

Observations from the application of a multimodal data approach for the examination of the 2024-2025 Highly Pathogenic Avian Influenza outbreak in the United States: Descriptive Study

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Abstract

Background: Highly pathogenic avian influenza (HPAI) outbreaks have primarily affected wild and domesticated bird populations, with occasional human spillover. In 2024, the United States (US) reported the first known HPAI H5N1 infection in dairy cattle, which rapidly evolved into a multispecies outbreak among cattle and poultry with spillover into humans. Publicly available data remained siloed and fragmented across agencies, which has implications for timely response. Innovative multimodal surveillance methods present an opportunity to enhance early situational awareness through comprehensive, standardized data collection, integration, and visualization.

Objective: This study aimed to describe observations from the application of enhanced surveillance methods that collect, integrate, and visualize multimodal data for real-time tracking of the 2024-2025 HPAI outbreak in the US as an innovative, transparent, repeatable, and scalable approach for open source public health surveillance for zoonotic or other emerging or re-emerging pathogens.

Methods: The Global.health consortium conducted real-time, multimodal data collection on the US HPAI outbreak between February 1, 2024 and February 28, 2025 using publicly available data for human cases, animal outbreaks, wastewater surveillance, genomic data, research updates, policy actions, and response measures. This digital data stream of traditional and non-traditional sources was used to create outbreak resources—a line-list, event timeline, and interactive map—using a One Health framework to track emerging hotspots

Results: Seventy human HPAI cases were confirmed across 13 US states, with exposure for nearly all (92.9%) cases associated with commercial agriculture and related operations. Only one human case of HPAI had ever been documented in the US prior to

2024, underscoring a sharp rise in incidence. We curated 682 Timeline entries across six distinct categories: human, cattle, response, birds, genome, wastewater, and mammals. California was identified as the outbreak epicenter with leading numbers in human cases (n= 38, 54.3%), cattle (n=748, 76.6%), and poultry infections (n=66, 20.3%) during the study period. Wastewater surveillance provided an early warning sign, identifying viral presence in California at least 81 days before the first dairy cattle case.

Conclusions: The integration of traditional and non-traditional public health surveillance data into a single view within a One Health framework improved contextual understanding and enhanced situational awareness during the 2024-2025 HPAI outbreak in the US. Wastewater detections identified early viral presence, marking a critical window for intervention, policy action, and response to curb spread. Access to an open source multimodal data platform - like that put forward by Global.health - in real-time can assist researchers, public health officials, and decision makers in understanding the origins, scope, and evolution of emerging zoonotic diseases that fragmented, more traditional surveillance systems may be unable to readily provide. Further research should be conducted to understand the full potential of multimodal data in real-time outbreak surveillance.

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Original Manuscript

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Abstract

Background

Highly pathogenic avian influenza (HPAI) outbreaks have primarily affected wild and domesticated bird populations, with occasional human spillover. In 2024, the United States (US) reported the first known HPAI H5N1 infection in dairy cattle, which rapidly evolved into a multispecies outbreak among cattle and poultry with spillover into humans. Publicly available data remained siloed and fragmented across agencies, which has implications for timely response. Innovative multimodal

surveillance methods present an opportunity to enhance early situational awareness through comprehensive, standardized data collection, integration, and visualization.

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This study aimed to describe observations from the application of enhanced surveillance methods that collect, integrate, and visualize multimodal data for real-time tracking of the 2024-2025 HPAI outbreak in the US as an innovative, transparent, repeatable, and scalable approach for open source public health surveillance for zoonotic or other emerging or re-emerging pathogens.

Methods

The Global.health consortium conducted real-time, multimodal data collection on the US HPAI outbreak between February 1, 2024 and February 28, 2025 using publicly available data for human cases, animal outbreaks, wastewater surveillance, genomic data, research updates, policy actions, and response measures. This digital data stream of traditional and non-traditional sources was used to create outbreak resources—a line-list, event timeline, and interactive map—using a One Health framework to track emerging hotspots.

Results

Seventy human HPAI cases were confirmed across 13 US states, with exposure for nearly all (92.9%) cases associated with commercial agriculture and related operations. Only one human case of HPAI had ever been documented in the US prior to 2024, underscoring a sharp rise in incidence. We curated 682 Timeline entries across six distinct categories: human, cattle, response, birds, genome, wastewater, and mammals. California was identified as the outbreak epicenter with leading numbers in human cases ($n=38$, 54.3%), cattle ($n=748$, 76.6%), and poultry infections ($n=66$, 20.3%) during the study period. Wastewater surveillance provided an early warning sign, identifying viral presence in California at least 81 days before the first dairy cattle case.

Conclusions

The integration of traditional and non-traditional public health surveillance data into a single view within a One Health framework improved contextual understanding and enhanced situational awareness during the 2024-2025 HPAI outbreak in the US. Wastewater detections identified early viral presence, marking a critical window for intervention, policy action, and response to curb spread. Access to an open source multimodal data platform - like that put forward by Global.health - in real-time can assist researchers, public health officials, and decision makers in understanding the origins, scope, and evolution of emerging zoonotic diseases that fragmented, more traditional surveillance systems may be unable to readily provide. Further research should be conducted to understand the full potential of multimodal data in real-time outbreak surveillance.

Keywords: One Health; Digital Health; Public Health Surveillance; Zoonotic Infectious Diseases; Zoonotic Spillover; Avian Influenza; Wastewater Surveillance; Data Curation; Data Analysis; Data Visualization

Introduction

Background

Early in 2024, farmers in the United States (US) began to report the emergence of a mysterious illness amongst their cattle herds. This cluster of symptoms would later be identified as the H5N1 strain of highly pathogenic avian influenza (HPAI) [1]. HPAI is better known for infecting wild and domesticated bird populations, with occasional and severe human spillovers. Since 2022, HPAI has been regularly reported on US poultry farms [2], however this was the first time that H5N1 had been identified in dairy cattle [3–6]. On April 1, 2024, the Texas Department of State Health Services announced the first human case of HPAI since the country's first confirmed human case in 2022 [7,8]. The individual was a dairy farm worker who had come in contact with infected cattle while at work. Genomic testing of the virus provided strong evidence that the farm worker had been infected via a spillover from dairy cattle [9]. This spillover into humans marked the start of a multi-state zoonotic outbreak infecting humans, cattle, poultry, and other mammals [10].

The emergence of a public health threat, such as a zoonotic outbreak, initiates a series of mitigation efforts. Within the US, multiple local, state, and federal agencies are responsible for protecting and monitoring human, environmental, and animal health [11–13]. This results in a complex and fragmented response and surveillance system for monitoring multi-species diseases such as HPAI. A key challenge arising from this surveillance landscape is that resulting data collected by responding agencies is siloed, which in turn can hamper timely analysis and response [14]. Barriers to implementing One Health surveillance systems—including data privacy, quality, and resource capacity—mirror longstanding challenges in the evolution of public health surveillance, highlighting the need for innovative methods to improve monitoring of zoonotic diseases [15,16].

Global.health (G.h) was formed during the early stages of the SARS-CoV-2 pandemic in 2020 to address the challenge of integrating fragmented data during multi-agency, multi-jurisdictional outbreak responses [14,17]. The technology powering G.h is an open source, scalable, and accessible platform for the rapid curation, analysis, and visualization of early outbreak data [18]. The platform has been deployed in response to mpox, Ebola, and Marburg, evolving to address the specific needs presented by each outbreak [19–21].

