10 HOT TOPICS in infectious diseases

14° edizione

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Centro Congressi Castello Simon Boccanegra
Ospedale Policlinico San Martino

L'aviaria (H5N1) e le altre zoonosi respiratorie potenzialmente patogene per l'uomo

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DISCLOSURES

Advisor/speaker (past 2 years)

Novartis, MSD, Astrazeneca

Le zoonosi sono definite come infezioni trasmesse naturalmente tra animali vertebrati e uomo

3 categorie:

a) <u>Zoonosi endemiche</u> presenti in molti luoghi e colpiscono molte persone ed animali

b) <u>Zoonosi epidemiche</u> con distribuzione temporale e spaziale sporadica

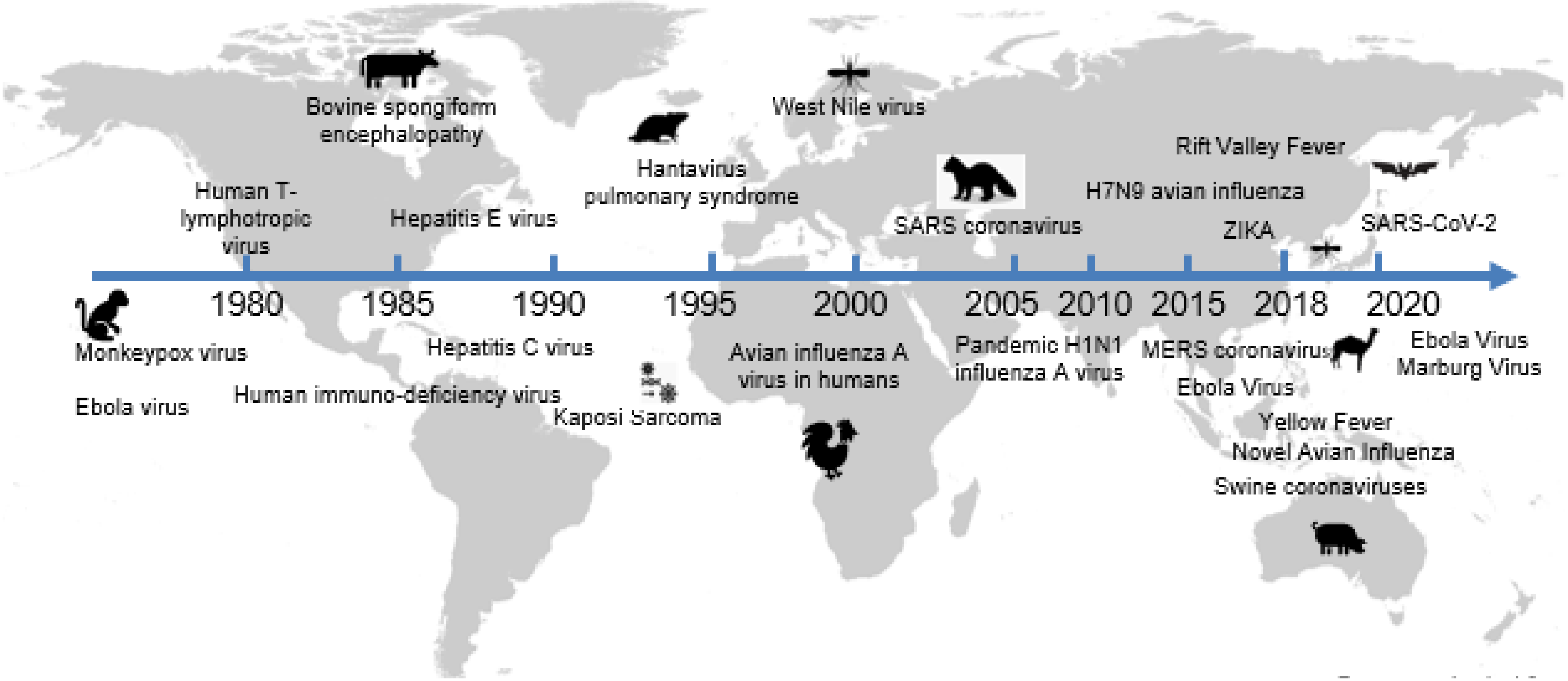
c) **Zoonosi emergenti e ri-emergenti che compaiono de novo in una popolazione o che sono esistite in precedenza, ma che aumentano rapidamente in termini di incidenza o di estensione geografica:**

