

A strain of highly pathogenic avian influenza has infected over 200 flocks in 25 states

As of April 21, 2022, in the US 150 commercial flocks and 79 backyard flocks in 29 states have returned positive tests for the presence of a highly pathogenic avian influenza strain (HPAI), H5N1. The number of birds on premises with confirmed infections exceeds 31 million (<https://tinyurl.com/2nfr2wh>).

Most of us vividly remember the December 2014-June 2015 HPAI (mostly the H5N2 strain) outbreak that resulted in the death of more than 50 million birds either from the disease or the depopulation of poultry facilities to control the spread of the disease, so the current numbers are cause for concern.

HPAI infections have been detected in at least 762 wild birds and has resulted in the death of more than 30 bald eagles. While the connection between the Mississippi flyway for wild fowl and the infected commercial flocks was clear in the 2014-2015 HPAI outbreak so far, no direct connection between infections in wild birds and domestic fowl has been made in the current outbreak though it is likely.

In the past we have written about various avian influenza outbreaks and identified the strain involved and we think it would be helpful to our readers to understand the naming convention used by scientists.

The Animal and Plant Health Inspection Service (APHIS) writes “Avian-origin influenza viruses are broadly categorized based on a combination of two groups of proteins on the surface of the influenza A virus: hemagglutinin or “H” proteins, of which there are 16 (H1-H16), and neuraminidase or “N” proteins, of which there are 9 (N1-N9). [144] different combinations of “H” and “N” proteins are possible. Each combination is considered a different subtype” (<https://tinyurl.com/yzmvyp7f>).

The subtype does not determine its pathogenicity, which is related other factors on the surface of the virus. In public communication the H#N# is a convenient way to identify an outbreak.

While a novel coronavirus is responsible for the current pandemic that has resulted in nearly 1 million deaths in the US and over 6 million deaths worldwide, an HPAI H1N1 strain was responsible for the 1918 pandemic that resulted in 675,000 deaths in the US and at least 50 million worldwide. Since then, many H1N1 strain viruses have been identified that are not highly pathogenic.

Centers for Disease scientists have studied the 1918 H1N1 strain and have determined that while it originated in birds, it was transmitted to mammals, most likely swine, where it gained its pathogenicity (<https://tinyurl.com/yc737mtc>). From there it was transmitted to the human population.

As a result of our direct observation of the 2014-2015 HPAI outbreak and our reading of the Centers for Disease Control and Prevention study of the virus that caused the 1918 pandemic, we have two interrelated concerns.

First, as a part of the agricultural community we need to ensure that we adequately fund APHIS as well as state agencies in their ongoing work to monitor HPAI and other plant and animal diseases. Reducing the cost of maintaining government agencies like APHIS and state departments of agriculture may make a good soundbite on the campaign trail this fall, but the work they do is essential to the health of the US agricultural sector.

Second, we need to fund the continuous monitoring of the potential transmission of diseases from one species to another, a process that can make the resulting disease more deadly for humans. Both the 1918 pandemic and COVID-19 were caused by zoonotic diseases that were transmitted to humans through a secondary host.

In the absence of a disease outbreak, it is easy for us to become complacent and want to redirect funding to more visible activities. But as we are seeing with COVID-19, the ultimate cost of complacency is paid in the number of lives lost.

Policy Pennings Column 1123

Originally published in MidAmerica Farmer Grower, Vol. 37, No. 369, April 29, 2022

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