 using no weighting of risk factors. Changes in relative risk ranking are apparent among years particularly in east Texas and states along the Atlantic coast

counties had positive linear correlation (mean = 0.36) in risk ranking among the first- and second-time lags. Partial autocorrelation also found a positive correlation with the first-time lag for most counties.

4 | DISCUSSION

Disease surveillance systems are a foundational element of the animal health infrastructure used to detect and respond to disease events and wildlife are an increasingly important component of these systems. Wildlife have the potential to be involved in at least 79% of OIE reportable diseases and once a livestock disease spills over into wildlife significant challenges for disease control or eradication can exist (Miller et al., 2013; VerCauteren & Miller, 2021). Once introduced, pathogens transmitted at the wildlife-domestic animal interface are challenging to manage and have a greater possibility for persisting and becoming enzootic due to spillover and spillback dynamics (Arias et al., 2018; Wiethoelter et al., 2015). Correspondingly, early identification of FADs in wildlife that is critical to minimize outbreak sever-

ity and potential impacts to wildlife, biodiversity and to animal agriculture. Surveillance frameworks are most useful when they are flexible, can be rapidly implemented and are targeted to the highest risk populations. The surveillance framework we developed addresses many of the challenges associated with identifying at-risk wildlife populations and designing surveillance systems for wildlife populations. Our framework supports representative sampling of at-risk populations, adapts to changes in risks through time, incorporates risk factors for both source and recipient populations and can be rapidly adjusted to address newly emerging diseases.

Applying this framework to determine targeted surveillance priorities in wild pigs we identified a small set of counties that remained high priority over a large range of weighting schemes. Identification of high priority areas demonstrates the value of using risk-based surveillance strategies to efficiently sample across national spatial extents. Only 1.2% of counties were in the upper 5% of risk ranking consistently. Strict opportunistic approaches to surveillance are likely to miss or under sample these high-risk populations. Additionally, we found a relatively large change in risk ranking annually across the 11 years we

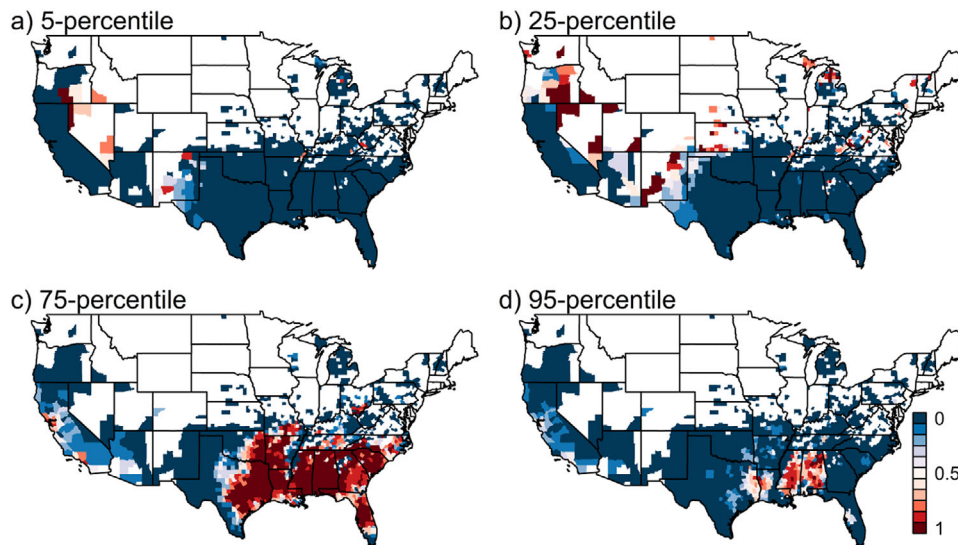


FIGURE 6 Annual mean probability a county is included in the upper and lower 5-percentile, upper and lower 25-percentile of relative risk ranking across all 110,000 possible weighting combinations for each county. Dark red indicates a high probability of being included in the relative risk rank percentile. Conversely dark blue indicates a low probability of being included in the relative risk rank percentile

investigated. This temporal change in risk highlights the importance of annually updating surveillance priorities based on changes in risk factors included in the framework. Relatively short (1–2 years) temporal autocorrelation of county level risk ranking in most counties indicates that static risk determination and surveillance prioritization may only be useful for a short period and may quickly result in misallocation of surveillance resources to areas that have become lower risk.