Kalawat U. and Mohan A. J Clin and Scient Res, 2023

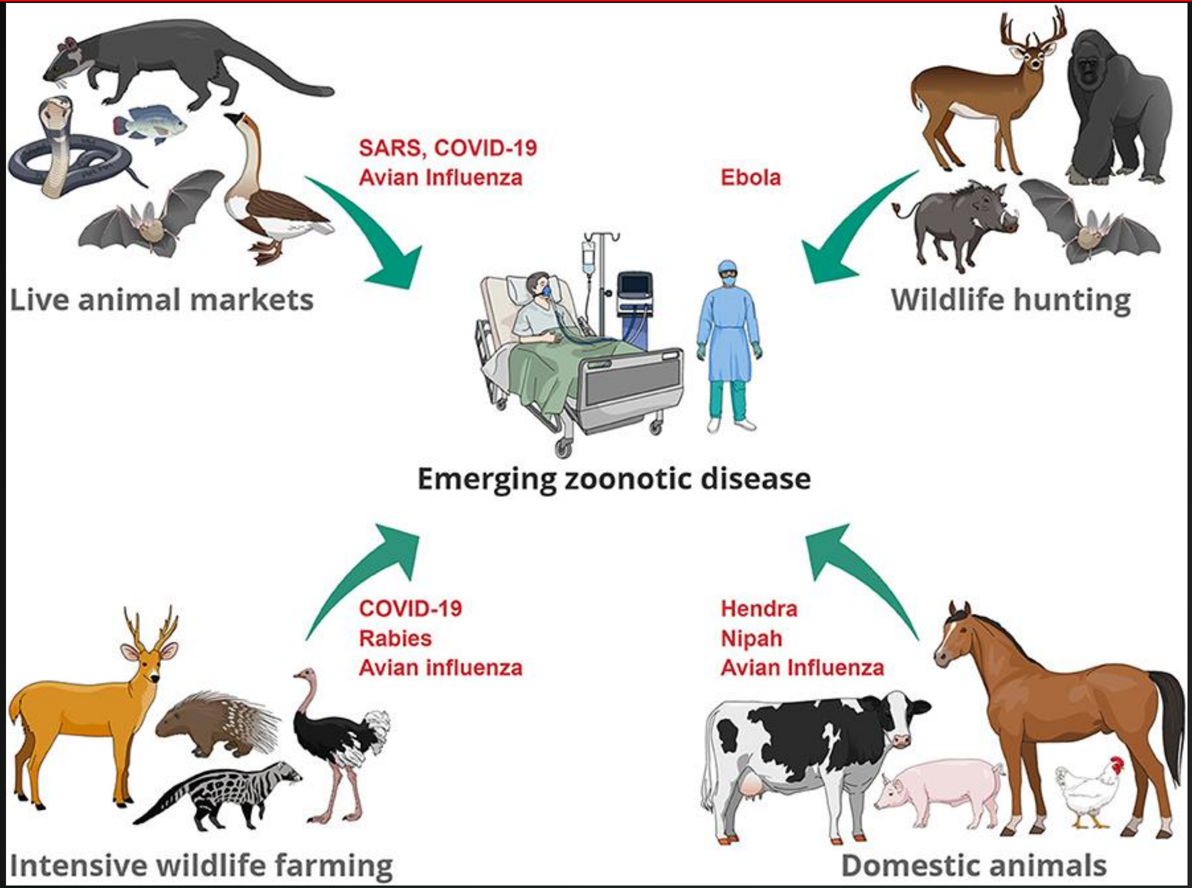
SARS, pandemic influenza H1N1 2009, Avian Influenza (H5N1) and H7N9, Middle East respiratory syndrome coronavirus (MERS-CoV), SARS-CoV-2, Hantavirus, Hendra virus, Nipah virus

WHO, 2020

Examples of zoonotic diseases & outbreaks



Emerging Zoonotic Diseases:
Should We Rethink the Animal–Human Interface?