Study Objectives

In order to increase access to data and support One Health analysis of the HPAI outbreak in the US, G.h launched a data collection effort that integrated human cases, animal outbreaks, wastewater surveillance, genomic data, research, response efforts, and policy actions. Accompanying this data collection effort was the creation of enhanced data visualizations to improve outbreak insights. In this paper, we examine G.h's multimodal data collection, integration, and visualization efforts. Subsequently, we discuss observations regarding the spread of HPAI over time. Using information collected between February 2024 and February 2025, this paper highlights the value of integrating disparate datasets into infectious disease surveillance systems for increased situational awareness.

Methods

Outbreak Initiation

A set of established protocols are used to analyze emerging public health events and determine if they require the launch of G.h outbreak response [18]. Early in 2024, the G.h team initiated an outbreak response to the HPAI outbreak in the US. The launch of an outbreak response triggers a

cascade of planning and preparatory measures outlined in Image 1a and 1b.

Figure 1a: Global.health Decision Instrument for the Assessment of an Emerging Infectious Disease Event

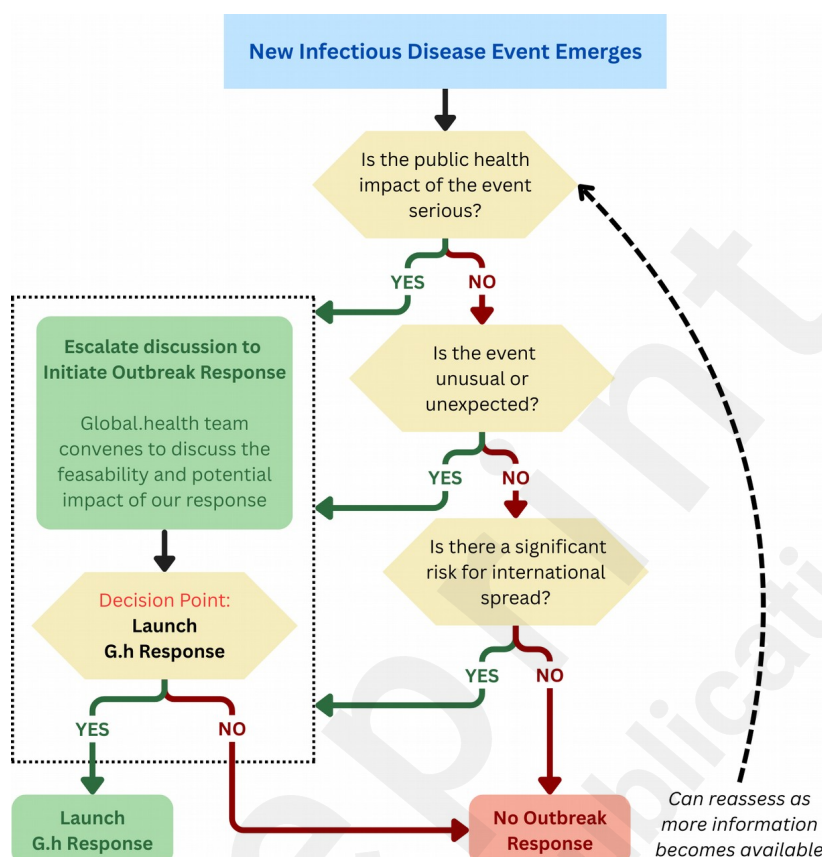


Figure 1a. Global.health Decision Instrument for the Assessment of an Emerging Infectious Disease Event. Modeled after the World Health Organization's International Health Regulations (2005) Third Edition Annex 2, a cascade of yes/no binary questions are asked to support informed decision making [22]. A "yes" response to these questions will escalate internal discussion around the feasibility and potential impact of our work that considers timing, team resources, publicly available information, and current event coverage. The outcome of this discussion reaches a Decision Point for yes/no to launch the G.h outbreak response. A "yes" decision will move forward with the launch of a G.h outbreak response outlined in Figure 1b. A "no" decision can be reassessed at any time as more information becomes available. Serious public health events include those with high case-fatality rates, limited access to effective prophylaxis or treatment, challenges in detecting the pathogen, spread in community and healthcare settings, and the need for an enhanced response at multiple levels. A subset of pathogens G.h considers as likely triggers for serious public health events are listed by the United Kingdom Health Security Agency as high consequence infectious diseases [23]. G.h may respond to other high consequence infectious diseases such as mpox and measles and vector borne diseases such as dengue, chikungunya, and yellow fever.

Figure 1b: Outbreak Response Workflow

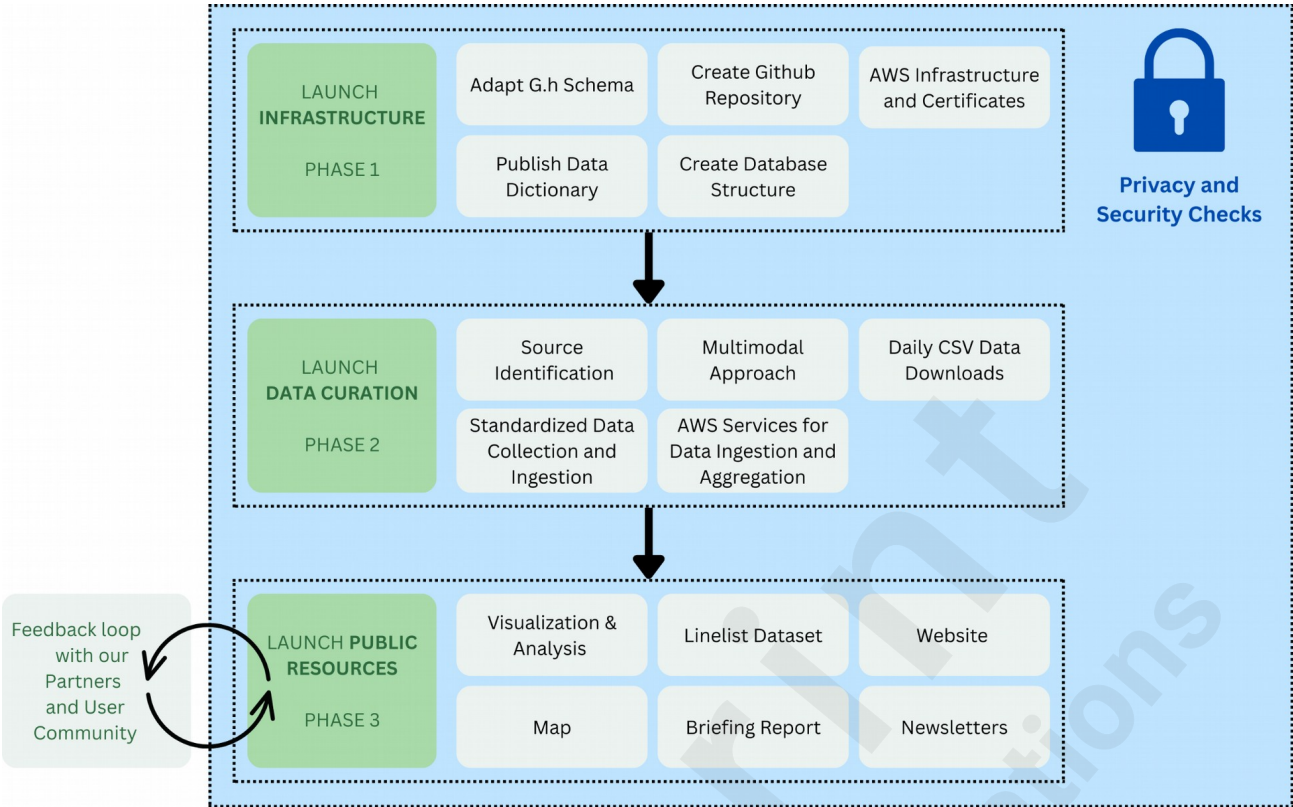


Figure 1b. Outbreak Response Workflow. Decision to launch a G.h response triggers a tri-phased series of actions that first set-up the infrastructure (Phase 1), then launch data curation efforts (Phase 2), and later provide public resources to our global user community (Phase 3). Examples of the types of activities or products created to support each phase are listed in the relevant section. A feedback loop is built into the model to support a transparent, crowdsourced approach to sharing outbreak information and welcome meaningful collaboration and fact checks through our platform. We consider relevant data privacy laws and regulations and employ robust data protection measures and mitigation strategies including deidentification, data validation, data quality checks, and access control.

