Rural and Remote Health
MEDLINE listed
Impact factor 0.878
The International Electronic Journal of Rural and Remote Health Research, Education, Practice and Policy
ISSN 1445-6354

SHORT COMMUNICATION

Avian influenza prevalence among hunter-harvested birds in a remote Canadian First Nation community

EN Liberda[1], R Meldrum[1], NA Charania[2], R Davey[3], LJS Tsuji[4]

[1]*School of Occupational and Public Health, Ryerson University, Toronto, Ontario, Canada*

[2]*Department of Public Health, Auckland University of Technology, Auckland, New Zealand*

[3]*Fort Albany First Nation, Fort Albany, Ontario, Canada*

[4]*University of Toronto, Scarborough, Toronto, Ontario, Canada*

Submitted: *6 January 2016;* ***Revised:*** *2 October 2016;* ***Accepted:*** *31 October 2016;* ***Published:*** *11 January 2017*

Liberda EN, Meldrum R, Charania NA, Davey R, Tsuji LJS

Avian influenza prevalence among hunter-harvested birds in a remote Canadian First Nation community
Rural and Remote Health **17: 3864. (Online) 2017**

Available: http://www.rrh.org.au

ABSTRACT

Introduction: Avian influenza virus (AIV) prevalence has been associated with wild game and other bird species. The contamination of these birds may pose a greater risk to those who regularly hunt and consumed infected species. Due to resident concerns communicated by local Band Council, hunter-harvested birds from a remote First Nation community in subArctic Ontario, Canada were assessed for AIV. Hunters, and especially those who live a subsistence lifestyle, are at higher risk of AIV exposure due to their increased contact with wild birds, which represent an important part of their diet.

Methods: Cloacal swabs from 304 harvested game birds representing several species of wild birds commonly hunted and consumed in this First Nation community were analyzed for AIV using real-time reverse transcription polymerase chain reaction. Subtyping was performed using reverse transcription polymerase chain reaction. Sequences were assembled using Lasergene, and the sequences were compared to Genbank.

Results: In total, 16 of the 304 cloacal swab samples were positive for AIV. Of the 16 positive samples, 12 were found in mallard ducks, 3 were found in snow geese (wavies), and 1 positive sample was found in partridge. The AIV samples were subtyped, when possible, and found to be positive for the low pathogenic avian influenza virus subtypes H3 and H4. No samples were positive for subtypes of human concern, namely H5 and H7.

Conclusions: This work represents the first AIV monitoring program results of hunter-harvested birds in a remote subsistence First Nation community. Community-level surveillance of AIV in remote subsistence hunting communities may help to identify future risks, while educating those who may have the highest exposure about proper handling of hunted birds. Ultimately, only low

pathogenic strains of AIV were found, but monitoring should be continued and expanded to safeguard those with the highest exposure risk to AIV.

Key words: Aboriginal, avian influenza, birds, Canada, First Nation, Indigenous.

Introduction

Recently, we reported that over half the subsistence hunters from Fort Albany First Nation were aware of avian influenza virus (AIV) being a potential health hazard[1]. Over a quarter of the total participants perceived a risk of contracting this virus while harvesting birds[1]. The perception of this risk is not unfounded as several studies have noted that hunters and some bird handlers, such as wildlife biologists, may be at increased risk of exposure to highly pathogenic avian influenza A (HPAI) viruses[2-6]. Within hunters, HPAI exposure risk varies greatly by location due to the viral prevalence observed during different hunting seasons in birds, species of bird, the average number of birds harvested per hunting period, and the age and ratio of juveniles to adult birds harvested[7,8]. The group of hunters in this study is particularly vulnerable to exposure due to their subsistence lifestyle combined with the knowledge that HPAI outbreaks have occurred in migratory waterfowl, which is their primary hunting target[9,10].

Although relatively rare in human occurrence, the high fatality rate associated with HPAI infection creates a continued cause for human health concern[11]. The most recent data (1 May 2015) from the WHO reports 840 cases of H5N1 resulting in 447 deaths since 2003 across the globe[12]. Furthermore, the high hunter contact rate of birds in this study may act as an additional danger due to these people's remoteness and isolation from adequate medical facilities that can recognize and combat this virus. Campagna and colleagues (2011) recently reported that seropositivity of 10 zoonotic infections from two First Nations communities in Quebec was associated with hunting practices[13]. Because many remote First Nations communities rely on hunted meats for subsistence, they are at an increased risk of AIV exposure as well. In response to community hunter and Band Council (locally elected government) concerns about HPAI (particularly the H5 and H7 subtypes) in the game birds harvested from the Fort Albany First Nation region of northern Ontario, Canada, we assessed a range of hunted fowl for influenza A virus.

