11-1-2018

Predicting the initial spread of novel Asian origin influenza A viruses in the continental USA by wild waterfowl

Alan. B. Franklin
APHISWS National Wildlife Research Center, alan.b.franklin@aphis.usda.gov

Sarah N. Bevins
APHISWS National Wildlife Research Center

Jeremy W. Ellis
APHISWS National Wildlife Research Center

Ryan S. Miller
APHIS-VS Center for Epidemiology and Animal Health

Susan A. Shriner
APHISWS National Wildlife Research Center

See next page for additional authors

Received: 11 May 2018 | Revised: 5 October 2018 | Accepted: 1 November 2018

DOI: 10.1111/tbed.13070

ORIGINAL ARTICLE

WILEY Transboundary and Emerging Diseases

Predicting the initial spread of novel Asian origin influenza A viruses in the continental USA by wild waterfowl

Alan. B. Franklin[1] | Sarah N. Bevins[1] | Jeremy W. Ellis[1] | Ryan S. Miller[2] | Susan A. Shriner[1] | J. Jeffrey Root[1] | Daniel P. Walsh[3] | Thomas J. Deliberto[1]

[1]U. S. Department of Agriculture, APHIS-WS National Wildlife Research Center, Fort Collins, Colorado

[2]U. S. Department of Agriculture, APHIS-VS Center for Epidemiology and Animal Health, Fort Collins, Colorado

[3]U. S. Geological Survey, National Wildlife Health Center, Madison, Wisconsin

Correspondence
Alan B. Franklin, U. S. Department of Agriculture, APHIS-WS National Wildlife Research Center, Fort Collins, CO.
Email: alan.b.franklin@aphis.usda.gov

Funding information
Animal and Plant Health Inspection Service

Summary

Using data on waterfowl band recoveries, we identified spatially explicit hotspots of concentrated waterfowl movement to predict occurrence and spatial spread of a novel influenza A virus (clade 2.3.4.4) introduced from Asia by waterfowl from an initial outbreak in North America in November 2014. In response to the outbreak, the hotspots of waterfowl movement were used to help guide sampling for clade 2.3.4.4 viruses in waterfowl as an early warning for the US poultry industry during the outbreak . After surveillance sampling of waterfowl, we tested whether there was greater detection of clade 2.3.4.4 viruses inside hotspots. We found that hotspots defined using kernel density estimates of waterfowl band recoveries worked well in predicting areas with higher prevalence of the viruses in waterfowl. This approach exemplifies the value of ecological knowledge in predicting risk to agricultural security.

KEYWORDS

Eurasia, influenza A virus, pathogen introduction, surveillance, waterfowl

1 | INTRODUCTION

Most countries, including the USA, have been at increasing risk of novel emerging pathogens that affect human, agricultural and wildlife health (Endy, Rochford, Yuen, & Lei, 2011; Jones et al., 2008), a number of which have severe economic consequences (Fonkwo, 2008). Oftentimes, wildlife serve as maintenance hosts for these pathogens, which can be directly or indirectly transmitted to agricultural operations and humans (Daszak, Cunningham, & Hyatt, 2000). After detection of a high-pathogenic H5N8 strain of influenza A (clade 2.3.4.4) in wild birds and poultry in Asia and Europe, a reassortant H5N2 virus was isolated from samples collected during domestic poultry outbreaks in British Columbia, Canada in November 2014 (Ip et al., 2015). Presumably, reassortant H5N1, H5N2, and H5N8 likely emerged in North America after introduction of a high-pathogenic clade 2.3.4.4 H5N8 from Asia (Lee et al., 2016). The high-pathogenic H5N2 and H5N8 reassortants (collectively referred to as clade 2.3.4.4 H5 viruses hereafter) subsequently spread through the Pacific Northwest and Midwestern USA (Hill et al., 2017; Lee et al., 2016; Ramey et al., 2017), where they caused devastating outbreaks for the poultry industry with economic losses of over $3 billion (Greene, 2015).

Wild waterfowl and shorebirds are the natural reservoirs for influenza A viruses, most of which are considered low-pathogenic (Webster, Bean, Gorman, Chambers, & Kawaoka, 1992). While clade 2.3.4.4 H5 viruses are high-pathogenic to domestic poultry, they cause negligible mortality in wild waterfowl, such as mallards (*Anas platyrhynchos*) (Kang et al., 2015; Pantin-Jackwood et al., 2016). Although mallards exhibited elevated body temperature and weight loss after infection with clade 2.3.4.4 H5 viruses, these signs probably did not substantially impede movement of viruses by infected individuals during migrations (Pantin-Jackwood et al., 2016). Phylogenetic analyses have shown intercontinental mixing of avian influenza viruses in waterfowl at the Alaskan-Siberian interface (Ramey, Pearce,

Ely et al., 2010; Ramey, Pearce, Flint et al., 2010), where ~1 million waterfowl annually commingle (Winker & Gibson, 2010). For these reasons, migratory waterfowl have been strongly implicated in the global spread and subsequent introduction of high pathogenic Asian origin H5 into the USA (Global Consortium for H5N8 and Related Influenza Viruses, 2016, Lee et al., 2015). Evidence for this putative role includes viral presence in multiple species of apparently healthy waterfowl, genetic similarities between waterfowl and poultry viruses on different continents, and correlation of outbreaks with waterfowl movement patterns (Lee et al., 2015; Verhagen, Herfst, & Fouchier, 2015). Thus, wild waterfowl with Holarctic distributions and the potential for intercontinental mixing of populations during migration, such as mallards, northern pintails (*Anas acuta*), and northern shovellers (*Anas clypeata*), were logical targets for surveillance to determine the potential spread of clade 2.3.4.4 H5 viruses from the initial outbreak area in North America.

Here, we tested a quantitative approach for predicting spatial spread of clade 2.3.4.4 H5 viruses by wild waterfowl during an emergency-response situation with the implicit assumption that presence of these viruses in wild waterfowl in an area poses a risk of transmission to poultry within that region. Once the initial outbreak was detected in British Columbia, the immediate question was: *Where would clade 2.3.4.4 H5 viruses likely be spread by waterfowl migrating from the outbreak area?* To address this question, we used band-recovery data from migratory waterfowl to identify areas (hotspots) of waterfowl movement where clade 2.3.4.4 H5 viruses might spread by waterfowl migrating from the outbreak area. These hotspots were one of several factors initially used to help guide sampling waterfowl for detection of clade 2.3.4.4 H5 viruses during the emergency response to the outbreak of these viruses. Since actual sampling, due to expediency of maximizing sample size, was conducted both outside and within hotspots, we were able to test whether our strategy using hotspots of concentrated waterfowl movement were useful for improving detection of clade 2.3.4.4 H5 viruses.