Data Collection: Outbreak Linelist, Human Data

G.h developed and maintains a common data schema used to structure infectious disease data. During a response, the G.h outbreak schema is applied and may be adapted for novel data streams or pathogens to create the Outbreak Linelist that records granular epidemiological data pertaining to human cases in a standardized manner, building on lessons learned from COVID-19 data curation [24]. The outbreak schema is utilized for every outbreak (Table 1, Appendix) and can be modified to add new fields of interest. For the HPAI outbreak, Pathogen_name was expanded to capture subtype detail for HPAI; Pathogen_subtype1 and Pathogen_subtype2 capture data for Hemagglutinin and Neuraminidase proteins, respectively. The Genomics field was expanded to capture distinct information for Sequence, Clade, and Genotype. The study period captures and reviews outbreak data between February 1, 2024 and February 28, 2025. Systematic data collection started in April 2024 and retrospectively added earlier events of significance. Data collection for this event also extended beyond the study period but is not evaluated in this study. Curators undergo extensive training for data collection and standardization and each entry is reviewed and validated by at least one additional curator prior to posting. This study used publicly available, de-identified data and did not involve human participants. As such, it was not subject to Institutional Review Board review or approval.

Table 1: Schema

Variable Name	Definition	Value
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ID	Unique identification number of the case	<i>Number</i> . Starting with 1 and incrementing for each new case.
Pathogen_name	Pathogen of case	<i>String</i> . Constant pre-filled value: Influenza A
Pathogen_subtype1	Pathogen subtype for Influenza A Hx. Hemagglutinin protein type	<i>String</i> . Hx
Pathogen_subtype2	Pathogen subtype for Influenza A, further classification HxNy. Hemagglutinin protein and neuraminidase protein types	<i>String</i> . HxNy
Case_status	Status of the case	<i>String</i> . Must be one of ["confirmed", "probable", "suspected", "discarded", "omit_error"]
Location_Admin0	Admin 0 location [country]	<i>String</i> , countries (states or territories) that have ISO 3166-1 codes, USA perspective is used for disputed areas
Location_Admin1	Admin 1 location [state / province]	<i>String</i> , first-level administrative areas that have ISO 3166-2 (ISO 3166-1 alpha-2) codes, usually states or provinces
Location_Admin2	Admin 2 location [county / district]	<i>String</i> , second-level administrative areas, like counties, districts, or cities
Location_Admin3	Admin 3 location [city]	<i>String</i> , third-level administrative areas, like townships, towns, municipalities or villages
Age	Age of individual	<i>String</i> . Specified as range, open-ended (<n, >n) or as a range delimited by a hyphen following 5 year increments (m-n). Open-ended values for 'adult' is >=18 and 'child' is <18.
Gender	Sex at birth of an individual	<i>String</i> . Must be one of ["male", "female", "other"]
Occupation	Individual's occupation	<i>String</i> . Free response entry
Symptoms	Comma separated list of symptoms as described by source	<i>String</i> . Individual symptoms separated by comma. List of individual symptoms recorded as of February 28, 2025 is presented in Table 5.
Date_onset	Date of onset of symptoms	<i>String</i> , format: iso8601date
Date_confirmation	Date case was confirmed	<i>String</i> , format: iso8601date
Pre_existing_condition	If the individual has any pre-existing conditions)	<i>String</i> . Must be one of ["Y", "N"]
Hospitalised	Whether individual was hospitalized	<i>String</i> . Must be one of ["Y", "N"]
Date_hospitalisation	Date individual was hospitalized	<i>String</i> , format: date
Intensive_care	Whether individual admitted to an intensive care unit or high dependency unit at hospital	<i>String</i> . Must be one of ["Y", "N"]
Isolated	Whether individual was isolated at home or in hospital	<i>String</i> . Must be one of ["Y", "N"]
Date_isolation	Date individual entered isolation	<i>String</i> , format: iso8601date
Treatment_antiviral	Has the individual received antiviral treatment	<i>String</i> , Must be one of ["Y", "N"]
Treatment_antiviral_name	Name of antiviral drug	<i>String</i> .
Vaccination	Has the individual received a dose of vaccine	<i>String</i> . Must be one of ["Y", "N"]
Vaccine_name	Name of the first vaccine	<i>String</i> .

Vaccine_date	Date of first vaccination	<i>String, format: iso8601date</i>
Outcome	Outcome of disease, recovered includes inactive case counts.	<i>String.</i> Must be one of ["recovered", "death", "ongoing post-acute condition"]. "Recovered" includes 'recovering' outcome status, as described by Source
Date_death	Date individual died	<i>String, format: iso8601date</i>
Contact_with_case	Has the individual had contact with a confirmed or suspected case	<i>String.</i> Must be one of ["Y", "N"]
Contact_ID	If specified, the ID of the confirmed or suspected contact	<i>String.</i>
Contact_setting	Setting where contact occurred	<i>String.</i> Must be one of ["HOUSE", "WORK", "SCHOOL", "HEALTH", "PARTY", "BAR", "LARGE", "LARGECONTACT", "OTHER", "UNK"]
Contact_animal	Whether the individual has known contact with animals	<i>String.</i> Must be one of ["COMMERCIAL", "BACKYARD", "PET", "PETRODENTS", "WILD", "WILDRODENTS", "OTHER"]
Contact_animal_species	Free text describing animal species with known contact	<i>String.</i>
Transmission	Most likely mode of transmission	<i>String.</i> Must be one of ["ANIMAL", "HAI", "LAB", "MTCT", "OTHER", "FOMITE", "PTP", "SEX", "TRANSFU", "UNK"]
Travel_history	Whether an individual has travel history, domestic and/or international	<i>String.</i> Must be one of ["Y", "N"]
Travel_history_entry	Date when individual entered the country	<i>String, format: iso8601date</i>
Travel_history_start	Date when individual began travel	<i>String, format: iso8601date</i>
Travel_history_location	Location of travel obtained from geocoding API such as Mapbox	<i>String,</i> free-text field for location information <i>Object (GeoJSON)</i>
Genomic_Sequence	Sequence name and accession number(s) uploaded to public database	<i>String.</i>
Genomics_Clade	Which clade the viral strain belongs to	<i>String.</i>
Genomics_Genotype	Which genotype the viral strain belongs to	<i>String.</i>
Confirmation_method	Test used to perform diagnosis	<i>String.</i>
Source	URL of news story or government source where this case was confirmed	<i>String, format: url</i>
Source_Date report	Date of report for Source (I)	<i>String, format: iso8601date</i>
Source_Government	Indicate whether Source (I) is an official government source	<i>String.</i> Must be one of ["Y", "N"]
Source_II	URL of news story or government source where this case was confirmed	<i>String, format: url</i>
Source_III	URL of news story or government source where this case was confirmed	<i>String, format: url</i>
Source_IV	URL of news story or government source where this case was confirmed	<i>String, format: url.</i>
Source_V	URL of news story or government source where this case was confirmed	<i>String, format: url.</i>
Source_VI	URL of news story or government source where this case was confirmed	<i>String, format: url.</i>