Methods

All sampling was conducted under the guidance of a trained local community coordinator, all hunting was performed by local traditional hunters, and the project was approved by the Fort Albany Band Council. Cloacal swabs (Starplex Scientific, Etobicoke, Canada) were taken in the spring and autumn hunting seasons of 2013 and in the spring hunting season of 2014. Samples were frozen at –20°C and shipped directly to the laboratory for analysis. Total nucleic acids were extracted from the cloacal swab samples using the MagMAX-96 viral ribonucleic acid (RNA) Isolation Kit in a MagMAX Express-96 Magnetic Particle Processor (Applied Biosystems Inc., Foster City, California). Extracted nucleic acids were screened for the presence of influenza A virus RNA using a real-time reverse transcription polymerase chain reaction targeting a conserved region of influenza A virus M gene[14]. For hemagglutinin gene subtyping, influenza A virus RNA was amplified using a reverse transcription polymerase chain reaction (PCR)[15] and nucleotide sequences of PCR products were determined at the University of Guelph Laboratory Services sequencing facility. Sequences were assembled using the Lasergene software (DNAStar Inc., https://www.dnastar.com) and compared with hemagglutinin gene sequences in GenBank, the US National Institutes of Health genetic sequence database. In total, 304 cloacal swabs were analyzed; the number of samples by species is presented in Table 1. The results of this project were presented to the community under the direction of the community coordinator and the researchers.

Table 1: Number of cloacal swabs, by wild game bird type, obtained in a remote First Nation community in subArctic Ontario, Canada, 2013 and 2014

Common and species name	Number of samples
Canada goose (*Branta canadensis maxima and interior)*	192
Mallard duck (*Anas platyhynchos)*	42
Partridge/sharp-tailed grouse (*Tympanuchus phasianellus phasianellus*)	11
Snow goose (*Chen caerulescens caerulescens)*	16
Spruce grouse (*Falcipennis canadensis*)	43

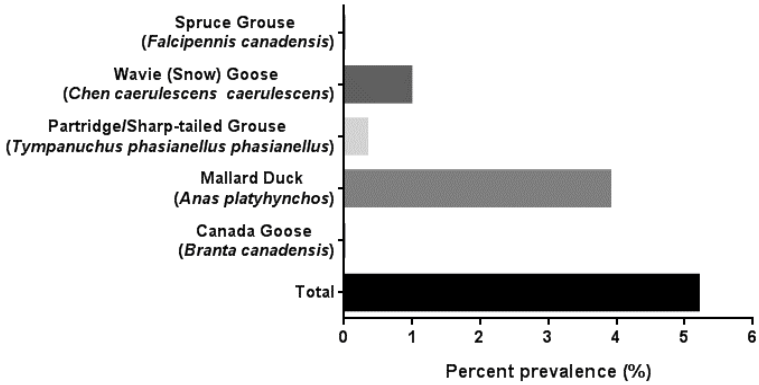

Figure 1: Point prevalence of avian influenza virus in individual bird species sampled and total sample population.

Results

A 5.26% (*n*=16) AIV prevalence was found in the 304 cloacal swab samples analyzed. Of the 16 positive samples, 12 were found in mallard ducks, 3 were found in snow geese (wavies), and 1 positive sample was found in partridge (Fig1). Three mallard ducks were successfully subtyped for H3 and one mallard duck was subtyped for H4. The remaining positive samples were unable to be subtyped either due to being positive for multiple strains of avian influenza A, or due to reduced sensitivities in the conventional PCR process used to generate the template for sequencing.

Discussion

To our knowledge, the pilot work presented herein is the first to examine hunter-harvested birds from a subsistence First Nation community. Globally, surveillance and reporting of avian influenza remains weak[16,17], and the community-level data presented here is the first step towards mapping risk and exposure by identifying which bird species may be acting as reservoirs or pathogen vectors[18]. Others have successfully used surveillance data to assess risk from avian influenza[19,20] and similar application of this data could provide added security to subsistence hunting communities.

HPAI remains a concern globally, and those who hunt and handle birds may be at additional risk. However, no HPAI subtypes were identified in any of the samples collected by community members of Fort Albany First Nation; only low pathogenic AIV was found. The H3 and H4 low pathogenic AIV subtypes are most commonly found among dabbling ducks[8], and this was represented in this study. Ferro et al. found that dabbling ducks and snow geese had lower

prevalences of AIV (10.9% and 0%, respectively) in hunter-harvested waterfowl from the Texas coast[21] when compared to our study (28.6% for mallard duck only and 6.3%, respectively). AIV prevalence within dabbling ducks varies, and others have reported a 24.3% prevalence in mallard ducks, which is similar to our value[22]. Stallknecht et al. found that prevalence of AIV varied by season[23], and others have noted that age, species, location, and number of birds harvested all cause variation in AIV prevalence[7,8,24]. While it is possible that we did not capture true prevalence of all birds from the Fort Albany community, the majority of the samples were collected during the two main hunting seasons (spring and autumn) and this represents the highest potential hazard period for hunters. Additionally, research suggests that northern breeding grounds in colder environments may act as reservoirs for some types of AIV, even though they might seem unfavorable[25].