2 | METHODS

Band-recovery data coupled with sampling of wild waterfowl for clade 2.3.4.4 H5 viruses served as the basis of our analyses. Band-recovery data have been programmatically collected and archived in North America since the 1920s (Tautin, Metras, & Smith, 1999); data on individually marked birds include the spatial locations of where an individual was banded and where it was recovered. For waterfowl, recoveries primarily occur through hunter harvesting and reporting of banded individuals.

2.1 | Developing hotspot sampling strategy

In response to the initial outbreak in British Columbia, Canada, we assembled the band-recovery data we had on hand, which included waterfowl band recoveries from 1976-2007 previously obtained from the US Geological Survey Bird Banding Laboratory (USGS BBL; https://www.usgs.gov/centers/pwrc/science/north-american-bird-band-laboratory). Although not current, the urgency of the situation did not allow for additional data acquisition, but the scale of the data encompassed the overall movement patterns of waterfowl from the outbreak area. From this initial database, we used band-recovery data from birds banded in southern British Columbia and northern Washington (Figure 1). This area was selected to include both the initial outbreak area in British Columbia (Fraser Valley), as well as the first detection of clade 2.3.4.4 H5 viruses on the US side of the border, which occurred several weeks later at Wiser Lake, Washington (Ip et al., 2015), and provided sufficient banding data for analysis. We further constrained these data using (a) only birds banded from May through December of each year to avoid spring migrants (i.e., we assumed birds banded between May-December would only include residents and fall migrants), and (b) data only from mallards (61.0% of species with H5 subtypes), American green-winged teal (8.9%), blue-winged teal (5.9%), Northern pintail (4.7%), Northern shoveller (4.7%), American wigeon (4.7%) and unidentified Teal (Table 1), based on the Holarctic distribution of some species and previous surveillance data on low-pathogenic H5 subtypes found in waterfowl (Bevins et al., 2014). We defined these species as our initial target species.

We used the band-recovery data (n = 8,841) from these initial target species banded in the H5 outbreak area (Figure 1) and examined areas across the USA and Canada for frequency of recoveries of these birds. We estimated frequency as (a) *density of recoveries* in 10-minute latitude-longitude blocks as defined by the USGS BBL (Gustafson, Hildenbrand, & Metras, 1997) to identify areas where banded birds from the outbreak were frequently recovered and (b) *relative density of recoveries* using a kernel density estimator within the Geospatial Modelling Environment programme (Beyer, 2014) with a plug-in bandwidth estimation algorithm (Chu, Henderson, & Parmeter, 2015), a cell size of 0.1 units and a Gaussian kernel. GIS layers were developed based on these two estimates to identify hotspots that could be sampled for clade 2.3.4.4 H5 viruses that may have been moved by wild waterfowl during fall migration.

Based on the distribution of band recoveries, we focused our subsequent analyses in the Pacific Flyway, because it was the primary migration corridor for waterfowl found in and around the initial outbreak. We also confined the analyses to the continental USA because of differing surveillance strategies in Canada and Mexico and the immediate need to understand movement of the virus relative to poultry production in the USA.

As recovery data for waterfowl in North America is primarily collected from hunter harvested birds, our density estimates may be biased by hunter attributes and behaviour and may not completely represent waterfowl movement (Lavretsky, Miller, Bahn, & Peters, 2014). Thus, an underlying assumption in using band-recovery data is that areas and seasons for waterfowl hunting also correspond to waterfowl concentration areas (Buhnerkempe et al., 2016; Farnsworth et al., 2011). Although imperfect, these data represent the best available large-scale movement data for waterfowl over both

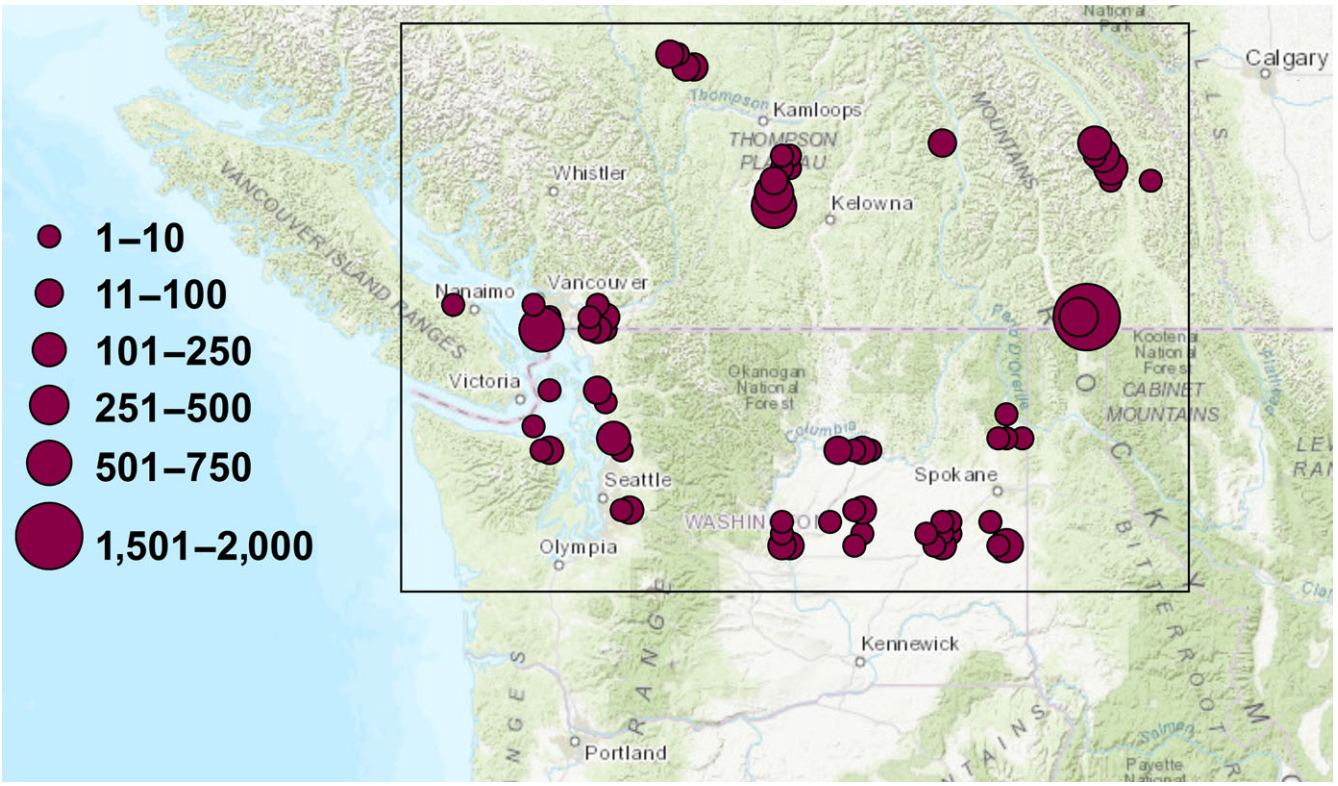


FIGURE 1 Area (black outline) of southern British Columbia and northern Washington from which data on banded waterfowl were used in analysis of band recoveries. Maroon circles are locations where waterfowl were initially banded with the circle size representing numbers banded that were subsequently recovered. Blue stars indicate the initial outbreaks of clade 2.3.4.4 H5 viruses in poultry and captive birds. Base map is the World Topographic Map from ESRI® (http://www.arcgis.com/home/item.html?id=30e5fe3149c34df1ba922e6f5bbf808f)

time and space and are useful for rapid risk assessment situations at regional and national scales (Miller, Sweeney, Akkina, & Saito, 2015).

