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News

Highly Pathogenic Avian Influenza in the Midwest for the Second Year in a Row

Dr. Mo El-Gazzar, Poultry Extension Veterinarian

On January 15, 2016, the USDA announced that highly pathogenic avian influenza (HPAI) was found on a commercial turkey farm located in Dubois, Indiana. The case was confirmed on January 14th and it was determined that the virus was an H7N8 subtype. This strain of virus is different from the H5 virus that caused the outbreak in 2015. The index case suffered from high mortality which prompted the testing and the detection of the virus. The index primes was quarantined and a 10 km (6 miles) surveillance zone was struck around it. Upon further testing in the surveillance zone, 9 more cases were detected on January 16, 2016. The viruses from the newly detected cases were H7N8 subtype as well and genetically related to the original index case virus. However, the newly detected cases were NOT of the Highly Pathogenic variety, which was slightly surprising. Due to the multiple new detections within the surveillance zone, the surveillance was expanded based on the new locations, but on top of that expansion there was an additional 10 km expansion to increase the surveillance zone to 20 km. While the surveillance efforts are still ongoing, no additional cases have been detected after January 16, 2016. As of January 20th all of the confirmed flocks have been depopulated and the process of disposal is underway. This includes a combined total of 414,503 turkeys and chickens. Prior to 2015, the last large scale HPAI outbreak in commercial poultry in the United States was in 1983, but we've now an outbreak in two successive years. At this time, CDC considers the risk to the general public from these H7 viruses to be low and there are no known cases of H7N8 infection in humans.

Influenza viruses are a diverse group of viruses. Among the 3 types (Type A, B and C) of Influenza, type A Influenza is the most diverse and versatile. Type A is further classified into subtypes based on the different variations of the surface antigens. Two surface antigens are involved in the subtyping of Influenza A; the Hemagglutinin (HA) and Neuraminidase (NA). Serologically, type A Influenza has 16 different HA subtypes and 9 different NA subtypes. The HA subtypes are designated H1 through H16 and NA subtypes are designated N1 through N9. Based on this classification, type A Influenza hypothetically could have 144 different combinations of H and N subtypes, interestingly all of the possible combinations have been actually isolated from wild migratory water fowl.

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This illustrates the high rate of genetic material exchange between Influenza A viruses and explains why the migratory water fowl are considered the Influenza A reservoir.

Influenza A sub-types can infect multiple hosts and can jump from one host to another. Swine Influenza, Equine Influenza, Avian Influenza and some Human Influenza are all Type A Influenza, just to mention a few. Avian influenza viruses are type A influenza viruses that can infect domestic poultry, including but not limited to chickens and turkeys. Within the Avian Influenzas there are two major categories; Highly Pathogenic Avian Influenza (HPAI) and Low Pathogenic Avian Influenza (LPAI). HPAI make domestic poultry severely sick resulting in high mortality and large economic losses. All of the HPAI viruses are either H5 or H7 subtypes, but not all H5 and H7 viruses are highly pathogenic. United States aims to keep the domestic poultry population free of this devastating disease. South East Asia including China seems to be a hot bed for generating these HPAI viruses. Several of these HPAI viruses are endemic in the Far East, representing a threat to animal and human health.

In early 2014, one of these viruses (H5N8 HPAI) was first reported in South Korea. This virus circulated in South East Asia for most of 2014, and by late summer to early fall, this virus was detected in Western Europe. In November 2014, this Eurasian H5 virus was detected for the first time in North America in British Columbia, Canada. Wild Migratory birds are hypothesized to be the culprit in transmitting the virus to North America; however, we don't have any evidence to support this hypothesis. Once the virus entered North America, it very quickly mixed with local North American viruses to produce a HPAI virus with genetics mixed between the North American and Eurasian lineages. We can identify the lineages of the viruses by sequencing the nucleic acid of the virus. This mixed lineage virus was dubbed the American/Eurasian H5 HPAI (AM/EA H5 HPAI). In early March, multiple detections of the virus, almost simultaneously, in 4 Midwestern States (MN, KS, MO, and AR) were reported. Once the virus was in poultry-dense areas of Minnesota, farm to farm transmission played the major role in spread. Multiple other Midwestern states were heavily affected including ND, SD, WI, and IA. Iowa in particular was severely affected, losing in excess of 30 million birds representing approximately one-half of its table egg layer population, creating a shortage in egg supply and soaring egg prices. By the time the outbreak had ended, more than 48 million birds were affected in 21 states; fortunately, Ohio was not one of the affected states. The estimated direct economic losses exceed one billion dollars, not counting indirect costs.

