

Highly Pathogenic Avian Influenza Virus, Midwestern United States

Chau M. Bui, Lauren Gardner, C. Raina MacIntyre

Author affiliations: University of New South Wales School of Public Health and Community Medicine, Sydney, New South Wales, Australia (C. Bui, C.R. MacIntyre); University of New South Wales School of Civil and Environmental Engineering, Sydney (L. Gardner)

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To the Editor: Novel highly pathogenic avian influenza (HPAI) viruses of subtypes H5N2, H5N8, and H5N1 have recently caused numerous outbreaks in commercial poultry farms in the United States and Canada (1). Risk for zoonotic transmission is low; humans are affected primarily from the extensive economic repercussions of suspending poultry-farming activities (1).

Large-scale research is under way, including case-control studies of infections on poultry farms and modeling studies to investigate the spread of virus in waterfowl (1,2). The US Department of Agriculture has published a report that summarizes various biosecurity measures of affected farms, results of airborne pathogen testing, and geospatial analyses correlating wind speed and direction to outbreaks (1). These studies found insufficient evidence to support

any particular modes of virus spread and suggest that farms are contaminated from infected migrating waterfowl and/or unauthorized movements (e.g., of vehicles, equipment, persons, or animals) between farms and that unusually high wind speeds are the likely mechanism of spread (1). The spread from farm to farm, but not from barn to barn within a single farm (3), further adds to the puzzle of how infection has been transmitted.

To better understand the outbreak behavior, we used publicly available sources (4–6) to create maps of outbreaks of HPAI virus, subtype H5, infections in relation to poultry distribution and wild bird migratory patterns (Figure; online Technical Appendix Figures 1, 2, <http://wwwnc.cdc.gov/EID/article/22/1/15-1053-Techapp1.pdf>; Video, <http://wwwnc.cdc.gov/EID/article/22/1/15-1053-V1.htm>). From November 30, 2014, through June 17, 2015, a total of 280 outbreaks caused by HPAI virus subtype H5 in Canada and the United States were reported to the World Organisation for Animal Health (4). Most outbreaks occurred during April (n = 116) in commercial turkey farms (n = 154) and were caused by HPAI virus subtype H5N2 (n = 256) (online Technical Appendix Figure 3). Related reassortant HPAI subtypes H5N8 and H5N1 were also found among infected poultry; however, these appeared infrequently. Subtype H5N1 appeared in 4 of 21 outbreaks in backyard and commercial farms and was found in 1 of 3 infections in a backyard farm. Backyard farms generally contain flocks for local consumption and implement fewer biosecurity measures (4).