2.2 | Testing the hotspot sampling strategy

We used 3,437 oral and cloacal swab samples collected from wild waterfowl over 43 days between 20 December 2014 and 1 February 2015 with known sample locations in Washington, Oregon, Idaho and California (Bevins et al., 2016). Although our initial sampling strategy was used to guide the collection of these samples, samples were collected throughout the region, both within the hotspots we identified and in multiple other areas. For example, sampling was done in 10 priority watersheds (Bevins et al., 2016), which included varying degrees of recovery density. We used the influenza A assay results from these samples (Bevins et al., 2016) to test whether areas with high densities of waterfowl recoveries yielded a higher probability of detecting clade 2.3.4.4 H5 viruses south of the outbreak areas, compared to areas predicted by our mapping to have few or no waterfowl recoveries.

We analysed these data using generalized linear models with a binomial distribution and logit link (SAS Institute Inc., 2013) to assess the predictive ability of density and kernel density of band recoveries in the probability of detecting clade 2.3.4.4 H5 viruses from sampled wild birds. We used a normalized transform of kernel density estimates and also classified kernel density estimates into three hotspot categories, where Hotspot1 retained the upper 95% of the kernel density estimates (corresponded closely to the original sampling areas proposed), Hotspot2 retained the upper 67% of the kernel density estimates and Hotspot3 retained the upper 33% of the kernel density estimates. Although the cut-off values were somewhat arbitrary, they represented terciles with Hotspot1 being the most inclusive and Hotspot3 being the most restricted. These variables were used to see if different hotspot configurations would improve the fit of the statistical models examined. We used a model selection framework with Akaike's Information criterion to asses which statistical models best fit the data (Burnham & Anderson, 2002). We initially examined logit, probit, and complementary log-log link functions in a global model; the latter link functions are often used when positive samples are rare. However, there was little difference in Akaike weights (w_i = 0.317–0.364) so we used a logit link in subsequent analyses. To keep the size of the model set reasonable, we used a three-stage approach in developing statistical models (Doherty, White, & Burnham, 2012). In the first stage, we examined models with either band-recovery density, transformed kernel density (Kernel) or the three categories of hotspots (where samples were either in or out of the hotspot) as single predictor variables in the

TABLE 1 Low-pathogenic H5 avian influenza virus subtypes found in waterfowl species in the USA during avian influenza virus surveillance in wild birds from 2007-2011 (Bevins et al., 2014), prior to the initial outbreak of clade 2.3.4.4 H5 viruses in North America

	H5 avian influenza virus subtype										
Species	H5N?	H5N1	H5N2	H5N2, N8	H5N3	H5N5	H5N6	H5N7	H5N8	H5N9	Total
Mallard		6	75	1	11	3	2	1	1	3	103
Green-winged teal			15								15
Blue-winged teal			8		2						10
Northern pintail			7		1						8
Northern shoveller	1		6		1						8
American wigeon			7		1						8
Black duck		1	5		2						8
Ring-necked duck			2								2
Canada goose		1	1								2
Unidentified duck			1								1
Mute swan			1								1
Cackling goose			1								1
Wood duck					1						1
Common eider			1								1
Total	1	8	130	1	19	3	2	1	1	3	169

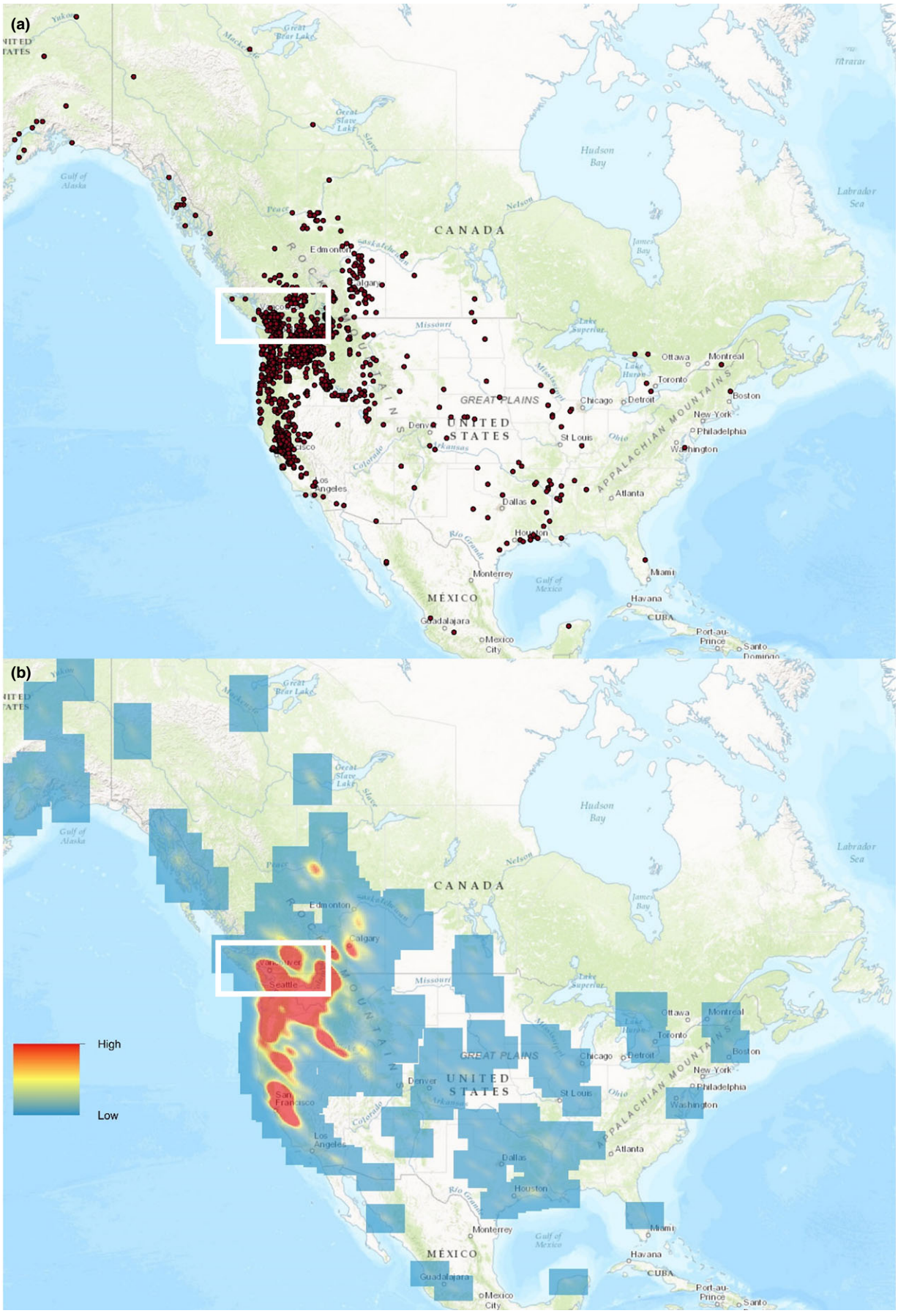
models. We then used the model with the highest Akaike weight in the second modelling stage where we examined the effect of states, either singly (state = WA, OR, ID and CA separately) or grouped (state1 = WA, OR and ID combined, versus CA; state2 = WA versus OR and ID combined versus CA; state3 = WA, OR, and CA combined versus ID). Using the model with highest Akaike weight from the second stage, we then explored additional models in the final stage that included the number of days since the start of the initial outbreak (Outbreak Days) as both a linear and quadratic variable and a categorical variable whether waterfowl sampled were target species or not (Target). Latitude was not included because it was correlated with Outbreak Days (r = –0.62). The model with the highest Akaike weight from this stage was considered the model best explaining the data. We examined the predictive capability of this model using receiver operating characteristic (ROC) curves (Park, Goo, & Jo, 2004), where the area under the ROC curve measures the overall diagnostic performance (ranging from 0.5 to 1.0) of our best model in predicting where clade 2.3.4.4 H5 viruses in wild waterfowl would occur, based on band-recovery data.