Conclusions

Community-level surveillance of AIV in remote subsistence hunting communities is an important aspect of identifying risks and working to control a potential outbreak that may otherwise lead to adverse social and economic effects[26]. While general Canadian pandemic plans[27] and recommendations for First Nations communities[28] have been developed, data such as that presented here can help address monitoring gaps and improve hunter education. This is an important first step to assessing risk as Aboriginal (First Nations, Inuit, and Metis} people have had the highest rate of H1N1 worldwide[29] and a HPAI outbreak in a remote community would have significant adverse consequences. Although only low pathogenic AIV was found in the 304 cloacal swab samples tested herein, ongoing monitoring of birds from areas with potentially high exposure groups such as subsistence hunters is recommended.

Acknowledgements

We wish to thank the hunters of Fort Albany First Nation who participated in this research project. Funding was provided by Health Canada's Regional First Nations Environmental Contaminants Program and a Ryerson University Faculty of Community Services Seed Grant.

References

1. Charania NA, Martin ID, Liberda EN, Meldrum R, Tsuji LJ. Bird harvesting practices and knowledge, risk perceptions, and attitudes regarding avian influenza among Canadian First Nations subsistence hunters: implications for influenza pandemic plans. *BMC Public Health* 2014; **14:** 1113. https://doi.org/10.1186/1471-2458-14-1113

2. Reed C, Bruden D, Byrd KK, Veguilla V, Bruce M, Hurlburt D, et al. Characterizing wild bird contact and seropositivity to highly pathogenic avian influenza A (H5N1) virus in Alaskan residents. *Influenza and Other Respiratory Viruses* 2014; **8(5):** 516-523. https://doi.org/10.1111/irv.12253

3. Shafir SC, Fuller T, Smith TB, Rimoin AW. A national study of individuals who handle migratory birds for evidence of avian and swine-origin influenza virus infections. *Journal of Clinical Virology* 2012; **54(4):** 364-367. https://doi.org/10.1016/j.jcv.2012.05.001

4. Gray GC, Ferguson DD, Lowther PE, Heil GL, Friary JA. A national study of US bird banders for evidence of avian influenza virus infections. *Journal of Clinical Virology* 2011; **51(2):** 132-135. https://doi.org/10.1016/j.jcv.2011.03.011

5. Gray GC, McCarthy T, Capuano AW, Setterquist SF, Alavanja MC, Lynch CF. Evidence for avian influenza A infections among Iowa's agricultural workers. *Influenza and Other Respiratory Viruses* 2008; **2(2):** 61-69. https://doi.org/10.1111/j.1750-2659.2008.00041.x

6. Gill JS, Webby R, Gilchrist MJ, Gray GC. Avian influenza among waterfowl hunters and wildlife professionals. *Emerging Infectious Diseases* 2006; **12(8):** 1284-1286. https://doi.org/10.3201/eid1708.060492

7. Dorea FC, Cole DJ, Stallknecht DE. Quantitative exposure assessment of waterfowl hunters to avian influenza viruses. *Epidemiology and Infection* 2013; **141(5):** 1039-1049. https://doi.org/10.1017/S0950268812001720

8. Kistler WM, Stallknecht DE, DeLiberto TJ, Van Why K, Yabsley MJ. Subtype-specific influenza A virus antibodies in Canada geese (*Branta canadensis*). *Veterinary Microbiology* 2015; **177(3-4):** 296-301. https://doi.org/10.1016/j.vetmic.2015.03.021

9. Chen H, Smith GJ, Zhang SY, Qin K, Wang J, Li KS, et al. Avian flu: H5N1 virus outbreak in migratory waterfowl. *Nature* 2005; **436(7048):** 191-192. https://doi.org/10.1038/nature03974

10. Normile D. Avian influenza. Evidence points to migratory birds in H5N1 spread. *Science* 2006; **311(5765):** 1225. https://doi.org/10.1126/science.311.5765.1225

11. Van Kerkhove MD. Brief literature review for the WHO global influenza research agenda – highly pathogenic avian influenza H5N1 risk in humans. *Influenza and Other respiratory Viruses* 2013; **7(Suppl 2):** 26-33. https://doi.org/10.1111/irv.12077

12. WHO, Global Influenza Programme. *Cumulative number of confirmed human cases for avian influenza A(H5N1) reported to WHO, 2003–2015*. (Internet) 2015. Available: http://www.who.int/influenza/human_animal_interface/EN_GIP_20150501CumulativeNumberH5N1cases.pdf?ua=12015 (Accessed 1 June 2015).