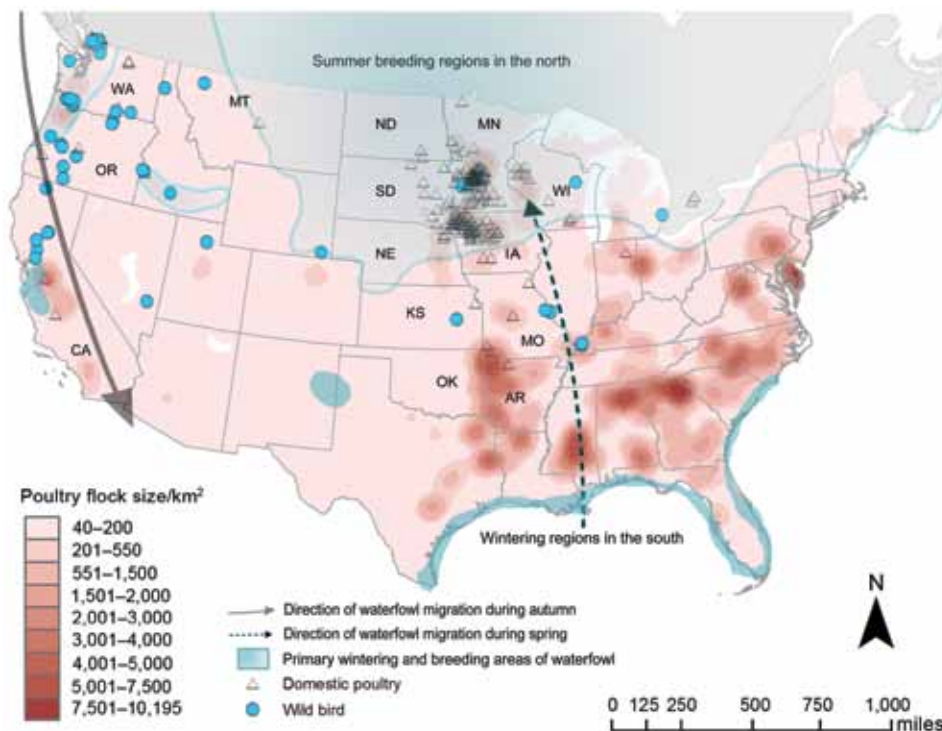


Figure. Distribution of highly pathogenic avian influenza (HPAI) H5 outbreaks in domestic poultry compared with domestic poultry flock density and direction of wild waterfowl migration, United States. Triangles represent HPAI H5 domestic poultry outbreaks; circles represent HPAI H5 wild bird outbreaks. Solid gray shading indicates migratory waterfowl wintering and breeding regions, and arrows represent general direction of seasonal movements. Gradient gray shading indicates density of domestic poultry holdings, with darker shades representing areas where flock densities are higher. A color version of this figure is available online (<http://wwwnc.cdc.gov/EID/article/22/1/15-1053-F1.htm>).

Initial outbreaks on poultry farms that began in November 2014, near the British Columbia–Washington State border, have been associated with timing of waterfowl migration and reported infection in migratory waterfowl (7,8). Subsequent surveillance of avian influenza virus in wild birds in the Pacific flyway has also shown sporadic infections caused by HPAI virus subtype H5, primarily in waterfowl species of the family Anseriformes (4) (online Technical Appendix Table 1).

In late February 2015, however, HPAI virus subtype H5, emerged in US midwestern states, leading to a substantial number of outbreaks in commercial poultry farms in the region. The spread from west to east does not correlate with the direction of typical waterfowl migration, in which movement occurs from south to north. Unlike the earlier outbreaks in poultry in Canada, in the outbreaks in midwestern states, corresponding high numbers of virus were not detected in samples of wild birds in surrounding regions (despite increased surveillance). Of 3,300 samples tested, 1 sample tested positive for HPAI virus subtype H5 (4,9). In addition, most poultry farms were affected in April, and migratory waterfowl typically appear in Minnesota in March and April (online Technical Appendix Figure 1). This February introduction of virus to Minnesota may be explained by an earlier-than-usual spring (10).

Minnesota and Iowa lie within regions where migrating waterfowl spend their breeding season, and waterfowl densities on commercial poultry farms are particularly high (online Technical Appendix Figure 2). In southern parts of the United States, where poultry density is also high, isolated outbreaks of HPAI have occurred in poultry, although the introduction of virus into these regions did not result in a surge of outbreaks. The timing of waterfowl migration enables the mixing of highly dense populations of wild waterfowl and poultry, which likely plays a key role in spreading virus onto farms.

Of particular note, outbreaks in poultry were densely concentrated within Minnesota and Iowa in a spatial pattern inconsistent with the much more geographically dispersed spread of infection in wild birds. The magnitude and clustered distribution of poultry outbreaks are suggestive of local spread, rather than multiple introductions from passing migratory waterfowl. Genetic analyses have similarly shown evidence for concurrent multiple introductions as well as common source exposures, and surveys of affected farms have shown that local spread could be facilitated by the sharing of equipment by multiple farms or through animals entering barns (1).

The combination of high poultry densities and timing of waterfowl migration have likely predisposed Minnesota and Iowa to outbreaks of avian influenza among poultry flocks. However, consistent with US Department of Agriculture findings, local factors have likely also contributed

to the large number of outbreaks in these states. We suggest that network modeling analyses would be valuable in exploring how virus may spread from farm to farm.