3 | RESULTS

Using the data from resident and non-resident waterfowl banded during May-December in and spatially proximate to the outbreak areas from 1976-2007, we mapped recovery locations to determine likely movement paths (Figure 2). Recoveries from individuals originally banded in the outbreak area were concentrated primarily in the Pacific Flyway (defined here as Washington, Oregon, California and Idaho) both spatially (Figure 2a) and by density (Figure 2b). However, it was evident from this mapping exercise that there was potential for waterfowl to move the viruses across the USA and into Mexico (Figure 2a). Fifteen (0.2%) of 8,841 recoveries were in states (North Dakota, South Dakota, Nebraska, Minnesota, Iowa, and Wisconsin) that experienced numerous outbreaks of clade 2.3.4.4 H5 viruses in commercial poultry farms (Bui, Gardner, & MacIntyre, 2016). In one case, a mallard banded in August 2000 in the British Columbia outbreak area was recovered in November that same year in Iowa, indicating that cross-continental movement of waterfowl does occur.

In coupling the band-recovery and clade 2.3.4.4 H5 data, the best-fitting model for explaining presence/absence of clade 2.3.4.4 H5 viruses included the upper 95% of the kernel density estimates, a quadratic relationship with the number of days since the initial outbreak, and a categorical state variable (Washington, Oregon and Idaho combined, and California) (Table 2, Figure 3). Of the samples used in our analysis, 923 samples were collected outside the hotspots while 2,514 samples were collected inside those areas. Parameter estimates for this model were precise (Table 3) and indicated that presence of clade 2.3.4.4 H5 viruses in wild waterfowl was more likely found in hotspots of waterfowl band recoveries (Figure 3). Based on the estimated odds ratio, clade 2.3.4.4 H5 viruses were 2.8 times (95%

FIGURE 2 Recoveries of waterfowl in North and Central America from birds banded in the initial clade 2.3.4.4 H5 outbreak area with (a) locations of recovered individuals, and (b) map of kernel density of recovered individuals. White rectangle encompasses the initial outbreak area where recovered individuals were originally banded. Base map is the World Topographic Map from ESRI® (http://www.arcgis.com/home/item.html?id=30e5fe3149c34df1ba922e6f5bbf808f)


(a)
CANADA
UNITED STATES
MÉXICO
GREAT PLAINS
APPALACHIAN MOUNTAINS
ROCKY MOUNTAINS
Edmonton
Calgary
Vancouver
Seattle
San Francisco
Los Angeles
Denver
Chicago
Detroit
Toronto
Ottawa
Montreal
Boston
New York
Philadelphia
Washington
St Louis
Atlanta
Dallas
Houston
Miami
Monterrey
Guadalajara
Mexico City
Havana
CUBA
Port-au-Prince
Hudson Bay
Labrador Sea
Gulf of Alaska
Great Bear Lake
Great Slave Lake
Lake Superior
Lake Huron
Missouri
Ohio
Colorado
Rio Grande
Gulf of Mexico
(b)
High
Low

confidence limits = 1.2, 8.3) more likely to be detected inside hotspots than outside hotspots. In addition, presence of clade 2.3.4.4 H5 viruses increased to a peak about a month after the initial outbreak and then decreased over time. Viral detection also increased as sampling progressed south from Washington to California (Figure 4). The odds of detecting clade 2.3.4.4 H5 viruses were 4.9 (95% confidence limits = 2.2, 12.0) and 4.3 (95% confidence limits = 1.6, 11.9) more likely to be detected in Oregon and California, respectively, than in Washington. The area under the ROC curve for this model was 0.733 (95% confidence intervals = 0.664, 0.802), indicating the model reasonably predicted the presence of clade 2.3.4.4 H5 viruses in waterfowl, especially in Oregon, Idaho, and California.