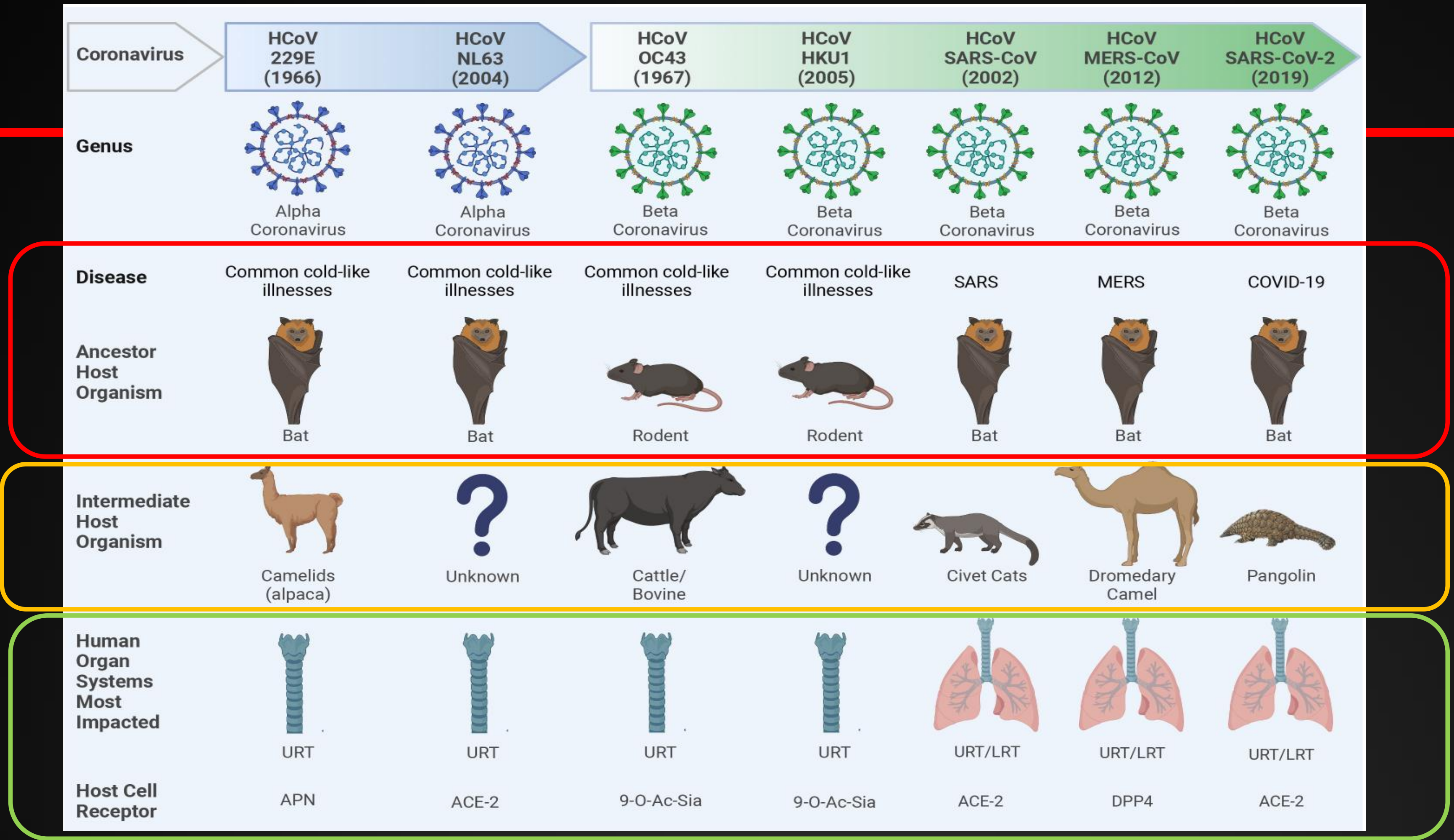
Magouras *et al*., Front Vet Sci, 2020

Le malattie zoonotiche sono (ri)-emerse all'interfaccia animale-uomo

Interfaccia animale-uomo :
è fondamento
della trasmissione tra specie

Vie di trasmissione includono: contatto diretto o indiretto animale/uomo (manipolazione di animali vivi/commercio di animali selvatici o domestici, preparazione di animali macellati, contatto con fluidi corporei)

Ecology of human coronaviruses (CoVs)



Coronavirus	HCoV 229E (1966)	HCoV NL63 (2004)	HCoV OC43 (1967)	HCoV HKU1 (2005)	HCoV SARS-CoV (2002)	HCoV MERS-CoV (2012)	HCoV SARS-CoV-2 (2019)
Genus	Alpha Coronavirus	Alpha Coronavirus	Beta Coronavirus	Beta Coronavirus	Beta Coronavirus	Beta Coronavirus	Beta Coronavirus
Disease	Common cold-like illnesses	Common cold-like illnesses	Common cold-like illnesses	Common cold-like illnesses	SARS	MERS	COVID-19
Ancestor Host Organism	Bat	Bat	Rodent	Rodent	Bat	Bat	Bat
Intermediate Host Organism	Camelids (alpaca)	Unknown	Cattle/ Bovine	Unknown	Civet Cats	Dromedary Camel	Pangolin
Human Organ Systems Most Impacted	URT	URT	URT	URT	URT/LRT	URT/LRT	URT/LRT
Host Cell Receptor	APN	ACE-2	9-O-Ac-Sia	9-O-Ac-Sia	ACE-2	DPP4	ACE-2