Wildlife disease surveillance efforts, particularly at the national scale, are fraught with challenges including difficulty designing representative sampling strategies, unvalidated diagnostic tools, inaccurate or incomplete denominator data and incomplete wildlife surveillance infrastructure (Ryser-Degiorgis, 2013; Stallknecht, 2007). When the goal of surveillance is early detection of an FAD in wildlife, obtaining the number of samples required for disease detection at a prevalence level (e.g., 0.01% with 95% confidence) useful for animal disease control may not be fiscally or logistically feasible at the national scale. Risk-based targeted surveillance approaches reduce the number of samples required for pathogen detection by focusing surveillance efforts to those populations at greatest risk for disease introduction while maintaining levels of detection useful for early detection of a FAD.

Once at-risk populations have been identified, an additional challenge for surveillance in wildlife populations is determination of a statistically valid sample size to meet surveillance system objectives (Sleeman et al., 2012). In the case of wildlife this is frequently due to the lack of population estimates for the at-risk population being surveyed. Targeted surveillance strategies help to lessen this challenge because the number of local populations to be surveyed is constrained reducing the geographic extent that population data are required. This allows for more focused development of data needed to develop population estimates to support determination of sample sizes required to meet surveillance system objectives.

Once populations important for surveillance are identified and sample sizes determined, a frequent limitation when conducting surveillance in wildlife is obtaining samples from at-risk host species. Sampling wildlife populations for disease is most frequently done using opportunistic surveillance of hunter harvested animals, through routine handling of wildlife during population monitoring activities (e.g., bird banding), or investigations of mass mortality events (Sleeman et al., 2012). Collecting samples via any of these methods can benefit from targeted sampling, due to logistical challenges of collecting from populations at national scales, especially when the objective of surveillance is early detection of a FAD that are expected to be a rare event. Targeting surveillance to those populations of greatest risk aids in reducing logistics at national scales. For example hunter harvest surveillance is typically implemented either through hunter check stations or in some cases self-reporting of harvest and presenting the animal for testing. Both approaches are logistically challenging and result in sampling that is unbalanced and spotty. However, focusing these methods to at-risk populations can improve sampling efficiency by improving logistics and increasing the capture of samples.

After samples have been acquired from at-risk populations a further complication is that diagnostic assays are frequently unvalidated in wildlife species which complicates interpretation of results and often results in reduced sensitivity of the overall surveillance system (Stallknecht, 2007). Consequently, sample sizes are frequently increased to compensate for reduced diagnostic sensitivity. While this may serve to improve the surveillance system sensitivity, the potential for false positive findings remains. False positive results can be a substantial consideration when conducting surveillance for OIE reportable diseases that can have negative economic impacts on domestic animal trade. This is of greatest concern when surveillance relies on serological assays of apparently healthy animals because tissue culture supporting confirmatory diagnostics may not be

available for the suspect animal and can take time to implement. However, with a targeted surveillance approach the at-risk population is defined and can be resampled to acquire the necessary tissues to support confirmatory diagnostic testing.

4.1 | Application of adaptive surveillance to address wildlife surveillance challenges

Adaptive management is an important concept that is often used to optimize temporal and spatial allocation of limited resources. In adaptive management frameworks, monitoring is structured to improve learning about the system by iterating between monitoring to reduce uncertainty about key drivers of management outcomes and then updating management strategies based on the improved knowledge (Williams et al., 2009). Adaptive management frameworks have been proposed as a tool to manage disease (Merl et al., 2009; Miller et al., 2013; Shea et al., 2014; Webb et al., 2017), optimize disease risk assessment (Miller & Pepin, 2019; Pepin et al., 2021) and apportion surveillance for pathogen detection (Gonzales et al., 2014), but have seldom been used in practice or implemented to design risk-based surveillance at national scales in domestic or wild species. Our framework incorporates adaptive management concepts by allowing new risk factors to be incorporated through time. Additionally, our results indicate updating surveillance priorities at regular intervals using the most recent risk factor data is important to prevent misallocation of limited surveillance resources. Designing surveillance plans that are adaptable is particularly important for emerging diseases because objectives will change from largely risk assessment to predominantly control if the disease is introduced into a new population (Clow et al., 2019).