4 | DISCUSSION

The use of band-recovery data to predict potential movement of influenza A viruses in North America has been previously proposed (Doherty et al., 2009; Miller et al., 2015) but never implemented in an emergency-response situation. Despite being a reactive approach to quickly respond to the initial outbreak of clade 2.3.4.4 H5 viruses in North America, our analyses demonstrated that the approach worked well in identifying areas where wild birds were likely to further spread clade 2.3.4.4 H5 viruses to high density poultry production areas, such as the Sacramento Valley in California, which is one of the top 10 poultry production areas in the USA (National

TABLE 2 Model selection results for the three stage model selection framework in selecting generalized linear models predicting presence of clade 2.3.4.4 H5 influenza A virus in wild waterfowl in the Pacific flyway of the USA

Model	−2lnL	K	AIC	AICc	ΔAICc	Akaike Weight
Stage 1						
Intercept	462.239	1	464.239	464.240	4.064	0.098
Hotspot1	**456.173**	**2**	**460.173**	**460.176**	**0.000**	**0.749**
Hotspot2	462.128	2	466.128	466.132	5.955	0.038
Hotspot3	462.032	2	466.032	466.036	5.859	0.040
Kernel	462.206	2	466.206	466.210	6.034	0.037
Density	462.137	2	466.137	466.140	5.964	0.038
Stage 2						
State+Hotspot1	446.650	5	456.650	456.667	1.616	0.208
State+Hotspot1 + State*Hotspot1	442.114	8	458.114	458.154	3.103	0.099
State1 + Hotspot1	456.045	3	462.045	462.051	7.000	0.014
State1 + Hotspot1 + State1*Hotspot1	449.260	4	457.260	457.271	2.219	0.154
State2 + Hotspot1	**447.040**	**4**	**455.040**	**455.052**	**0.000**	**0.467**
State3 + Hotspot1	453.908	3	459.908	459.914	4.863	0.041
State3 + Hotspot1 + State3*Hotspot1	453.668	4	461.668	461.679	6.628	0.017
Stage 3						
Outbreakdays	455.853	2	459.853	459.857	15.230	0.000
Ln(Outbreakdays)	457.162	2	461.162	461.165	16.539	0.000
Outbreakdays^2	450.980	3	456.980	456.987	12.361	0.001
Outbreakdays+Hotspot1	453.120	3	459.120	459.127	14.501	0.000
Outbreakdays^2+Hotspot1	448.902	4	456.902	456.913	12.287	0.001
Outbreakdays+State2 + Hotspot1	440.494	5	450.494	450.511	5.885	0.027
Outbreakdays^2+State2 + Hotspot1	**432.602**	**6**	**444.602**	**444.626**	**0.000**	**0.511**
Outbreakdays^2+State2 + Kernel	436.802	6	448.802	448.826	4.200	0.063
Outbreakdays^2+State2 + Density	437.928	6	449.928	449.953	5.326	0.036
Outbreakdays^2+State2	437.928	5	447.928	447.946	3.320	0.097
Outbreakdays+State2 + Hotspot1 + Outbreakdays*Hotspot1	437.738	6	449.738	449.762	5.136	0.039
Outbreakdays+State2 + Hotspot1 + Outbreakdays*State2	440.369	7	454.369	454.402	9.775	0.004
Target	462.2060	2	466.206	466.209	21.583	0.000
Target+Hotspot1	456.0980	3	462.098	462.105	17.479	0.000
Target+State2 + Hotspot1	446.8934	5	456.893	456.911	12.285	0.001
Target+Outbreakdays+State2 + Hotspot1	440.2692	6	452.269	452.294	7.667	0.011
Target+Outbreakdays^2+State2 + Hotspot1	432.3826	7	446.383	446.415	1.789	0.209

Bolded values indicate the best model within each stage based on minimum AICc.

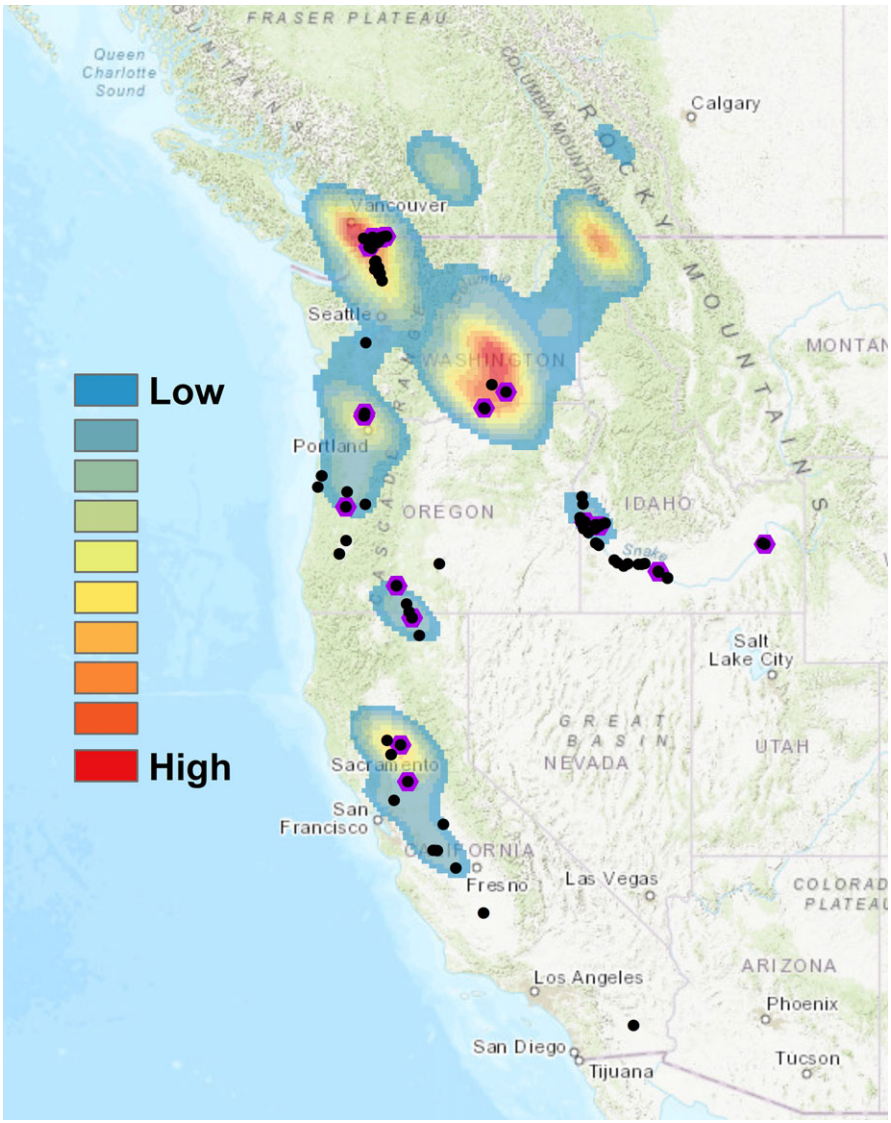


FIGURE 3 Hotspots of the upper 95% of kernel density estimates of band recoveries (Hotspot1) and locations of clade 2.3.4.4 H5 positive (purple polygons) and negative (black dots) samples. Some sample locations contain multiple samples. Base map is the World Topographic Map from ESRI® (http://www.arcgis.com/home/item.html?id=30e5fe3149c34df1ba922e6f5bbf808f)

Agricultural Statistics Service, 2015). While we found generally lower detectability in Washington, this may have been a function of the timing of wild bird sampling occurring; viruses had already started to move through the region after the initial outbreak in British Columbia, Canada and became more prevalent further south during fall migration.