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References

1. United States Department of Agriculture, Animal and Plant Health Inspection Service. Epidemiological and other analyses of HPAI affected poultry flocks: June 15, 2015 report [cited 2015 Jul 7]. http://www.aphis.usda.gov/animal_health/animal_dis_spec/poultry/downloads/Epidemiologic-Analysis-June-15-2015.pdf
2. United States department of Agriculture. Surveillance plan for highly pathogenic avian influenza in waterfowl in the United States, June 2015 [cited 2015 Jul 6]. http://www.aphis.usda.gov/animal_health/downloads/animal_diseases/ai/2015-hpai-surveillance-plan.pdf
3. Center for Infectious Disease Research and Policy. Role of wild birds in US H5N2 outbreaks questioned [cited 2015 May 15]. <http://www.cidrap.umn.edu/news-perspective/2015/03/role-wild-birds-us-h5n2-outbreaks-questioned>
4. World Organization of Animal Health (OIE). OIE reports. 2015 [cited 2015 Jul]. <http://www.oie.int/en/animal-health-in-the-world/update-on-avian-influenza/2014/>
5. Bruhn MC, Munoz B, Cajka J, Smith G, Curry RJ, Wagener DK, et al. Synthesized population databases: a geospatial database of US poultry farms. RTI Press publication no. MR-0023-1201. Research Triangle Park (NC): RTI Press; 2012 [cited 2015 Jul 7]. <http://www.rti.org/pubs/mr-0023-1201-bruhn.pdf> <http://dx.doi.org/10.3768/rtipress.2012.mr.0023.1201>
6. Johnsgard PA. Waterfowl of North America, rev. ed. Lincoln (NE): University of Nebraska; 2010 [cited 2015 Jul 7] <http://digitalcommons.unl.edu/biosciwaterfowlna/1>
7. Pasick J, Berhane Y, Joseph T, Bowes V, Hisanaga T, Handel K, et al. Reassortant highly pathogenic influenza A H5N2 virus containing gene segments related to Eurasian H5N8 in British Columbia, Canada. *Sci Rep*. 2014;5:9484.
8. Ip HS, Torchetti MK, Crespo R, Kohrs P, DeBruyn P, Mansfield KG, et al. Novel Eurasian highly pathogenic influenza A H5 viruses in wild birds, Washington, USA, 2014. *Emerg Infect Dis*. 2015;21:886–90. <http://dx.doi.org/10.3201/eid2105.142020>
9. Minnesota Department of Natural Resources. After initial testing, DNR researchers still investigating avian flu in wildlife. June 18, 2015 [cited 2015 Jul 7]. <http://news.dnr.state.mn.us/2015/06/18/after-initial-testing-dnr-researchers-still-investigating-avian-flu-in-wildlife/>
10. Zimpfer NL, Rhodes WE, Silverman ED, Zimmerman GS, Richkus KD. Trends in duck breeding populations, 1955–2015. US Fish & Wildlife Service Division of Migratory Bird Management Administrative Report, July 2, 2015 [cited 2015 Jul 7]. http://flyways.us/sites/default/files/uploads/trends_in_duck_breeding_populations_2015.pdf

Address for correspondence: Chau Bui, School of Public Health and Community Medicine, Samuels Bldg F25, Kensington Campus, University of New South Wales, Sydney, NSW, Australia; email: chau.bui@unsw.edu.au

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Technical Appendix

Materials

Coordinate data on confirmed outbreaks caused by highly pathogenic avian influenza (HPAI), subtype H5, were available from the World Organisation for Animal Health (OIE) (1). Poultry farm locations and flock sizes were obtained from a modeled dataset designed for use in research (2). This dataset contains estimated coordinate locations of poultry farms, along with estimates of farm-holding size and reflect US census data. Estimated distributions of wild bird populations were derived from bird-banding data supplied by the US Geological Survey, Patuxent Wildlife Research Centre and Bird Banding Laboratory Canadian Wildlife Service, National Wildlife Research Centre (available on request at <http://www.pwrc.usgs.gov/>). A list of all wild bird species reporting HPAI H5 viruses (Technical Appendix Table 1) was compiled using information from <http://www.aphis.usda.gov/>. Generalized distributions of waterfowl wintering and breeding regions were obtained from the revised edition of *Waterfowl of North America* (3). Data on flyways in North America were available at <http://www.ducks.org/>.

Methods

ArcMap software (Version 10.2) was used to create maps (Figures 1; Technical Appendix Figures 1, 2) and a time-series video of outbreaks (Video). Base maps of the United States and Canada were obtained from the GADM database of Global Administrative Areas (<http://www.gadm.org/>). The North America Lambert Conformal Conic projection (www.esri.com) was used for all layers. Adobe Photoshop, version CS5 (<https://www.adobe.com>), was used for graphics editing.

