



July 2017 – June 2018

Last Updated: 5/18/2018

Total birds sampled: 31,438

Total HPAI positive cases (HA gene sequence confirmed): 0

icA molecular detection^d only (HA gene sequence unsuccessful/no virus isolated) cases: 0

Total birds sampled by flyway

Atlantic: 8,012

Mississippi: 8,616

Central: 7,175

Pacific: 7,632

American Oceania^f: 3

WILD BIRD HIGHLY PATHOGENIC AVIAN INFLUENZA CASES IN THE UNITED STATES^a

LINE	COLLECTION DATE	SPECIES	COUNTY	STATE	SUBTYPE ^b	CONFIRMATION DATE	COLLECTING AGENCY	COLLECTION STRATEGY ^c
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^a Avian H5 influenza (H5N8) originating from Eurasia (EA) spread rapidly along wild bird migratory pathways during 2014. Introduction of this virus into the Pacific Flyway sometime during 2014 has allowed mixing with North American (AM) origin viruses and generated new (novel) combinations with genes from both EA and AM origin (or “reassortant” viruses). These findings are not unexpected as the EA-H5 viruses continue to circulate in the flyways. This group of EA-H5 viruses is highly pathogenic in poultry. The ‘novel EA/AM H5N1’ is different from the ‘Asian HPAI H5N1’ and is a mixture of Eurasian and low pathogenic North American origin viruses.

^b EA = Eurasian; AM=North American; the EA-H5 (2.3.4.4) are highly pathogenic to poultry

^c M = morbidity/mortality; H = hunter harvest ; L = live bird released; A = agency harvested

^d Sequencing was unsuccessful and no virus was isolated; RNA was detected by 3 assays targeting 2 different genes including the H5 (icA) molecular assay which is specific for the Eurasian H5 clade 2.3.4.4 viruses first detected in the US in December 2014.

^e Cases posted in most recent update.

^f American Oceania flyway consists of Hawaii, Guam, Marshall Islands, and American Samoa.

For past updates, please refer to [Wild Bird Positive Highly Pathogenic Avian Influenza Cases in the United States: July 2016 to June 2017](#).