Although sampling effort was higher in the hotspots in our best model, hotspot identification was only one of several criteria used to determine sampling locations. The resultant distribution of sampling locations both inside and outside hotspots provided the opportunity to retrospectively test our approach. In addition, the imbalance of sampling effort does not by itself bias the parameter estimates in logistic regression and oversampling can improve estimates if the oversampling resembles the underlying distribution of the original population (Crone & Finlay, 2012; Oommen, Baise, & Vogel, 2011).

In emergency outbreak situations, decisions and strategies must be developed and implemented rapidly; band-recovery data were an easily accessible resource that could be integrated into a targeted sampling strategy that could be deployed quickly. A number of studies (Bridge et al., 2014; Gunnarsson et al., 2012) have employed satellite telemetry, genetics and stable isotopes to link waterfowl movement with large-scale spatial and temporal distributions of

TABLE 3 Maximum likelihood parameter estimates for the best-fitting generalized linear model predicting presence of clade 2.3.4.4 H5 influenza A viruses in wild waterfowl in the Pacific flyway of the USA

Parameter	Estimate	Standard error	Profile likelihood 95% confidence intervals
Intercept	−10.860	2.640	−16.034, -5,687
Number of Outbreak Days	0.326	0.146	0.039, 0.612
(Number of Outbreak Days)^2	−0.005	0.002	−0.009, −0.001
California[a]	1.457	0.504	0.470, 2.444
Oregon & Idaho	1.583	0.429	0.742, 2.424
Kernel Density Hotspot	1.022	0.492	0.058, 1.986

[a]Parameter estimates for California and Oregon & Idaho are relative to Washington state.

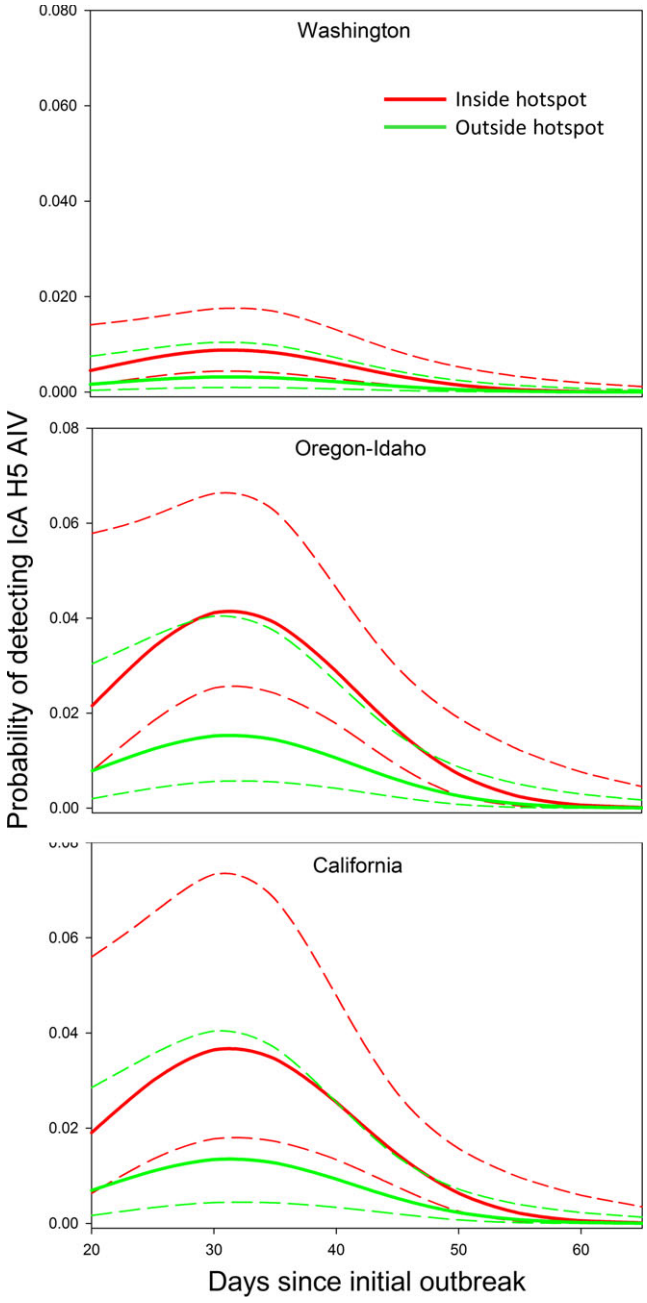


FIGURE 4 Probability of detecting clade 2.3.4.4 H5 influenza A virus in wild birds as a function of state, days since the initial outbreak in British Columbia, Canada, and whether the sample was collected inside or outside a hotspot (Hotspot1) boundary. Dashed lines represent 95% confidence intervals

avian influenza viruses. While excellent tools for research, these techniques are not always feasible to rapidly inform emergency-response situations because they provide information after sampling has taken place rather than guiding sampling in the beginning. The accumulation of data sets on waterfowl movement using these techniques in publicly available repositories, such as MoveBank (www.movebank.org), can provide additional information that can be combined with band-recovery data to incorporate into emergency-response exercises. However, waterfowl recovery data are currently the best available data to capture broad-scale distributions of waterfowl populations in the USA (Farnsworth et al., 2011).

Of interest was the within-season movement of a mallard from the outbreak area to Iowa. This suggests migratory west-to-east movement of viruses carried by waterfowl might occasionally occur in addition to typical north-to-south migratory pathways (Buhnerkempe et al., 2016; Bui et al., 2016) and offers one explanation of how clade 2.3.4.4 H5 viruses could have jumped from the outbreak area to the Midwestern USA, where extensive outbreaks in poultry occurred 4 months after the initial outbreak.