Disease event data from OIE (1) were transcribed into a line list on Microsoft Excel (Microsoft Corp., Redmond, WA, USA). OIE reports from the United States and Canada contain the following: start date of disease event, sample collection location (country, state, county, and occasionally a more specific location name), coordinate data, the species of bird affected, and if a farm was reported, the farm type affected (commercial or backyard). Coordinate data of disease events were used to plot the location of HPAI H5 outbreaks. Epidemic curves were created by using Microsoft Excel (Technical Appendix Figure 3).

Coordinate data representing synthetic poultry farm locations were plotted for each of the 3 domestic poultry groups: chicken farms (broilers, layers, pullets), turkey farms, and other poultry farms (duck, geese, other) (Technical Appendix Figure 2, panels A, C, E). We additionally plotted large flock farms that house >10,000 poultry on separate maps for each of the 3 poultry groups (Technical Appendix Figure 2, panels B, D, F). Kernel density transformations were also performed, using all 3 poultry groups together (Figure 1).

Coordinate data from the bird-banding dataset was used to create maps displaying wild bird encounter locations for each month of the study period (Technical Appendix Figure 1, panels A–F). Encounter locations refer to locations where banded wild birds have been found (dead, hunted, or recaptured). Further information can be found at <http://www.pwrc.usgs.gov/BBL/MANUAL/Howobt.cfm>. Data were limited to recent bird-banding data (January 2013 onwards) and restricted to the 11 Anseriformes species (waterfowl) that have had reported HPAI H5 viruses as species from the Anseriformes and Charadriiformes families (shorebirds), which are considered to be the natural reservoirs of avian influenza viruses. For each month, the kernel density of bird encounters (per km²) were calculated and displayed with the plotted disease incidence for that particular month. Generalized waterfowl seasonal distributions from Waterfowl of North America, revised edition (3) and direction of seasonal movement were digitized by using Adobe Photoshop (version CS5) (see Figure 1).

References

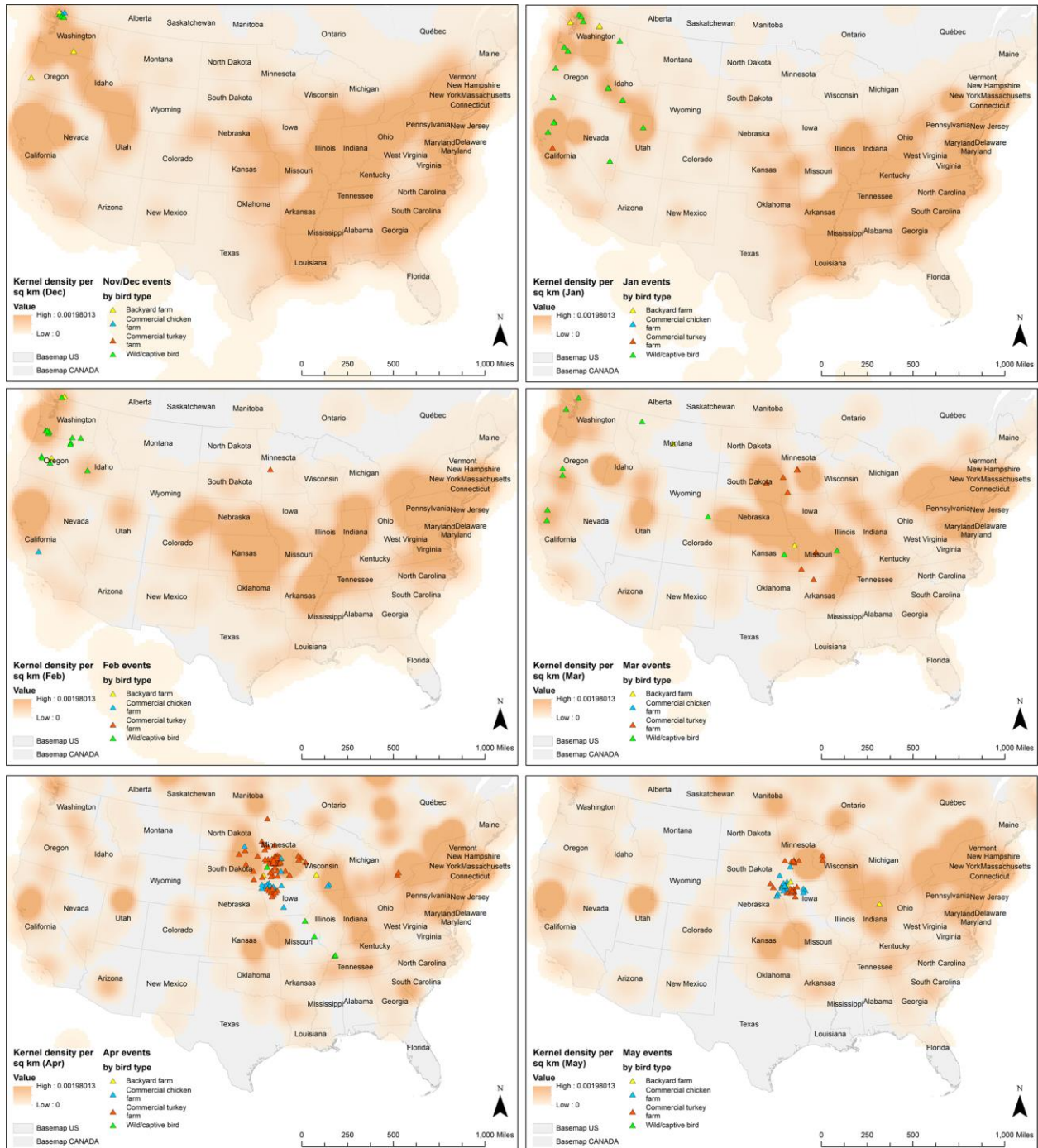
1. World Organisation for Animal Health (OIE). OIE reports. 2015. [cited 2015 Jul]. <http://www.oie.int>
2. Bruhn MC, Munoz B, Cajka J, Smith G, Curry RJ, Wagener DK, et al. Synthesized population databases: a geospatial database of US poultry farms. RTI Press publication no. MR-0023-1201.