Source_VII	URL of news story or government source where this case was confirmed	<i>String, format: url.</i>
Source_VIII	URL of news story or government source where this case was confirmed	<i>String, format: url.</i>
Source_IX	URL of news story or government source where this case was confirmed	<i>String, format: url.</i> Additional sources may be added.
Location_Comment*	Location detail for case	<i>String.</i> For internal use only.
Contact_comment*	Free text describing any additional contact information	<i>String.</i> For internal use only
Travel_history_comment*	Travel history detail for case	<i>String.</i> For internal use only
Confirmation_comment*	Testing or confirmation detail for case	<i>String.</i> For internal use only
Date_entry*	Date case was entered into linelist	<i>String, format: iso8601date</i>
Date_last_modified*	Last date when case was modified in linelist	<i>String, format: iso8601date.</i>
Curator_initials*	Curator initials of those who contributed to curating case	<i>String.</i> For internal use only
Verified*	Whether case has been verified by second curator	<i>String.</i> Must be one of ["Y", "N"]. For internal use only
Verified_by*	Initials of verifier	<i>String.</i> For internal use only
Curator Comment*	Curator notes about case	<i>String.</i> For internal use only
Table 1 outlines all schema variables used by the G.h curators during the 2024 - 2025 outbreak response to HPAI * Indicates that this variable was private and could only be viewed by the curation team		

Data Collection: Outbreak Timeline, Multimodal Data

Complementing the Outbreak Linelist, and to help place the events in context, an Outbreak Timeline was created [25]. Because the Outbreak Linelist is exclusive to human cases, we also developed an Outbreak Timeline that utilized multimodal data to enhance outbreak surveillance methods and exploit publicly available sources during the early response phase [26]. The Outbreak Timeline weaves together diverse data sources (outlined in Figure 2) into a single, integrated chronology to inform response in real-time and considers a One Health approach to highlight the interconnectedness of humans, animals and our shared environment for this zoonotic outbreak [27].

Figure 2: Multimodal Data Approach for Infectious Disease Surveillance

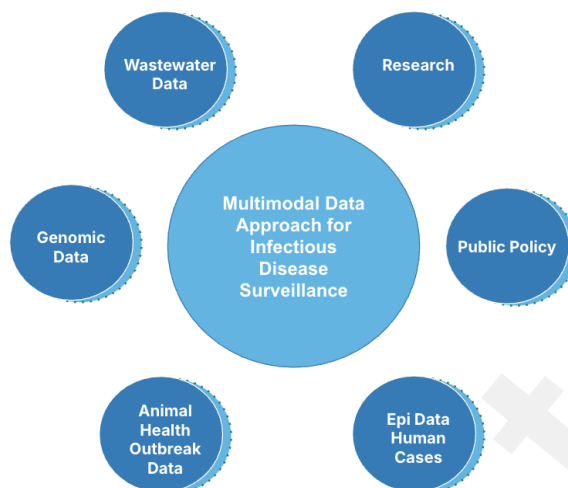


Figure 2. A multimodal data approach for integrated infectious disease surveillance. This figure outlines the types of sources collected to track the emerging H5 outbreak in the US. Disparate data sources that include epidemiological data for human cases, animal health outbreak data, genomics data, wastewater surveillance data, research and response highlights, and public policy actions are brought together in a timeline view for a comprehensive picture of the emerging event.

Outbreak Timeline entries were organized under four variables: Date, Event, Read More (source link), and Category. Each entry was tagged under one of the following categories for easy filtering and organization: Human, Cattle, Response, Birds, Wastewater, Genome, and Mammals.

The primary source used to identify animal outbreaks was the United States Department of Agriculture (USDA) [28]. The USDA website reports HPAI in commercial and backyard flocks, wild birds, mammals, and livestock. For poultry outbreaks, using the USDA website, curators were able to ascertain the confirmation date, state and county location, production type, control area release, and the number of birds affected [2]. Only poultry or birds classified under commercial production, including the World Organization for Animal Health (WOAH) poultry category, were included in the descriptive analyses for this study. For livestock (cattle), curators used the USDA website to ascertain confirmation date, state location, production type, and species [29]. Outbreaks among “cattle” species and “dairy milking cows” as the production type were included in these analyses. These commercial industry productions supply the food chain and create hot-spots for increased risk of occupational exposure to HPAI among farm workers.

Wastewater surveillance systems can indicate the presence of a pathogen at the population level that is not influenced by the reporting of symptoms, access to diagnostic tests, nor treatment-seeking behavior [30,31]. For the collection of wastewater data, curators manually reviewed publicly available WastewaterSCAN reports from 192 wastewater testing sites across the US [32]. Filters were selected for Pathogen: Influenza; View by: Location; Subtype: H5; Location(s): National, All Wastewater Sites (192). Data is available from WastewaterSCAN as of May 7, 2024. The first H5 detection was observed on May 16th, 2024 in Jackson, Michigan.

Genomic data, for humans and animals, can support preparedness and response and provide insight into genetic diversity, viral mutations, transmission and spread, and help to inform targeted interventions [33]. For the collection of genomic data, including clade and genotype information, sequence name, and accession number, the curation team gathered details from research and technical updates and information submitted to the Global Initiative on Sharing All Influenza Data (GISAID) virus genomic database or to GenBank, the genetic sequence database run by the US

National Institutes of Health (NIH) [34,35]. Data collection and reconciliation efforts for HPAI are ongoing.

Global.health collaborated with Think Global Health to publish a weekly version of the Outbreak Timeline [25].

Visualizing Multimodal Data

The Outbreak Visualization Map was created to accompany the Outbreak Linelist and multimodal Outbreak Timeline as publicly available resources [36]. Based on our development experience with maps from COVID-19, Mpox (2022 and 2024), Ebola (Uganda 2022), and Marburg (Equatorial Guinea 2023), we used Mapbox Boundaries and Mapbox GL JS library to create a state-level human HPAI map and later added new data overlays for county-level animal outbreaks in commercial cattle and poultry.

In order for data to be properly displayed on the map, it needs to contain identifying information about affected locations. G.h utilizes admin0 to admin3 administrative resolutions (those correspond to: *admin0* - country - ISO_3166-1, *admin1* - states or provinces - ISO_3166-2, *admin2* - counties, districts, or cities, *admin3* - townships, towns, municipalities or villages). For this event, animal outbreak data are available and displayed at admin2 (county), and human cases are displayed at admin1 (state). The location data identifiers are then parsed to the mapbox compatible format using their proprietary data format [37]. The parsing process is scheduled to take place daily at 1AM UTC, and we make sure to save parsed data snapshots everyday to be able to access it if necessary. Different colors are used to depict the different species affected (human: blue, cattle: orange, poultry: green). A color gradient and scale are applied to human cases at the state level (*admin1*). The date range captured on the map spans from March 7, 2024 to February 28, 2025. USDA identified a poultry outbreak, classified under the “WOAH Poultry” category, in Essex County, Massachusetts confirmed on March 7, 2024. No data for confirmed human, cattle, or poultry cases were identified prior to this date inside the study period following our inclusion criteria.

Results

Outbreak Linelist, Human Data

As of February 28, 2025, there were a total of $n = 70$ confirmed human cases of HPAI reported in 13 states across the US [10]. Nearly all confirmed human cases (92.9%) were from exposure associated with commercial agriculture and related operations. Fifty-eight point six percent ($n = 41$) of confirmed human cases occurred after exposure to infected commercial dairy herds. Thirty-four point three percent ($n = 24$) of confirmed human cases were the result of exposure to infected commercial poultry farms and culling operations. Two human cases were exposed to other animals (such as backyard flocks, wild birds, other mammals). For three cases, one Missouri resident and two Californian children, the source of exposure was unknown [10].