4.2 | Application for rapidly implementing surveillance for emerging diseases

Our surveillance framework is founded in epidemiological theory (Pepin et al., 2021; Plowright et al., 2017) and utilizes the principle components of initial disease introduction, presence of suitable host populations and contact among host populations to identify at-risk populations that can be prioritized for surveillance (see Figure 1). Empirical data can be used to inform these transmission risk components or, in the case of emerging diseases that have limited or no empirical data available, proxy information representing likely or hypothesized risk factors can be used. In its most basic implementation presence/absence information for the at-risk host populations and proxy information on pathways of introduction (e.g., airline passenger movements or product shipments from regions where the disease occurs) can be used to rapidly identify and triage populations for surveillance. As new information emerges on risk factors associated with transmission, host range, environmental persistence, or pathways of introduction (anthropogenic or wildlife movement) data representing these risk factors can be incorporated into the framework

and surveillance targeting further improved (Cook et al., 2019). Additionally, risk factor uncertainty can be addressed by conducting a sensitivity analysis to identify those regions and populations that are invariant to changes in risk factor ranking (see Figure 6).

4.3 | Future improvements: Incorporating dynamical models

Our adaptive risk-based targeted surveillance framework greatly improves upon traditional surveillance strategies that are largely opportunistic or utilize coarse risk factors that are static through time, however, there are opportunities to improve. The current framework does not currently incorporate potential consequences of a disease introduction—that is surveillance should also be focused on populations where the consequences (outbreak size, economic costs, etc) are large. Our framework can be further improved by incorporating mechanistic models—that is, articulating the potential hierarchical or non-linear relationships that may exist between risk factors or different species involved in the disease system. Models that allow risk to vary through time based on epidemiological mechanisms (e.g., compartmental models that track susceptible and infected individuals) can improve effective risk-based surveillance approaches by concurrently evaluating how changes in introduction risk, host populations, implementation of surveillance, species sampled and subsequent disease control affect time-to-detection and potential outbreak severity (Comin et al., 2012; Miller & Pepin, 2019). Mechanistic modelling approaches allow the inclusion of factors that may influence the likelihood of transmission among wildlife and domestic animals such as poor domestic animal biosecurity or frequency of contact. Furthermore, because the mechanisms governing transmission risks are explicitly included a more integrated approach to surveillance is possible allowing allocation of surveillance effort to both domestic and wildlife species proportional to their risk.

Using mechanistic models, a fully probabilistic approach can be implemented that would improve upon the relative risk approach we developed. Furthermore, formal optimization approaches can be used to determine the optimal spatial distribution and frequency of sampling that minimizes costs while maximizing risk reduction (Gonzales et al., 2014). The integration of mechanistic models into surveillance optimization has significant benefits for emergency preparedness. In the event of a FAD introduction, the models can be immediately used with existing surveillance data to predict areas where the disease may be present but undetected. Mechanistic approaches capture the variation that could occur over space and time because risk predictions will change with the state of the system. Changes in the state of the system can result from intrinsic processes (e.g., birth pulses) that do not correlate explicitly with a covariate-only statistical approach. Additionally, because mechanistic approaches capture variation in the underlying process of the system quantities such as time-to-detection of cases can be estimated and used to inform predictions of outbreak severity and, in turn, allocation of resources to improve response activities. Finally, mechanistic models are useful for evaluating control actions allowing

alternative control policies to be evaluated quickly. Mechanistic models can be adjusted as new surveillance data become available improving our understanding of the systems epidemiology (e.g., which transmission factors are more important), that can provide more precise predictions for risk assessment and improve our knowledge for developing the best control strategies.

5 | CONCLUSION

Surveillance frameworks that are founded in epidemiological theory and can be rapidly scaled to meet new and emerging disease threats are most useful for national scale FAD surveillance and are particularly useful for wildlife. Our adaptive risk-based targeted surveillance approach is flexible, accounts for changing disease risks through time, can be scaled from local to national extents and permits the inclusion of quantitative data or when information is limited to expert opinion. Additionally, it can be used to alleviate many of the challenges associated with identifying at-risk wildlife populations of importance for surveillance. Our framework is an advancement for developing surveillance systems in wildlife at national scales. There remains an opportunity to advance our framework using mechanistic modelling approaches that would integrate surveillance targeting and disease control evaluation thus improving both efficiency of the surveillance system as well as emergency preparedness.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

ETHICAL STATEMENT

The authors confirm to adhere to the ethical policies of the journal. No ethical approval was required as this is an original research article that did not use experimental data.

DATA AVAILABILITY STATEMENT

The data that support the findings will be available in [repository name] at [DOI/URL] following an embargo from the date of publication to allow for commercialization of research findings.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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