Lessons Learned from the 2015 Outbreak

As mentioned, the US aims to keep the domestic poultry population free from this devastating disease to avoid the international trade implications. For that reason, the strategy for the US is to eradicate the virus by quickly identifying the infected premises, depopulate infected flocks, properly dispose of carcasses and manure, clean and disinfect the premises, and to impose a 21-day period of down time with confirmed negative testing before repopulating the premise again. Among the important lessons learned during the 2015 outbreak was to realize the importance of speedy detection, depopulation, and disposal steps to control the further spread of the disease. All poultry producing states along with USDA and other organizations have been preparing for any potential future outbreaks, taking to heart all the lessons learned from the 2015 outbreak. OSU Extension is one of multiple organizations including the Ohio Department of Agriculture (ODA), USDA APHIS Veterinary Services, and Ohio Poultry Association (OPA), working closely together to help prepare for any future HPAI outbreaks in Ohio. Each of these organizations has a role to play in the event of an outbreak, so they we are working closely to coordinate and communicate expected roles in the control and potential eradication of the disease.

Better Preparations, Better Response

As the poultry industry, USDA, state departments of agriculture, and Universities across the country place a lot of effort into preparations for any new influenza outbreaks; the response to this new H7N8 HPAI appear to be better compared to last year's. It is true that this virus is different from the virus that caused the outbreak last year, but also the speed, thoroughness, and detailed actions that were taken in the response appear better. As mentioned, by January 20, 2016 all of the confirmed flocks have been depopulated and the process of disposal is underway. This includes a total of more than 414,000

turkeys and chickens. By sequencing the nucleic acid of the H7N8 virus, National Veterinary Services Laboratory in (NVSL) Ames, Iowa found the virus to be of North American Lineage. This is different from the Virus from last year that had mixed American and Eurasian lineages. The H7N8 combination is not a very common combination in wild birds; however, it was recently detected in wild birds in two locations in North America. Finding both the highly pathogenic and low pathogenic versions of this particular virus in domestic poultry population at such proximity suggests that change from low pathogenicity to high pathogenicity may have happened in the domestic poultry population. This could also mean that the virus was detected soon after its transformation. This early detection could potentially help the efforts to stop this outbreak and eradicate the virus from the poultry population.

Biosecurity

At this time, all poultry producers, regardless if commercial operation or noncommercial flock, should increase their level of biosecurity and vigilance. While surveillance, quick diagnosis, and quick response are essential tools to detect the virus and limit the infection and eventually control the outbreak, it's the BIOSECURITY efforts that will prevent the infection from reaching your flock, whether it is commercial or noncommercial. Biosecurity is the sound sanitary practices that are used to stop the infectious agent from reaching the host. Before understanding biosecurity and the logic behind it, one must understand the dynamics of disease transmission. Infectious diseases in bird populations can be transmitted primarily by two ways:

1. Direct transmission, which means the infectious agents are transmitted through direct physical contact between infected individuals and uninfected susceptible individuals.
2. Indirect transmission, which means the infectious agents are transmitted through indirect transportation vehicles to reach the susceptible individuals. In case of diseases that affect birds including avian influenza, the indirect transportation vehicles include:
 - Humans
 - Domestic animals including pets
 - Wild animals including varmints and rodents
 - Physical objects including equipment (fomites)
 - Feed
 - Water
 - Environments including shared pastures and water ponds.

Accordingly, biosecurity practices are divided into:

1. Practices that aim to prevent direct transmission.
 - Avoid contact between your flock and other birds, wild, domestic or otherwise.
 - Prevent your birds from mixing with other poultry or wild birds. Mixing of birds often happens around open water bodies and in open pasture.
 - Whenever possible prevent mixing between species within the same flock, and between multiple ages within the same species.
 - Try to acquire birds from National Poultry Improvement Plan (NPIP) disease free sources.
 - If you bring new birds to your flock, quarantine the new birds for a week before mixing with the rest of the flock.
 - If you show birds, attend fairs or perform any activity where birds from different places come together in one place, quarantine the birds for a week before mixing back with the rest of the flock.