H5N1 was the only pathogen subtype that had been identified among these human cases. The sequencing of specimens showed that clade 2.3.4.4b of H5N1 was responsible for many of these infections, which was the same clade reportedly causing the outbreaks in cattle, poultry, and wild birds [38–40]. During the study period, of these sequenced human specimens, three genotypes of clade 2.3.4.4b had been identified: B3.13, D1.1, and D1.3 [40–42]. There was no evidence of human-to-human transmission of the virus as of February 28, 2025 [10]. All confirmed human cases to date with a known exposure source had come from zoonotic, animal-to-human transmission. As of February 28, 2025, there had only been one death reported within the US [10]. The case fatality rate for the US outbreak was 1.4%. Sixty-one confirmed human cases reported some kind of symptom

associated with HPAI as of February 28, 2025. When specific symptoms were noted (Table 2 in the Appendix), the three most common symptoms reported were fever, conjunctivitis / eye discomfort / watery discharge, and cough. G.h findings align with those reported in a publication in the New England Journal of Medicine (NEJM) whose researchers conducted patient interviews with individuals with confirmed HPAI infections. Among the 45 patients involved in the NEJM in that study population, the most common symptoms reported were conjunctivitis, fever or feeling feverish, and respiratory symptoms [43].

Table 2: Symptoms

Variable	Definition
pink_eye_conjunctivitis	"pink eye" "conjunctivitis" "eye discomfort" "eye redness"
watery_eyes	"watery discharge" "eye tearing" "drainage" "discharge"
subconjunctival_hemorrhage	"subconjunctival hemorrhage"
upper_respiratory_tract	"upper respiratory tract symptoms" "mild upper respiratory symptoms"
respiratory_symptoms	"common respiratory infection symptoms" "severe respiratory illness" "respiratory symptoms"
sore_throat	"sore throat"
runny_nose	"runny nose"
chest_pain	"chest pain"
nausea	"nausea"
weakness	"weakness"
vomiting	"vomiting"
diarrhea	"diarrhea"
nasal_congestion	"nasal congestion"
fatigue	"fatigue"
fever	"fever"
cough	"cough"

Outbreak Timeline, Multimodal Data

Early in the outbreak, the G.h team partnered with Think Global Health, a digital publication by the Council on Foreign Relations supported by Bloomberg Philanthropies. Think Global Health is an online bulletin that examines the ways in which changes in health are reshaping economies, societies, and the everyday lives of people around the globe. Think Global Health published data curated by the G.h team, creating the Outbreak Timeline (Image 1) [25]. During the study period, the Outbreak Timeline was the 16th most viewed story on the Think Global Health website. It also experienced periodic surges in traffic such as when it was first published in June 2024, then spiking again in October 2024 and January 2025. The Outbreak Timeline is accessible directly through the G.h website, GitHub, and ThinkGlobalHealth.org [17,25,44].

Image 1: Think Global Health H5N1 Influenza Outbreak Timeline

Timeline: H5N1 Influenza in the U.S., February 2024—Present

Filter by category:

Human Cattle Response Birds Genome Wastewater Mammals All

Filter by month:

2024: February March April May June July August September October November December
2025: January February March April May All

Month: February 25

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Date	Event	Read More	Category
February 28, 2025	The New Jersey Department of Health confirmed the state's first case of H5 HPAI in a feral cat from Hunterdon County. The cat developed severe neurological symptoms and was euthanized. Other cats on the property were also reported ill, including an indoor/outdoor cat that later tested positive for H5. Current public health risk remains low. Officials advise residents to monitor their pets and report any signs of illness.	New Jersey Department of Health	Mammals
February 28, 2025	CDC provides an updated risk assessment of HPAI A(H5N1) viruses in the U.S. The risk to the general population is low, but the risk to individuals in contact with potentially infected animals or contaminated surfaces or fluids is moderate to high. CDC has moderate confidence in this assessment, and stress that this risk could change in the future. The statement outlines that response to outbreaks in poultry and dairy cows has societal, policy, and economic implications for the U.S. general population, including the rise of egg prices, a decrease in milk production, and food recalls.	CDC	Response
February 28, 2025	USDA confirms 977 positive dairy farms in 17 states (Colorado (64), Idaho (36), Iowa (13), Kansas (4), Michigan (31), Minnesota (9), New Mexico (9), North Carolina (1), Ohio (1), South Dakota (7), Texas (27), Wyoming (1), Oklahoma (2), California (748), Utah (13), Nevada (10), Arizona (1)).	APHIS	Cattle
February 28, 2025	Wastewater SCAN confirms 1 site out of the 192 was positive for H5: California (1) in Turlock.	WastewaterSCAN	Wastewater

Caption: The Outbreak Timeline. This image displays the Outbreak Timeline as published on the Think Global Health website [25]. Readers can sort entries by category or month. Each entry includes the date, event, read more (with a link to the source), and category.

As of February 28, 2025, the Outbreak Timeline data consisted of a total of 682 entries across all categories (Table 2 of the Appendix). Sixty entries in the “human” category included information related to HPAI infections in humans (e.g., case counts and research updates). As case counts rapidly increased in the fall of 2024, some timeline entries reported multiple newly confirmed human infections on the same day, which is why the number of human infections exceeds the number of entries tagged in the “human” category. However, summing the case reports included in our 60 “human” entries provides the total number of confirmed cases reported in the US. For animal outbreak data, there were 116 entries in the “birds” category, with the latest timeline entry capturing a total of 325 positive commercial poultry farms across 37 states and one US territory (Figure 3). There were 191 entries under the “cattle” category, with the latest timeline entry capturing a total of 977 positive commercial dairy farms across 17 states (Figure 3).

Figure 3: HPAI Infected Poultry and Cattle Farms Per State

Human Cases Per State

38	California	1	Texas	1	Iowa	1	Wyoming
11	Washington	1	Missouri	1	Wisconsin		
10	Colorado	1	Oregon	1	Nevada		
2	Michigan	1	Louisiana	1	Ohio		

Infected Poultry Farms Per State

70	Ohio	5	Utah	3	Delaware	1	Kansas
66	California	4	Idaho	3	North Carolina	1	Montana
26	Minnesota	4	Colorado	2	Florida	1	Tennessee
24	Missouri	4	Illinois	2	Washington	1	Alabama
17	South Dakota	4	Oklahoma	2	Oregon	1	New York
16	Indiana	3	New Mexico	2	Arizona	1	Virginia
13	Michigan	3	North Dakota	2	Mississippi	1	West Virginia
13	Iowa	3	Nebraska	2	Georgia	1	Puerto Rico
11	Pennsylvania	3	Wisconsin	1	Texas		
5	Maryland	3	Arkansas	1	Massachusetts		

Cattle Farms Per State

748	California	13	Iowa	7	South Dakota	1	Wyoming
64	Colorado	13	Utah	4	Kansas	1	Arizona
36	Idaho	10	Nevada	2	Oklahoma		
31	Michigan	9	Minnesota	1	North Carolina		
27	Texas	9	New Mexico	1	Ohio		

Caption: HPAI Infections among Human, Poultry, and Cattle by State. These charts depict the number of human cases (blue), infected poultry cases (green), and infected cattle farms (red) per state. Shading indicates the number of outbreaks per state where the shading gets darker for states with more infections.