In May 2017, there were 161 ongoing outbreaks of very similar H5N8 influenza A viruses and its reassortants in both wild birds and poultry in Europe, Asia, and Africa with almost 4 million poultry destroyed to contain the outbreaks (World Organisation for Animal Health, 2017). Thus, the potential for introduction of these viruses into the USA or further spread of clade 2.3.4.4 H5 viruses within the USA by wild waterfowl remains a looming threat. While our reactive approach worked well, it could be improved considerably by (a) proactively integrating it with current surveillance strategies (e.g., Bevins et al., 2014), (b) integrating it with larger scale band-recovery models that could track cross-continental spread (e.g., Doherty et al., 2009), and (c) incorporating more rigorous estimators into the predictive modelling process (e.g., Buhnerkempe et al., 2016). Approaches, such as those presented here, can be used to predict general foci where pathogens are likely to be moved by migratory waterfowl. As seen in the introduction of clade 2.3.4.4 H5 viruses into North America, prediction of specific hotspot locations for the spatial spread of novel pathogens will be an increasingly important part of early-warning systems for enhancing biosecurity at agricultural operations in those locations. By integrating ecological knowledge into predictions of outbreak risk of pathogens carried by wildlife, more proactive management of novel pathogen introductions can be realized and can mitigate the severity of economic consequences (Grant et al., 2017).

ACKNOWLEDGEMENTS

This research was supported by the intramural research programme of the US Department of Agriculture, Animal and Plant Health Inspection Service. All data are archived at the Information Services Unit of the National Wildlife Research Center, Fort Collins, Colorado. We thank numerous personnel from the Idaho Department of Fish and Game, the Oregon Department of Fish and Wildlife, USDA-Wildlife Services and USGS National Wildlife Health Center who collected samples in the field (Bevins et al., 2016). We also thank Jeffrey Hall for reviewing earlier drafts of the manuscript. Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the US Government.

CONFLICT OF INTEREST

The authors declared no potential conflict of interest with respect to the research, authorship and/or publication of this article.

ORCID

Alan. B. Franklin http://orcid.org/0000-0001-9491-795X
Susan A. Shriner http://orcid.org/0000-0003-0349-7182
J. Jeffrey Root http://orcid.org/0000-0003-4177-1824

REFERENCES

Bevins, S. N., Dusek, R. J., White, C. L., Gidlewski, T., Bodenstein, B., Mansfield, K. G., … Deliberto, T. J. (2016). Widespread detection of highly pathogenic H5 influenza viruses in wild birds from the Pacific Flyway of the United States. *Scientific Reports*, *6*, 28980. https://doi.org/10.1038/srep28980

Bevins, S. N., Pedersen, K., Lutman, M. W., Baroch, J. A., Schmit, B. S., Kohler, D., … DeLiberto, T. J. (2014). Large-scale avian influenza surveillance in wild birds throughout the United States. *PLoS ONE*, *9*, e104360. https://doi.org/10.1371/journal.pone.0104360

Beyer, H. L. (2014). *Geospatial modeling environment*, *ver 0.7.2 RC2*. Spatial Ecology LLC..

Bridge, E. S., Kelly, J. F., Xiao, X., Takekawa, J. Y., Hill, N. J., Yamage, M., … Newman, S. H. (2014). Bird migration and avian influenza: A comparison of hydrogen stable isotopes and satellite tracking methods. *Ecological Indicators*, *45*, 266–273. https://doi.org/10.1016/j.ecolind.2014.04.027

Buhnerkempe, M. G., Webb, C. T., Merton, A. A., Buhnerkempe, J. E., Givens, G. H., Miller, R. S., & Hoeting, J. A. (2016). Identification of migratory bird flyways in North America using community detection on biological networks. *Ecological Applications*, *26*, 740–751. https://doi.org/10.1890/15-0934

Bui, C. M., Gardner, L., & MacIntyre, C. R. (2016). Highly pathogenic avian influenza virus, midwestern United States. *Emerging Infectious Diseases*, *22*, 138–139. https://doi.org/10.3201/eid2201.151053

Burnham, K. P., & Anderson, D. R. (2002). *Model selection and multimodel inference: A practical information-theoretic approach*, 2nd edn.. New York, NY: Springer.

Chu, C.-Y., Henderson, D., & Parmeter, C. (2015). Plug-in bandwidth selection for kernel density estimation with discrete data. *Econometrics*, *3*, 199. https://doi.org/10.3390/econometrics3020199

Crone, S. F., & Finlay, S. (2012). Instance sampling in credit scoring: An empirical study of sample size and balancing. *International Journal of Forecasting*, *28*, 224–238. https://doi.org/10.1016/j.ijforecast.2011.07.006

Daszak, P., Cunningham, A. A., & Hyatt, A. D. (2000). Emerging infectious diseases of wildlife - threats to biodiversity and human health. *Science*, *287*, 443–449. https://doi.org/10.1126/science.287.5452.443

Doherty, P. F., White, G. C., & Burnham, K. P. (2012). Comparison of model building and selection strategies. *Journal of Ornithology*, *152*, 317–323. https://doi.org/10.1007/s10336-010-0598-5

Doherty, P. F. J., Wilson, K. R., Davis, A. J., Farnsworth, M. L., Franklin, A. B., Gilbert, M. M., … Webb, C. T. (2009). *Avian influenza risk assessment for the United States: Modeling pathways of disease spread by wild birds*. Fort Collins, Colorado: Colorado State University.

Endy, T. P., Rochford, R., Yuen, K. Y., & Lei, H. Y. (2011). Emerging infectious diseases as a global health threat. *Experimental Biology and Medicine (Maywood, N.J.)*, *236*, 897–898. https://doi.org/10.1258/ebm.2011.011i01

Farnsworth, M. L., Kendall, W. L., Doherty, P. F., Miller, R. S., White, G. C., Nichols, J. D., … Franklin, A. B. (2011). Targeted surveillance for highly pathogenic avian influenza in migratory waterfowl across the conterminous United States. In S. K. Majumdar, F. J. Brenner, J. E. Huffman, R. G. McLean, A. I. Panah, P. J. Freda Pietrobon, S. P. Keeler & S. E. Shive (Eds), *Pandemic influenza viruses: Science, surveillance and public health* (pp. 143–155). Easton, PA: The Pennsylvania Academy of Sciences.

Fonkwo, P. N. (2008). Pricing infectious disease: The economic and health implications of infectious diseases. *EMBO Reports*, *9*, S13–S17. https://doi.org/10.1038/embor.2008.110

Global Consortium for H5N8 and Related Influenza Viruses (2016). Role for migratory wild birds in the global spread of avian influenza H5N8. *Science*, *354*, 213–217.

Grant, E. H. C., Muths, E., Katz, R. A., Canessa, S., Adams, M. J., Ballard, J. R., … White, C. L. (2017). Using decision analysis to support proactive management of emerging infectious wildlife diseases. *Frontiers in Ecology and the Environment*, *15*, 214–221. https://doi.org/10.1002/fee.1481

Greene, J. L. (2015). *Update on the highly-pathogenic avian influenza outbreak of 2014–2015 CRS Report*. Washington, D.C.: Congressional Research Service.