Research Triangle Park (NC): RTI Press; 2012 [cited 2015 Jul]. <http://www.rti.org/pubs/mr-0023-1201-bruhn.pdf> <http://dx.doi.org/10.3768/rtipress.2012.mr.0023.1201>

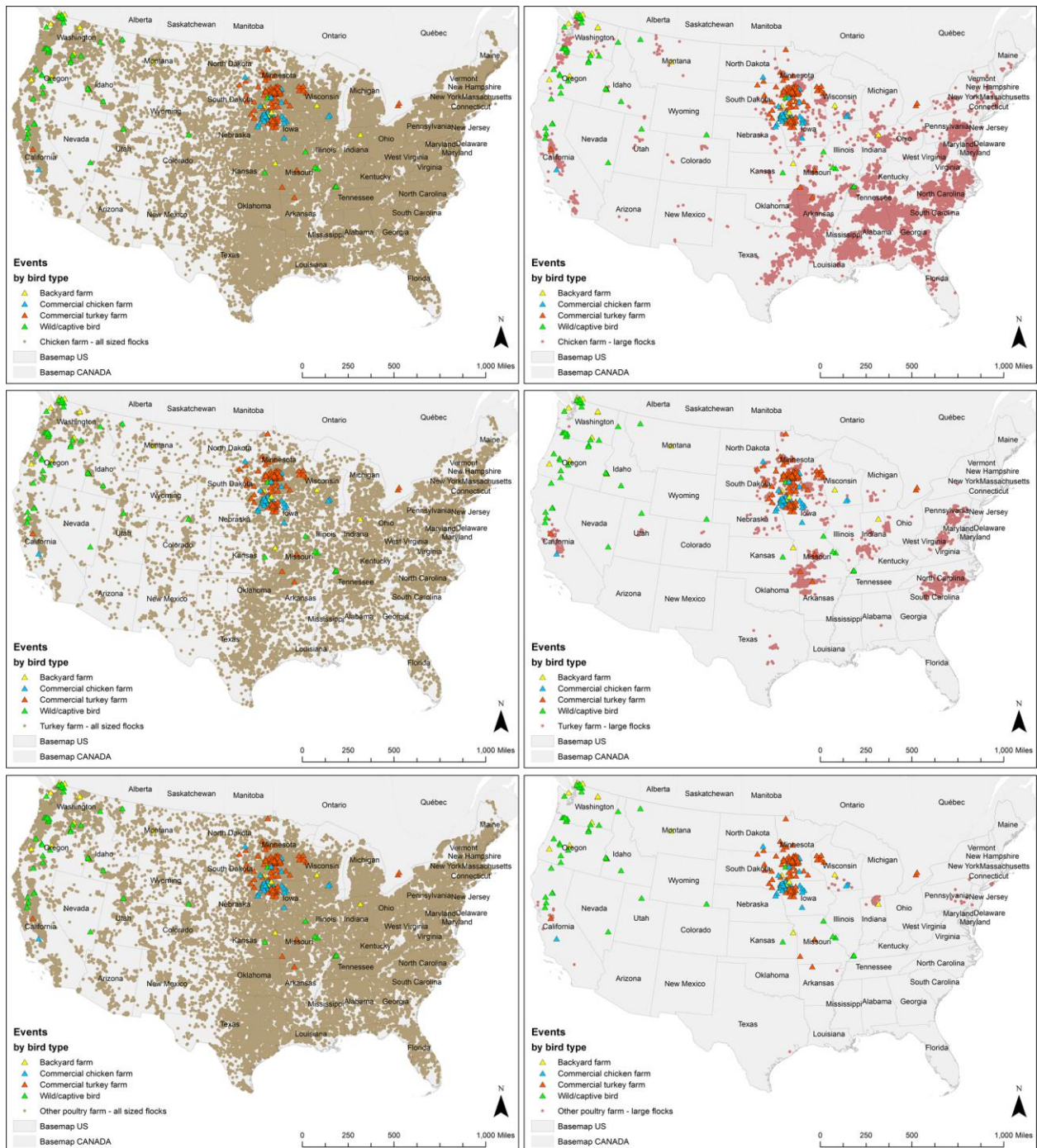
3. Johnsgard PA. Waterfowl of North America, rev. ed. Lincoln (NE): University of Nebraska; 2010 [cited 2015 Jul]. <http://digitalcommons.unl.edu/biosciwaterfowlna/1>