One hundred eighty nine entries in the “wastewater” category displayed wastewater detections across the country. Using WastewaterSCAN data, we observed wastewater sites with positive H5 detections in Michigan, Idaho, Texas, Minnesota, Iowa, California, South Dakota, Colorado, Arkansas, Florida, Nevada, Tennessee, Utah, Maine, Delaware, New Jersey, Illinois, Kansas, Connecticut, and Massachusetts as of February 28, 2025 [32].

The timeline also incorporated 31 entries in the “genome” category detailing genomic information about the outbreak and research related to the avian influenza genome. There were 29 entries in the “mammals” category that provided updates on HPAI in other mammals besides cattle and humans, such as domestic and feral cats, black rats, pigs, zoo animals (harbor seal), house mice, deer mice, prairie vole, and desert cottontail. Sixty-six entries in the “response” category highlighted response efforts, including policy mandates, or changes to recommendations and guidelines as the outbreak evolved.

Visualizing Multimodal Data

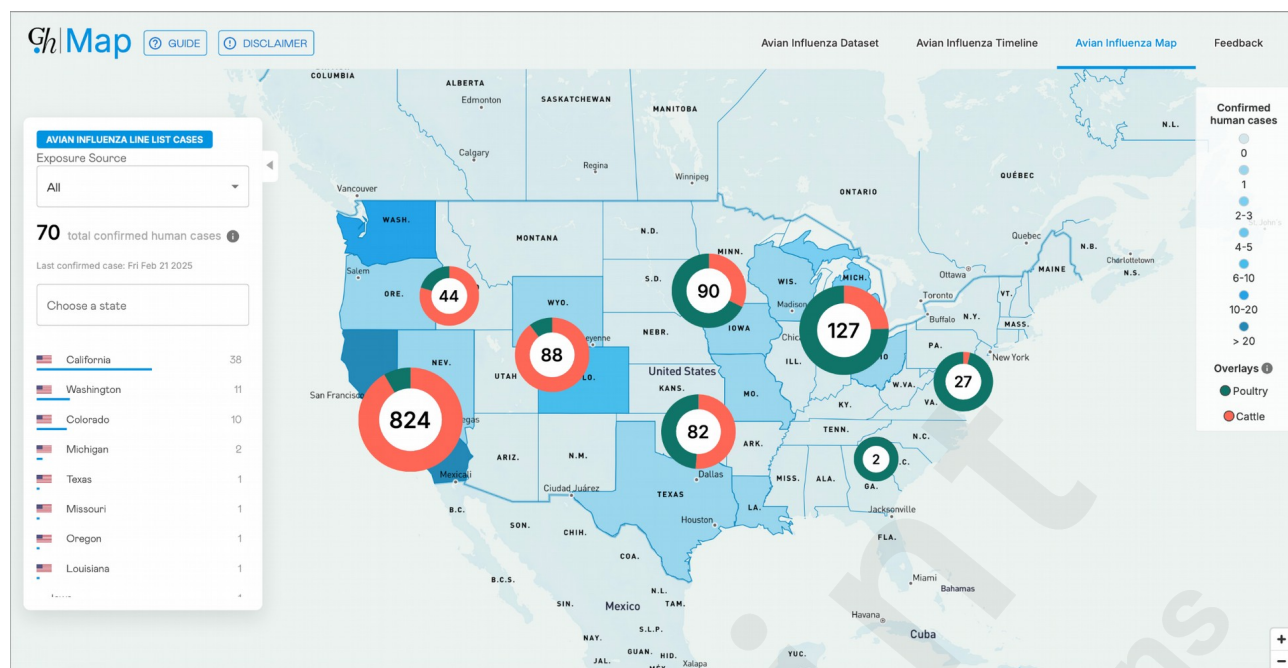
The Outbreak Visualization Map allows users to explore human cases and animal outbreaks in a single-view, supporting a One Health approach to outbreak surveillance [36]. The total number of

human HPAI cases across all affected US states is listed on the left side menu bar of the map. Human HPAI cases can be filtered by Exposure Source, currently containing five possible values: All, Cattle, Poultry, Other Animal Exposure, and Exposure Source Unknown. Additional exposure sources are added automatically as they appear in the Outbreak Linelist. State-level breakdowns can be accessed by clicking on the state area on the choropleth map or selecting it from the side menu.

Two overlays for commercial cattle and poultry outbreaks are available to select on the right side menu of the map. Each overlay represents data in *admin2* (county) administrative level. Those overlays can be toggled on and off using a side menu. Overlays are represented as markers that display the number of outbreaks and a doughnut chart showing the cattle-to-poultry ratio. Overlays form clusters that are grouped together according to the current map zoom level, clicking on the cluster zooms in the map view to the level where clusters can be split into smaller clusters and eventually individual affected areas. Hovering over animal overlay markers triggers a popup that contains additional information (commercial poultry and cattle outbreak count, affected state(s) and county(s), and last recorded outbreak). Map data is refreshed daily. The map interface also provides quick links to the Outbreak Linelist, Outbreak Timeline, and provides users with a map guide and disclaimer to help them understand and interact with this tool.

Image 2 shows the spatial distribution of reported cases of HPAI in humans, commercial poultry, and cattle outbreaks as of February 28, 2025 (confirmation date was used to pinpoint cases in time). During the study period, there were 13 states with confirmed human cases, 17 states with infected cattle, and 37 states plus one US Territory with infected poultry. Of the confirmed human cases, 41 were the result of exposure to commercial dairy herds (cattle), 24 were the result of exposure to commercial poultry farms and culling operations, two resulted from exposure to other animals (i.e. other non-commercial birds, including backyard poultry), and three had an unknown exposure source. California (CA) emerged as a hotspot during the study period, reporting the highest numbers of human cases and commercial cattle outbreaks in the US. Fifty-four point three percent of all human cases in the US were reported in CA (Total number of CA Human cases $n = 38$; Human Cases with Cattle exposure $n = 36$; Exposure Source Unknown $n = 2$) [10].

Image 2: Outbreak Visualization Map



Caption: The Outbreak Visualization Map for HPAI. This image displays the Outbreak Visualization Map with data as of February 28, 2025. The map overlays human, poultry, and cattle outbreak data in a single-view.

Case Study: California

We observed human, animal, and wastewater data reported between the study period, February 1, 2024 through February 28, 2025 with a filter on location: California. We also observed major research, response, and policy actions that may have an impact on events in California. Early in the spring of 2024, before any human or animal cases had been identified in CA, the federal government announced actions for HPAI control. On April 24, 2024, the USDA's Animal and Plant Health Inspection Service issued a federal order for mandatory testing for interstate movement of dairy cattle [45]. Additionally, it mandated reporting of positive Influenza A test results in cattle. Following these mandates, on April 26, 2024, the Centers for Disease Control and Prevention (CDC) expanded interim guidance to protect farm workers from sick animals or contaminated environments [46]. The CDC also provided guidance for employers to update or develop workplace health and safety plans. At the end of July 2024, CDC announced that it was investing \$10M into the federal "bird flu" response [47]. Allocations of these funds included \$5M towards a vaccination program targeting livestock industry workers for seasonal flu vaccines. These actions by the CDC were taken in hopes of preventing potential co-infection of seasonal and bird flu strains and potential recombination that could occur as a result. The remaining funds were distributed to partner organizations to focus on outreach and education of farmworkers to improve health and safety [47]. Just as these preventative measures were being deployed, evidence that the HPAI outbreak had infected California started to emerge.

