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H5N1 Bird Flu in 2026: A Comprehensive Status Report on the US Outbreak

Biology * Public Health * Evolution

The Clade 2.3.4.4b Panzootic Landscape

Originating from the 1996 goose/Guangdong lineage, highly pathogenic avian influenza A(H5N1) clade 2.3.4.4b entered North America via migratory waterfowl in late 2021, triggering the largest animal health emergency in United States history and a complex public health challenge.[1][2][8] By November 2026, viral evolution had expanded the outbreak from wild birds and poultry into a multi-species epidemiological crisis spanning over 1,000 dairy cattle herds across 22 states -- including fall 2026 detections in Yakima County, Washington, and Oregon -- alongside domestic swine, marine and terrestrial mammals, and 74 reported human A(H5) cases (including three fatalities since 2024).[3][4][5][7]

Genomic Reassortment and Molecular Mammalian Adaptation

As a segmented eight-strand negative-sense RNA virus, influenza A undergoes rapid antigenic shift (reassortment) within its genome when co-infecting host cells.[11][12] In March 2024, a single wild-bird spillover into Texas and Kansas cattle established genotype B3.13.[13] B3.13 acquired a notable amino acid substitution -- the PB2 M631L mutation in its RNA-dependent RNA polymerase complex -- alongside PA K497R, enhancing binding to bovine ANP32A cellular proteins to drive high-titer replication in mammary glands and primary human airway cultures.[9][14] In early 2025, surveillance identified independent D-lineage spillovers from wild birds, including D1.1 in Nevada and Arizona dairy herds, D1.2 in Oregon swine, and D1.3 in Ohio poultry.[11][12][15]

| Genotype | | Primary Host Reservoirs | | Molecular & Epidemiological Significance |

| B3.13 | | Dairy Cattle | | Drives the multi-state bovine epizootic; carries PB2 M631L and PA K497R mammalian polymerase adaptations.[9][13] |

| D1.1 | | Wild Birds, Poultry, Cattle | | Independent 2025 cattle spillover in NV/AZ; caused the first fatal U.S. human H5N1 case in Louisiana.[12][15] |

| D1.2 | | Migratory Birds, Swine | | Infected domestic pigs in Oregon (Oct 2024), posing reassortment risks in mixing-vessel hosts.[11] |

| D1.3 | | Commercial Poultry | | Reassortant lineage responsible for severe hospitalization of an Ohio poultry worker (Feb 2025).[12] |

The Bovine Epizootic and Non-Bovine Mammalian Spillovers

Exhibiting strong mammary tropism, H5N1 sheds high viral loads in unpasteurized milk; retrospective PCR detected viral RNA in 36% of retail milk samples across 13 states in spring 2024.[16][17] In December 2024, the USDA launched the five-stage

National Milk Testing Strategy (covering 28 states and 65% of U.S. milk production by January 2025) to screen processing plant silos and farm bulk tanks.[15][18][19][20] Over 1,000 herds had tested positive by early 2026 (including 759 in California), with ongoing silo testing detecting Oregon's first dairy herd infection in late 2026.[3][4] While commercial pasteurization inactivates the virus, raw milk remains a major vector.[21]

Across the wider ecosystem, H5N1 breached the species barrier into domestic pigs in Crook County, Oregon (October 2024, genotype D1.2).[11] Because porcine respiratory epithelia co-express avian 2,3-linked and human 2,6-linked sialic acid receptors, swine act as "mixing vessels" capable of reassorting avian and seasonal human viruses.[11] Meanwhile, raw milk and raw pet food caused fatal neurological disease in domestic cats -- including a Los Angeles County cluster across late 2024 and early 2025 linked to raw dairy and raw pet food that also resulted in seropositive asymptomatic infection in an exposed veterinary worker -- and wildlife surveillance confirmed fatal infections in a Florida bottlenose dolphin (meningoencephalitis), alpacas, Catalina Island foxes, red foxes, skunks, and house mice.[6][22][23][24]

Human Epidemiology, Agricultural Impacts, and One Health Surveillance

From February 2024 through early November 2026, the U.S. recorded 74 confirmed human A(H5) cases -- 67 identified via exposed-worker monitoring and seven via routine influenza surveillance -- spanning dairy workers (predominantly B3.13 presenting as acute conjunctivitis from milking-parlor splashes), commercial poultry workers (including a hospitalized Ohio worker with deep alveolar D1.3 infection), backyard/wild-bird exposures, and a fall 2026 cluster of three dairy-linked cases in Yakima County, Washington.[5][7][12][14] Three U.S. human cases have proved fatal: an older Louisiana patient infected with D1.1 from backyard/wild birds (January 2025), a Washington State patient who died in November 2025 from the world's first human influenza A(H5N5) infection, and a hospitalized Yakima County resident with underlying conditions who died in early November 2026 following exposure to infected dairy cattle.[5][7][26] Sequencing of human isolates has detected the mammalian upper-airway temperature adaptation PB2 E627K and minor oseltamivir-sensitivity shifts (NA-S247N), though no human-to-human transmission has been documented.[1][7][16][27]

| Outbreak Metric (2022 - Nov 2026) | | Quantified Scale | | Epidemiological & Economic Context |

| Human Cases (U.S. Cumulative Total) | | 74 Confirmed Cases | | Mostly mild conjunctivitis in dairy and poultry workers; 3 fatalities (LA H5N1 D1.1, WA H5N5, and Yakima WA H5N1).[5][7][26] |

| Commercial & Backyard Poultry Culled | | >168 Million Birds | | Spans all 50 states & Puerto Rico, dwarfing the 2014-2015 loss of 50.5M birds.[3][8] |

| Direct Economic & Federal Response Cost | | >1.4B USD Indemnity + 1B USD USDA Plan | | Covers mass depopulation, biosecurity, egg supply shocks, and livestock vaccines.[8][29] |

| Active Human & Wastewater Monitoring | | Monthly Worker + NWSS Surveillance | |

Paired with wastewater-based epidemiology across CDC National Wastewater Surveillance System sites.[25][28] |

Eroding Barriers and the One Health Imperative

While subclinical waterfowl carriage continuously re-seeds farms and threatens avian biodiversity, the convergence of >168 million culled birds, >1,000 infected dairy herds across 22 states, and polymerase mutations (PB2 M631L and E627K) demonstrates that H5N1 continues to erode cross-species barriers.[2][3][4][9] Sustaining the 2025 National One Health Framework, bulk milk screening, viral genomics, and livestock vaccine deployment remains vital to prevent a pandemic reassortment event.[10][29]

Updates... (Nov 22, 2026): Enriched Works Cited entries with exact verified CrossRef, CDC, USDA APHIS, WHO, and CIDRAP publication dates (in addition to earlier Nov 19, 2026 replacement of the Los Angeles County DPH soft-404 with CDC MMWR doi:10.15585/mmwr.mm7517a1).

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