2. Practices that aim to prevent indirect transmission.

- It is highly recommended NOT to bring any visitors to your bird flock. They could be carriers of diseases on their cloths, their shoes, on their hands or any objects they bring with them.
- It's recommended to have specific cloths and shoes dedicated to working with your birds.
- Additionally, using disposable coveralls, gloves and shoe covers are highly recommended.
- Wash your hands before and after handling your birds, or their feed or their water.
- Wash your hands before and after handling any equipment, bedding material housing material on any object that comes in contact with the birds.
- Foot paths and hand sanitizing stations should be in place and used every time the poultry house is entered or exited.
- Don't bring your pets or allow them access to your birds.
- It is essential to house the birds in animal proof/bird proof houses.
- It is very important to have effective rodent control program. Rodents are notorious for transmitting not only human disease but also poultry diseases.
- Equipment, bedding material housing material on any object that comes in contact with the birds should be thoroughly cleaned and properly disinfected before using with your birds.
- Acquire you feed from trusted sources and properly store the feed in dry, cool and clean place, shielded form access by other birds and animals particularly rodents.
- Drinking water for birds should be the same quality as drinking water for human. Surface water from rivers, ponds or puddles is particularly dangerous as it often contains infectious disease agents from migratory wild birds.

These practices should be adopted by anyone who owns, grows, or handles poultry. Finally, if your birds are dying at an alarming rate, you should immediately contact any of the following:

Ohio Department of Agriculture
Animal Disease Diagnostic Laboratory:
(614) 728-6220; After Hours (888) 456-3405

USDA APHIS Veterinary Services
(866)-536-7593

Ohio Poultry Association
info@ohiopoultry.org
(614) 882-6111

If your birds are suspected of having influenza, they will be tested at ODA's Animal Disease Diagnostic Laboratory (ADDL).

For more information regarding Avian Influenza, please visit our website <<https://vet.osu.edu/extension/poultry-resources>> and download the [brochure](#).

Research

Cole, K. J., & Hogan, J. S. (2016). **Short communication: Environmental mastitis pathogen counts in freestalls bedded with composted and fresh recycled manure solids.** *Journal of Dairy Science*. Advanced online publication. doi: 10.3168/jds.2015-10238

BACKGROUND: Composting can be a beneficial method in decreasing bacterial load in organic materials such as recycled manure solids (RMS) used as bedding. Reports are limited comparing fresh RMS and composted RMS under similar environmental conditions using the same cows within one farm.

PURPOSE: The purpose was to investigate if composted RMS decreases bacterial counts of mastitis pathogens compared with fresh RMS used as freestall bedding for dairy cows.

RESULTS: Mean total gram-negative bacterial counts were approximately 0.5 log₁₀ cfu/g of dry matter lower in the composted recycled manure solids on day 0 compared with fresh recycled manure solids. *Klebsiella* species, coliform, and *Streptococcus* species counts were at least 1.0 log₁₀ cfu/g of dry matter lower in composted compared with fresh recycled manure solids on day 0. Only gram-negative bacterial counts on day 1 were reduced in composted recycled manure solids compared with fresh recycled manure solids. Differences were not observed between treatments in gram-negative bacterial, coliform, *Klebsiella* species, or *Streptococcus* species counts on day 2 and 6. Ash content was higher in composted recycled manure solids compared with fresh recycled manure solids on day 0, 1, 2, and 6.

CONCLUSIONS: The authors concluded that despite the increase in ash after composting, bacterial counts of mastitis pathogens in composted recycled manure solids were comparable with those in fresh recycled manure when used as freestall bedding. Regardless of the management strategies tested in attempt to reduce bacterial counts in RMS bedding, bacterial counts of common environmental pathogens in freestalls increased rapidly once RMS is used as bedding and counts remained elevated throughout the current and previous trials.

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Jackson, K., Carstens, G., Tedeschi, L., & Pinchak, W. (2016). **Changes in feeding behavior patterns and dry matter intake prior to clinical symptoms associated with bovine respiratory disease in growing bulls.** *Journal of Animal Science*. Advance online publication. doi: 10.2527/jas.2015-9993

BACKGROUND: Subclinical bovine respiratory disease (BRD) cases often go undetected when diagnosis is dependent upon visual observations of clinical symptoms. Thus, there is a critical need to develop animal-health monitoring systems capable of accurate preclinical detection of morbidity earlier in the disease process to enhance efficacy of antimicrobial therapy, and mitigate the economic impact of BRD. Altered behavioral patterns associated with feeding activities are among the earliest indicators of the onset of clinical illness expressed in cattle.