Gunnarsson, G., Latorre-Margalef, N., Hobson, K. A., Van Wilgenburg, S. L., Elmberg, J., Olsen, B., … Waldenström, J. (2012). Disease dynamics and bird migration - Linking mallards *Anas platyrhynchos* and subtype diversity of the influenza A virus in time and space. *PLoS ONE*, *7*, e35679. https://doi.org/10.1371/journal.pone.0035679

Gustafson, M. E., Hildenbrand, J., & Metras, L. (1997). *The North American bird banding manual* (Electronic Version 1.0). Patuxent, MD: U. S. Geological Survey Bird Banding Laboratory.

Hill, N. J., Hussein, I. T. M., Davis, K. R., Ma, E. J., Spivey, T. J., Ramey, A. M., … Runstadler, J. A. (2017). Reassortment of influenza A viruses in wild birds in Alaska before H5 Clade 2.3.4.4 outbreaks. *Emerging Infectious Diseases*, *23*, 654–657. https://doi.org/10.3201/eid2304.161668

Ip, H. S., Torchetti, M. K., Crespo, R., Kohrs, P., DeBruyn, P., Mansfield, K. G., … Sleeman, J. M. (2015). Novel Eurasian highly pathogenic avian influenza A H5 viruses in wild birds, Washington, USA, 2014. *Emerging Infectious Diseases*, *21*, 886–890. https://doi.org/10.3201/eid2105.142020

Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, *451*, 990–994. https://doi.org/10.1038/nature06536

Kang, H.-M., Lee, E.-K., Song, B.-M., Jeong, J., Choi, J.-G., Jeong, J., … Lee, Y.-J. (2015). Novel reassortant influenza A(H5N8) viruses among inoculated domestic and wild ducks, South Korea, 2014. *Emerging Infectious Diseases*, *21*, 298–304. https://doi.org/10.3201/eid2102.141268

Lavretsky, P., Miller, J. H., Bahn, V., & Peters, J. L. (2014). Exploring fall migratory patterns of American black ducks using eight decades of band-recovery data. *The Journal of Wildlife Management*, *78*, 997–1004. https://doi.org/10.1002/jwmg.752

Lee, D.-H., Bahl, J., Torchetti, M. K., Killian, M. L., Ip, H. S., DeLiberto, T. J., & Swayne, D. E. (2016). Highly pathogenic avian influenza viruses and generation of novel reassortants, United States, 2014–2015. *Emerging Infectious Diseases*, *22*, 1283–1285. https://doi.org/10.3201/eid2207.160048

Lee, D.-H., Torchetti, M. K., Winker, K., Ip, H. S., Song, C.-S., & Swayne, D. E. (2015). Intercontinental spread of Asian-origin H5N8 to North America through Beringia by migratory birds. *Journal of Virology*, *89*, 6521–6524. https://doi.org/10.1128/JVI.00728-15

Miller, R. S., Sweeney, S. J., Akkina, J. E., & Saito, E. K. (2015). Potential intercontinental movement of influenza A(H7N9) virus into North America by wild birds: Application of a rapid assessment framework. *Transboundary and Emerging Diseases*, *62*, 650–668. https://doi.org/10.1111/tbed.12213

National Agricultural Statistics Service. (2015). *Poultry and egg production 2012. Census of Agriculture Highlights*. Washington, DC: U.S Department of Agriculture, National Agricultural Statistics Service.

Oommen, T., Baise, L. G., & Vogel, R. M. (2011). Sampling bias and class imbalance in maximum-likelihood logistic regression. *Mathematical*

Geosciences, *43*, 99–120. https://doi.org/10.1007/s11004-010-9311-8

Pantin-Jackwood, M. J., Costa-Hurtado, M., Shepherd, E., DeJesus, E., Smith, D., Spackman, E., … Swayne, D. E. (2016). Pathogenicity and transmission of H5 and H7 highly pathogenic avian influenza viruses in mallards. *Journal of Virology*, *90*, 9967–9982. https://doi.org/10.1128/JVI.01165-16

Park, S. H., Goo, J. M., & Jo, C.-H. (2004). Receiver operating characteristic (ROC) curve: Practical review for radiologists. *Korean Journal of Radiology*, *5*, 11–18. https://doi.org/10.3348/kjr.2004.5.1.11

Ramey, A. M., Hill, N. J., Cline, T., Plancarte, M., De La Cruz, S., Casazza, M. L., … Boyce, W. M. (2017). Surveillance for highly pathogenic influenza A viruses in California during 2014–2015 provides insights into viral evolutionary pathways and the spatiotemporal extent of viruses in the Pacific Americas Flyway. *Emerging Microbes & Infections*, *6*, e80. https://doi.org/10.1038/emi.2017.66

Ramey, A. M., Pearce, J. M., Ely, C. R., Sheffield Guy, L. M., Irons, D. B., Derksen, D. V., & Ip, H. S. (2010). Transmission and reassortment of avian influenza viruses at the Asian-North American interface. *Virology*, *406*, 352–359. https://doi.org/10.1016/j.virol.2010.07.031

Ramey, A. M., Pearce, J. M., Flint, P. L., Ip, H. S., Derksen, D. V., Franson, J. C., … Trust, K. A. (2010). Intercontinental reassortment and genomic variation of low pathogenic avian influenza viruses isolated from northern pintails (*Anas acuta*) in Alaska: Examining the evidence through space and time. *Virology*, *401*, 179–189. https://doi.org/10.1016/j.virol.2010.02.006

SAS Institute Inc. (2013). *SAS/STAT® 13.1 user's guide: The GENMOD procedure*. Cary, NC: SAS Institute Inc.

Tautin, J., Metras, L., & Smith, G. (1999). Large-scale studies of marked birds in North America. *Bird Study*, *46*, S271–S278. https://doi.org/10.1080/00063659909477254

Verhagen, J. H., Herfst, S., & Fouchier, R. A. M. (2015). How a virus travels the world. *Science*, *347*, 616–617. https://doi.org/10.1126/science.aaa6724

Webster, R., Bean, W. J., Gorman, O. T., Chambers, T. M., & Kawaoka, Y. (1992). Evolution and ecology of influenza A viruses. *Microbiological Reviews*, *56*, 152–179.

Winker, K., & Gibson, D. D. (2010). The Asia-to-America influx of avian influenza wild bird hosts is large. *Avian Diseases*, *54*, 477–482. https://doi.org/10.1637/8741-032509-Reg.1

World Organisation for Animal Health. (2017). *OIE situation report for avian influenza*. Paris, France: World Organisation for Animal Health.

How to cite this article: Franklin AB, Bevins SN, Ellis JW, et al. Predicting the initial spread of novel Asian origin influenza A viruses in the continental USA by wild waterfowl. *Transbound Emerg Dis*. 2019;66:705–714. https://doi.org/10.1111/tbed.13070