Technical Appendix Table. Summary of the number of disease outbreaks caused by highly pathogenic avian influenza virus, subtype H5, reported in North America according to species of wild bird

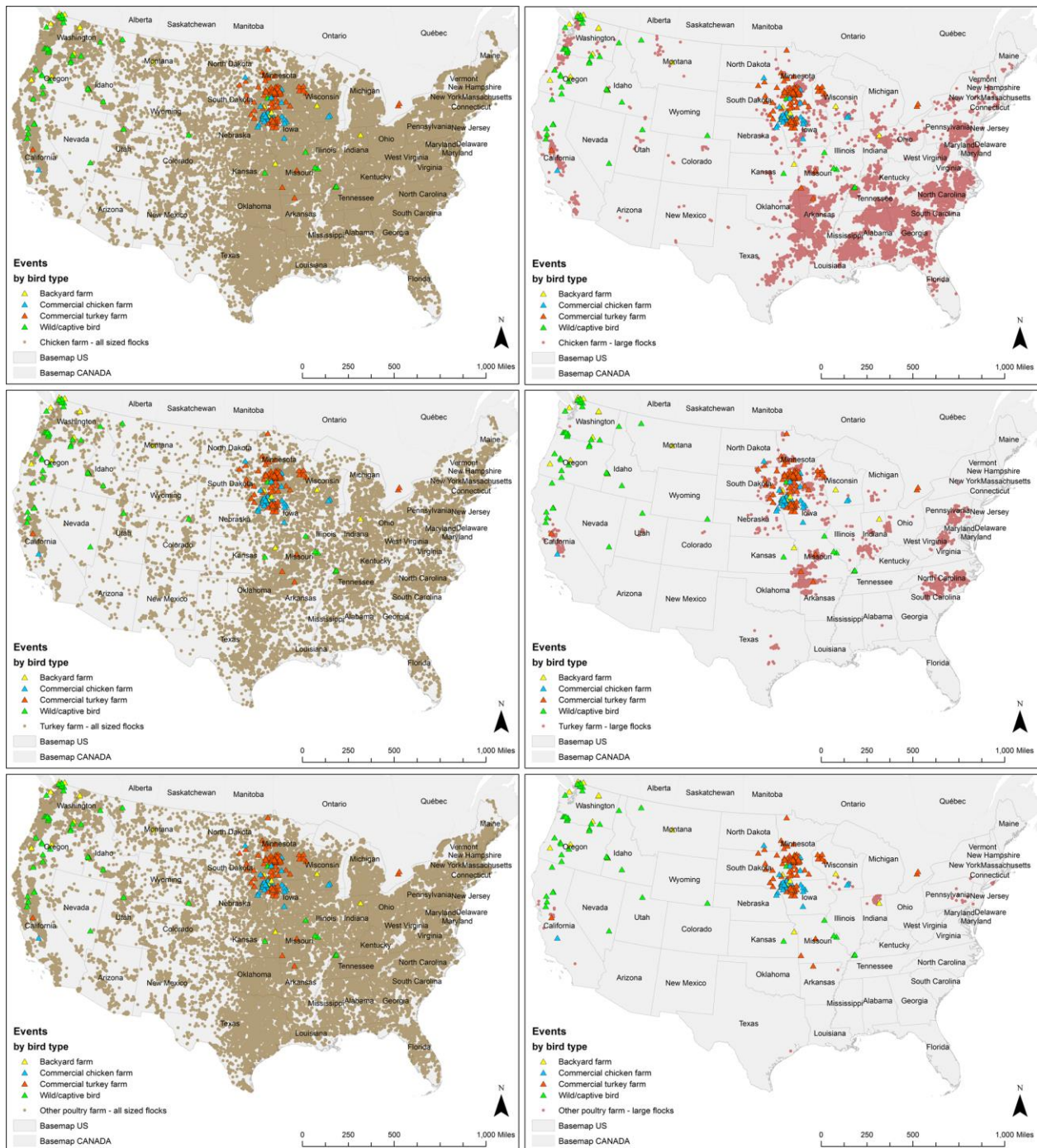
Family	Species	No. reports
Anseriformes	Mallard	16
Anseriformes	American wigeon	11
Anseriformes	Northern pintail	5
Anseriformes	Canada goose	5
Anseriformes	American green-winged teal	4
Anseriformes	Lesser snow goose	4
Anseriformes	Wood duck	3
Anseriformes	Northern shoveler	3
Falconiformes	Red-tailed hawk	2
Falconiformes	Cooper's hawk	2
Falconiformes	Bald eagle	1
Anseriformes	Ring-necked duck	1
Strigiformes	Snowy owl	1
Anseriformes	Gadwall	1
Anseriformes	Cinnamon teal	1
Falconiformes	Peregrine falcon	1



Technical Appendix Figure 1. Distribution of outbreaks caused by highly pathogenic avian influenza (HPAI) virus, subtype H5, layered over the monthly geographic distributions of reported wild bird encounters in December (A), January (B), February (C), March (D), April (E), and May (F). Yellow, blue, red, and green triangles represent HPAI H5 outbreak locations in backyard farms, commercial chicken farms, commercial turkey farms and wild/captive birds, respectively. Orange shading indicates the density of reported encounters with wild birds in December (A), January (B), February (C), March (D), April (E), and May (F). Darker shading indicates higher density of bird encounters.