PURPOSE: The objective was to characterize time-series patterns in behavioral parameters associated with DMI and feeding behavior patterns relative to the onset of clinical symptoms of illness in beef cattle.

RESULTS: The model-detected inflection points for DMI were 6.8 and 3.8 d prior to observed clinical illness and metaphylactic treatment, and the reductions in DMI from detected inflection points to the day of observed clinical illness and day of metaphylactic treatment were 39.3 and 49.8%, respectively. Furthermore, the model detected inflection points for individual feeding behavior 33 traits that ranged from 1.3 to 14.2 d prior to observed clinical illness, and from 3.8 to 12.6 d prior to metaphylactic treatment.

CONCLUSIONS: The authors concluded that the results suggest that deviations in feeding behavior patterns preceding the display of clinical symptoms of illness in beef

cattle may be useful in development of predictive algorithms for preclinical detection of BRD.

[ACCESS THE ARTICLE...](#)

Bliss, N., Nelson, S. W., Nolting, J. M., & Bowman, A. S. (2016). **Prevalence of influenza A virus in exhibition swine during arrival at agricultural fairs.** *Zoonoses Public Health*. Advance online publication. doi: 10.1111/zph.12252

BACKGROUND: The largest outbreaks of swine-to-human transmission of influenza A virus (IAV) have occurred at agricultural fairs. While it seems likely that IAV is amplifying through swine populations at livestock exhibitions, little is known about IAV prevalence in swine arriving at exhibitions before swine have commingled and IAV spread through the population.

PURPOSE: The objective was to estimate the prevalence of IAV in exhibition swine as they enter fairs as a prelude to understanding the transmission of IAV at the fair with an ultimate goal of preventing intrafair transmission.

RESULTS: The overall IAV prevalence detected among swine arriving at exhibitions was 5.3% (188/3547) via rRT-PCR and 1.5% (53/3547) via virus isolation, with IAV being detected and recovered from swine at 5 of the 9 exhibitions. Within the fairs with IAV-positive swine, the individual exhibition IAV prevalence ranged from 0.2% (1/523) to 34.4% (144/419) using rRT-PCR and 0.2% (1/523) to 10.3% (43/419) with virus isolation. Single IAV subtypes were detected at three of the fairs but subtype diversity was detected among the pigs at two fairs as both H1N1 and H3N2 were recovered from incoming swine. At two of the exhibitions, a temporal relationship was observed between the order of the individual swine in sampling and the associated IAV rRT-PCR results, indicating the fomite transmission of IAV through common contact surfaces may occur.

CONCLUSIONS: The authors concluded that the current project demonstrated that a small number of swine arrived at an exhibition actively infected with IAV. However, the estimated prevalence of IAV at individual fairs ranged widely and may in part be due to the slight difference in sampling procedures used at each fair. In particular, sampling that occurred in chutes resulted in a far greater prevalence of IAV when compared with sampling in pen or on a trailer. The authors hypothesize this to be the result of IAV contamination in the chute. If true, fomite transmission of IAV may occur whenever swine are moved through the barn such as during weighing, washing, walking to and from the show ring and at times when animals encounter contaminated sites. These activities could be heightened areas for IAV transmission between swine, and thus, potential time points and locations to target for controlling swine-to-human zoonosis.

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Calendar



A full calendar of all upcoming events and continuing education opportunities offered by the College of Veterinary Medicine is available on the website at <http://vet.osu.edu/>

[Ohio Dairy Health and Management Certificate Program](#)

Module 7 – Economics of Dairy Business
March 10-11, 2016
Shisler Conference Center, Wooster, Ohio
Spots are always available for specific module plan.

[Dairy Cattle Welfare Symposium](#)

Intersection of Best Practices and Sustainability
May 20-21, 2016
Ohio Union, Columbus, Ohio
Registration deadline April 1st (limited to 265 attendees).

Food Armor® Phase I & II Program for Veterinarians

April 27-28, 2016
OVMA, Columbus, Ohio
Details and agenda will be posted soon.

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