13. Campagna S, Levesque B, Anassour-Laouan-Sidi E, Cote S, Serhir B, Ward BJ, et al. Seroprevalence of 10 zoonotic infections in 2 Canadian Cree communities. *Diagnostic Microbiology and Infectious Disease* 2011; **70(2):** 191-199. https://doi.org/10.1016/j.diagmicrobio.2011.01.009

14. Weingartl HM, Berhane Y, Hisanaga T, Neufeld J, Kehler H, Emburry-Hyatt C, et al. Genetic and pathobiologic characterization of pandemic H1N1 2009 influenza viruses from a naturally infected swine herd. *Journal of Virology* 2010; **84(5):** 2245-2256. https://doi.org/10.1128/JVI.02118-09

15. Phipps LP, Essen SC, Brown IH. Genetic subtyping of influenza A viruses using RT-PCR with a single set of primers based on conserved sequences within the HA2 coding region. *Journal of Virological Methods* 2004; **122(1):** 119-122. https://doi.org/10.1016/j.jviromet.2004.08.008

16. Huston P. The advance of H5N1/La progression du H5N1. *Canadian Journal of Public Health* 2005; **Nov-Dec:** 405.

17. Butler D. 'Refusal to share' leaves agency struggling to monitor bird flu. *Nature* 2005; **435(7039):** 131. https://doi.org/10.1038/435131a

18. Caron A, de Garine-Wichatitsky M, Chiweshe N, Gaidet N, Cumming GS. Estimating dynamic risk factors for pathogen transmission using community-level bird census data at the wildlife/domestic interface. *Ecology and Society* 2010; **15(3)**.

19. Cumming GS, Hockey PAR, Bruinzeel LW, Du Plessis MA. Wild bird movements and avian influenza risk mapping in Southern Africa. *Ecology and Society* 2008; **13(2)**. https://doi.org/10.5751/ES-02536-130226

20. Peterson AT, Williams RAJ. Risk mapping of highly pathogenic avian influenza distribution and spread. *Ecology and Society* 2008; **13(2)**. https://doi.org/10.5751/ES-02532-130215

21. Ferro PJ, Khan O, Peterson MJ, Batchuluun D, Reddy SM, Lupiani B. Avian influenza virus surveillance in hunter-harvested waterfowl, Texas Coast, September 2009 – January 2010. *Avian Diseases* 2012; **56(4s1):** 1006-1009.

22. Wilcox BR, Knutsen GA, Berdeen J, Goekjian V, Poulson R, Goyal S, et al. Influenza-A viruses in ducks in Northwestern Minnesota: fine scale spatial and temporal variation in prevalence and subtype diversity. *PLoS ONE* 2011; **6(9):** e24010. https://doi.org/10.1371/journal.pone.0024010

23. Stallknecht DE, Shane SM, Zwank PJ, Senne DA, Kearney MT. Avian influenza viruses from migratory and resident ducks of coastal Louisiana. *Avian Diseases* 1990; **34(2):** 398-405. https://doi.org/10.2307/1591427

24. Olsen B, Munster VJ, Wallensten A, Waldenstrom J, Osterhaus AD, Fouchier RA. Global patterns of influenza A virus in wild birds. *Science* 2006; **312(5772):** 384-388. https://doi.org/10.1126/science.1122438

25. Henaux V, Samuel MD, Dusek RJ, Fleskes JP, Ip HS. Presence of avian influenza viruses in waterfowl and wetlands during summer 2010 in California: are resident birds a potential reservoir? *PloS ONE* 2012; **7(2):** e31471. https://doi.org/10.1371/journal.pone.0031471

26. Fukuda K, WHO, Global Influenza Programme. *Pandemic influenza preparedness and response, a WHO guidance document*. (Internet) 2009. Available: http://public.eblib.com/choice/publicfullrecord.aspx?p=434246 (Accessed 24 June 2015).

27. Public Health Agency of Canada. *The Canadian Pandemic Influenza Plan for the Health Sector pandemic influenza – Pandémie d'influenza*. (Internet) 2006. Available: http://www.deslibris.ca/ID/205568 (Accessed 24 June 2015).

28. Charania NA, Tsuji LJS. Recommended mitigation measures for an influenza pandemic in remote and isolated First Nations communities of Ontario, Canada: a community-based participatory research approach. *International Indigenous Policy Journal* 2014; **5(3):** 1-22. https://doi.org/10.18584/iipj.2014.5.3.2

29. Kermode-Scott B. Canada has world's highest rate of confirmed cases of A/H1N1, with Aboriginal people hardest hit. *British Medical Journal* 2009; **339(jul06 2):** b2746-b.