Technical Appendix Figure 2. Distribution of outbreaks caused by highly pathogenic avian influenza (HPAI) virus, subtype H5, layered over the geographic distributions of: all chicken farms (A), chicken farms with large flocks (B), all turkey farms (C), turkey farms with large flocks (D), all ducks/geese/other farms (E), and ducks/geese/other farms with large flocks (F). Yellow, blue, red, green triangles represent HPAI H5 outbreak locations in backyard farms, commercial chicken farms, commercial turkey farms, and wild/captive birds, respectively. Brown dots represent the estimated location of farms in the United States: all chicken farms (A), chicken farms with large flocks (B), all turkey farms (C), turkey farms with large flocks (D), all ducks/geese/other farms (E), and ducks/geese/other farms with large flocks (F).



Technical Appendix Figure 3. Daily distribution of outbreaks caused by highly pathogenic avian influenza (HPAI) virus, subtype H5, from November, 30, 2014, through June 18, 2015. A) Distribution grouped by bird type: wild birds (n = 49), backyard farm birds (n = 20), commercial turkey farms (n = 154), and commercial chicken farms (n = 57) in North America. The 2 commercial mixed poultry farms were grouped as commercial chicken farms. B) Distribution by HPAI virus subtypes H5N2 (n = 256), H5N8 (n = 21), and H5N1 (n = 3).