The first signs that the HPAI dairy cattle outbreak had begun in CA came on June 10, 2024 when WastewaterSCAN reported the first positive wastewater site specifically for H5 in CA [32]. Positive detections from wastewater surveillance continued to occur in CA in July and September as early detections of the virus in the area, prior to confirmed infections in animals and humans [32]. Eighty-one days later, on August 30, 2024, the CA Department of Food and Agriculture confirmed the state's first infected dairy cattle in Sacramento County in the Central Valley [48]. Less than three weeks later, USDA reported a positive commercial poultry farm on September 18, 2024 in Merced County in the Central Valley [2]. The CA Department of Public Health then announced the state's first confirmed human cases of HPAI in the Central Valley on October 3, 2024 in two adult dairy farm

workers who had contact with infected cattle [49]. CA had positive H5 wastewater detections for the remainder of the study period (through February 28, 2025) with an increasing trend observed in October continuing through the surge in H5 detections observed from November 2024 into January 2025 [32]. Human infections among farm workers with increased risk for occupational exposure also peaked during this period in October (n = 16 confirmed human cases), November (n = 12 confirmed human cases), and December (n = 8 confirmed human cases) [10]. As with the case in Texas, pathogen genome sequencing supported spillovers from dairy cattle as the source of the infection for these farm workers [50].

Figure 4: Graph of Key Events in the California Outbreak of HPAI

California Highly Pathogenic Avian Influenza
Human, Poultry, Cattle and Wastewater

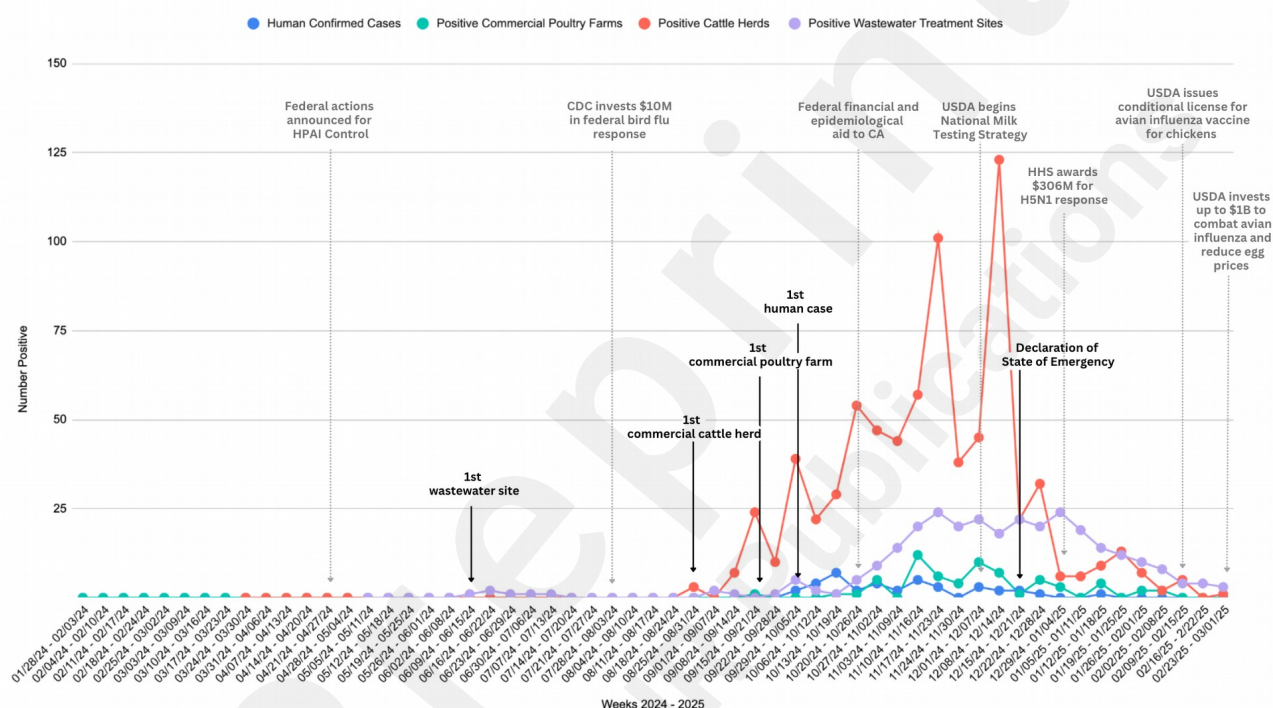


Figure 4: Graph of the number of positive human cases, commercial poultry farms, commercial dairy cattle farms, and wastewater treatment site detections of HPAI (H5) in California (CA). The study period is from February 1, 2024 through February 28, 2025 and dates were matched to CDC epidemiological weeks with a date range from January 28, 2024 (Week 5, 2024) through March 1, 2025 (Week 9, 2025). Data from WastewaterSCAN is not available prior to May 7, 2024. Cattle data from USDA is not available prior to March 25, 2024. First detections in CA and significant state- or federal-level response measures and policy changes are also annotated on the graph.

On August 30, 2024 the CA Department of Food and Agriculture confirmed the first detection of H5 HPAI in dairy cattle [48]. This first detection in dairy cattle occurred 81 days after the first wastewater detection in the state. A little over a month later, on September 18, 2024, the USDA reported the first commercial poultry farm to test positive for HPAI [2]. This announcement regarding the first detection in commercial poultry came 100 days after the first wastewater detection. On October 3, 2024, the CA Department of Public Health announced the confirmation of two human infections of HPAI [49]. Both individuals worked at dairy facilities experiencing bird flu outbreaks amongst cattle. Both individuals had been in contact with infected dairy cattle, and there was no known link or contact between the two individuals that could suggest human-to-human transmission [49]. These cases came 115 days after the first wastewater detection in CA. At the end of October, the USDA and the Department of Health and Human Services (HHS) released a fact sheet outlining the actions they have taken to assist CA in its response against HPAI [51]. These

actions included deploying an “epi strike team,” case management team, and multilingual epidemiological field team. The USDA provided support and financial assistance for veterinarian fees and shipping costs from testing dairy cattle, planning and placing biosecurity measures, and personal protective equipment (PPE) for workers. CA reportedly requested and started to receive PPE from HHS Administration for Strategic Preparedness and Response as early as May 2024, ahead of human cases and the animal outbreak in the state [51]. On December 6, 2024, the USDA announced the launch of a National Milk Testing Strategy to enhance testing and monitoring for H5N1 [52].

On December 18, 2024, CA Governor Gavin Newsom declared a State of Emergency due to the HPAI outbreak. This order was intended to prevent the further spread of HPAI and expedite the state’s response to the virus [53]. This order came 191 days after the first wastewater detection and 110 days after the first cattle outbreak. In just four months, outbreak numbers had climbed from first detection to 699 positive commercial dairy farms and 54 positive commercial poultry farms reported in CA as of December 31, 2024, showing rapid spread of the virus in the animal population [2,29]. These increasing trends are displayed in Figure 4.

Early in 2025, HHS announced \$306M in funding to enhance H5N1 monitoring and preparedness [54]. It allocated \$183M to regional, state, and local programs, \$111M to the CDC for monitoring and testing, and \$11M to the NIH for research into medical countermeasures. In February 2025, the USDA made two major announcements. The first occurred on February 14, 2025 when Zoetis received a conditional license from the USDA for an avian influenza vaccine, H5N2 subtype, for chickens [55]. The second came on February 26, 2025 when the U.S Secretary of Agriculture outlined a new \$1B strategy to mitigate the spread of bird flu and lower egg prices [56]. The plan has five main points (1) addressing biosecurity measures, (2) financial relief for affected farmers, (3) vaccine research, (4) reducing regulatory burdens, (5) exploring egg import options. When viewed in its entirety, the CA outbreak outlines a mix of proactive and reactionary measures taken in response to the emerging outbreak.

Discussion

Outbreak Resources

In this paper, we examined the G.h response to the HPAI outbreak in the US between February 2024 and February 2025, noting that systematic data collection started in April 2024 and captured events dating back to February. The data collection efforts resulted in the development of publicly accessible resources to track the outbreak, such as the Outbreak Linelist dataset (human) and Outbreak Timeline (multimodal data collection - human, animal, wastewater, genomic, research, response, and policy). The data collected was also utilized to produce an Outbreak Visualization Map (human and animal) which overlaid instances of human, cattle, and poultry for increased data visualization and insight capabilities. The integration and overlay of disparate data improved contextual understanding and can support early detection, interventions, and informed decision-making.

Case Study: California

When disparate data points were examined holistically, in real-time - tracking human, animal, and wastewater data together - it helped to identify emerging hotspots and highlighted outbreak trends. CA is examined in this study as an outbreak hotspot that quickly became an epicenter. Wastewater was the earliest indication of the virus in the state, reported in June 2024 [32]. The virus spread rapidly among commercial dairy cattle in the state, then affecting poultry and humans. The multi-species nature of the outbreak created public health, agricultural, and economic damage [57]. CA

declared a state of emergency on December 18, 2024, 191 days after the first wastewater detection, after 664 dairy farms had been infected and 33 dairy farm workers contracted the virus through occupational exposure [10,29,32,53]. The months between initial detection in wastewater and cases in animals and humans highlights a critical window of opportunity for early response. However, this outbreak demonstrated a key challenge with wastewater surveillance of HPAI: an inability to distinguish between human and animal detections. Although waste processing from industrial dairy farms in the US is highly regulated and, as a result, most farms have internal systems such that waste is not dumped into municipal sewage systems, research has demonstrated that animal inputs have been responsible for some wastewater detections [31,58,59]. Future work should focus on determining the origin of H5 in US municipal wastewater systems and include efforts to sequence viral genome fragments present in the wastewater samples. Targeted intervention and resource allocation, and preparedness measures from local, state, and federal agencies can help mitigate virus spread and reduce pandemic potential.

Flexibility and Scalability

G.h has developed flexible open source tools that are able to adapt and scale in real-time as an outbreak evolves and presents new challenges, integrating new data sources for enhanced surveillance, in line with broader calls to modernize pandemic intelligence by leveraging cross-sectoral and non-traditional data streams [60]. We were able to quickly adapt our outbreak schema for standardized collection of key information pertinent to this pathogen. In this study, we highlighted observations and insights gained from the integration of data from official and non-official media sources, including CDC, USDA, WOA, WastewaterSCAN, and GISID. Our open source format supports a transparent approach to information sharing, especially in the early days when there may be delays in official reporting and data vacuums. This integration and methodology presents an innovative, valuable, and repeatable approach for open source public health surveillance for zoonotic or other emerging or re-emerging pathogens.

Limitations

G.h strives to ensure that the data collated and shared on our platform are timely and accurate. As part of quality assurance, data requires continuous reconciliation and validation across local, state, national, and international datasets to ensure alignment and to track changes. All G.h data collection relies upon publicly available data. Further research is needed to realize the full potential of open source, multimodal data integration to support outbreak response and the impact it can have on public health as a whole. Curators faced many challenges with building an emerging infectious disease dataset in real-time, including: delays in reporting for human cases, animal outbreaks, and wastewater detections, delays in confirmatory testing, limited data standardization within and across government organizations, lack of precision of language in the media (e.g., H5, H5N1 being used interchangeably with avian influenza), presentation of aggregated case data, limited case metadata, and retroactive removal and addition of impacted herds, flocks, and wastewater sites. G.h conducted regular data reconciliation efforts to mitigate retroactive, unannounced, and unexplained changes and data discrepancies between G.h and our primary sources (WastewaterSCAN and USDA). The average look-back period was one week for Global.health to check and update data, and was limited by time and available resources. USDA published the total number of cattle outbreaks on their website, and we were able to align counts on a daily basis. However, cumulative numbers were not available from USDA (Poultry) or WastewaterSCAN. Therefore, public data that are currently available from these sources may differ from the results of this study. These challenges reflect longstanding gaps in U.S. surveillance systems; however, advanced tools and approaches create opportunities to integrate data not traditionally accessible to public health [61]. Innovative methods, such as artificial intelligence and automated quality control tools, may also help enhance data quality

in real-time [62,63]. To ensure data transparency, all outbreak resources are publicly accessible and point back to the original source(s) of information.

Conclusions

As outbreaks and the public health landscape evolve so too must our surveillance methods; how we gather, analyze, and visualize data matters. Further, the US HPAI outbreak emphasized the importance of a One Health approach as the pandemic potential of zoonotic outbreaks grows [64]. Focusing on the interplay of humans, animals, and our shared environment will assist in the ability of researchers, public health officials, and decision makers, to better understand the origins, evolution, and scope of emerging zoonotic events. Additionally, wastewater surveillance data has proven to be an important tool for identifying early indications of disease in a community, and multimodal datasets should explore and include these data when available. Accurate, accessible, real-time data is the cornerstone to prudent outbreak response. Early, open access to data and visualization tools, such as what is put forward by G.h, can demonstrate value in a public health response approach that is adaptable and resilient in the face of emerging threats.

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Conflicts of Interest: None declared.

Data Availability

Data collected for this study will be made available to others with publication. Our data products include the linelist dataset (human cases), data dictionary, interactive map, and event timeline. No additional related documents will be available. Data can be accessed through the Global.health website <https://global.health>. All of the data we collect is openly accessible under Creative Commons Attribution license (CC-BY-4.0) If you choose to access, download, or use G.h data, we ask that you adhere to our Terms of Use, Privacy Policy, and Citation Guidelines provided on our website.

Authors' Contributions (recommended):

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Samuel V. Scarpino, John S. Brownstein (Methodology), Juliana Sopko, Aimee Han, Jacqueline Powers, Mansi Avunoori, Stanislaw Zakrzewski (Visualization), Juliana Sopko, Aimee Han, Jacqueline Powers, Stanislaw Zakrzewski (Writing - original draft), Juliana Sopko, Aimee Han, Jacqueline Powers, Mansi Avunoori, Stanislaw Zakrzewski, Kara Sewalk, Autumn Gertz, Benjamin Rader, Moritz U.G. Kraemer, Samuel V. Scarpino, John S. Brownstein, (Writing - review & editing), Juliana Sopko, Aimee Han, Kara Sewalk, John S. Brownstein (Project administration), John S. Brownstein (Resources), Juliana Sopko, John S. Brownstein (Supervision), Moritz U.G. Kraemer, Samuel V. Scarpino, John S. Brownstein (Funding acquisition).

Abbreviations

CA: California

CDC: Centers for Disease Control and Prevention

G.h: Global.health

GISAID: Global Initiative on Sharing All Influenza Data

HHS: Department of Health and Human Services

HPAI: highly pathogenic avian influenza

NEJM: New England Journal of Medicine

NIH: National Institutes of Health

PPE: personal protective equipment

US: United States

USDA: United States Department of Agriculture

WOAH: World Organization for Animal Health

Data Availability

The datasets discussed in this study are available through the G.h website or through corresponding authors upon reasonable request. Global.health commits to releasing code and software tools under MIT License (<https://opensource.org/licenses/MIT>) and data where possible under CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/>). Both, University of Oxford and Boston Children's Hospital serve as data controllers.

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Supplementary Files