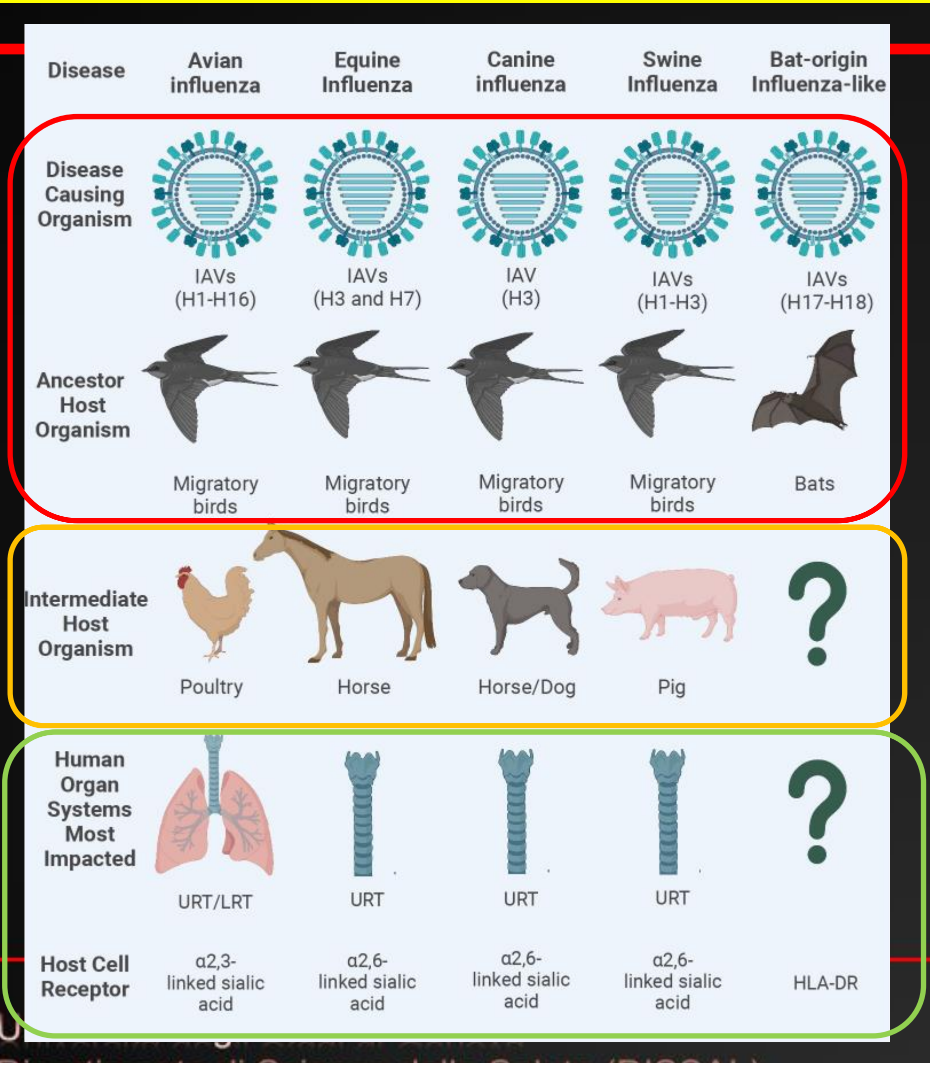
Seven CoVs that belong to alpha-CoVs (229E and NL63) and beta-CoVs (OC43, HKU1, SARS-CoV, MERS- CoV, and SARS-CoV-2) genera could escape species barriers to infect humans following non-hygienic contact with the intermediate host

Khalil A.M. et al. Frontiers in Cellular and Infection Microbiology, 2024

Carlo Urbani
Le malattie dimenticate
Poesia e lavoro di un medico in prima linea
Feltrinelli

Zoonosis and zooanthroponosis (reverse zoonosis) of emerging respiratory viruses

Ecology of influenza A viruses (IAVs) and origin of the 2009 pandemic influenza virus (A/H1N1)



Disease	Avian influenza	Equine Influenza	Canine influenza	Swine Influenza	Bat-origin Influenza-like
Disease Causing Organism	IAVs (H1-H16)	IAVs (H3 and H7)	IAV (H3)	IAVs (H1-H3)	IAVs (H17-H18)
Ancestor Host Organism	Migratory birds	Migratory birds	Migratory birds	Migratory birds	Bats
Intermediate Host Organism	Poultry	Horse	Horse/Dog	Pig	?
Human Organ Systems Most Impacted	URT/LRT	URT	URT	URT	?
Host Cell Receptor	α2,3-linked sialic acid	α2,6-linked sialic acid	α2,6-linked sialic acid	α2,6-linked sialic acid	HLA-DR

Khalil A.M. et al., Frontiers in Cellular and Infection Microbiology 2024

Following transmission from their natural reservoirs (e.g. migratory birds or bats)

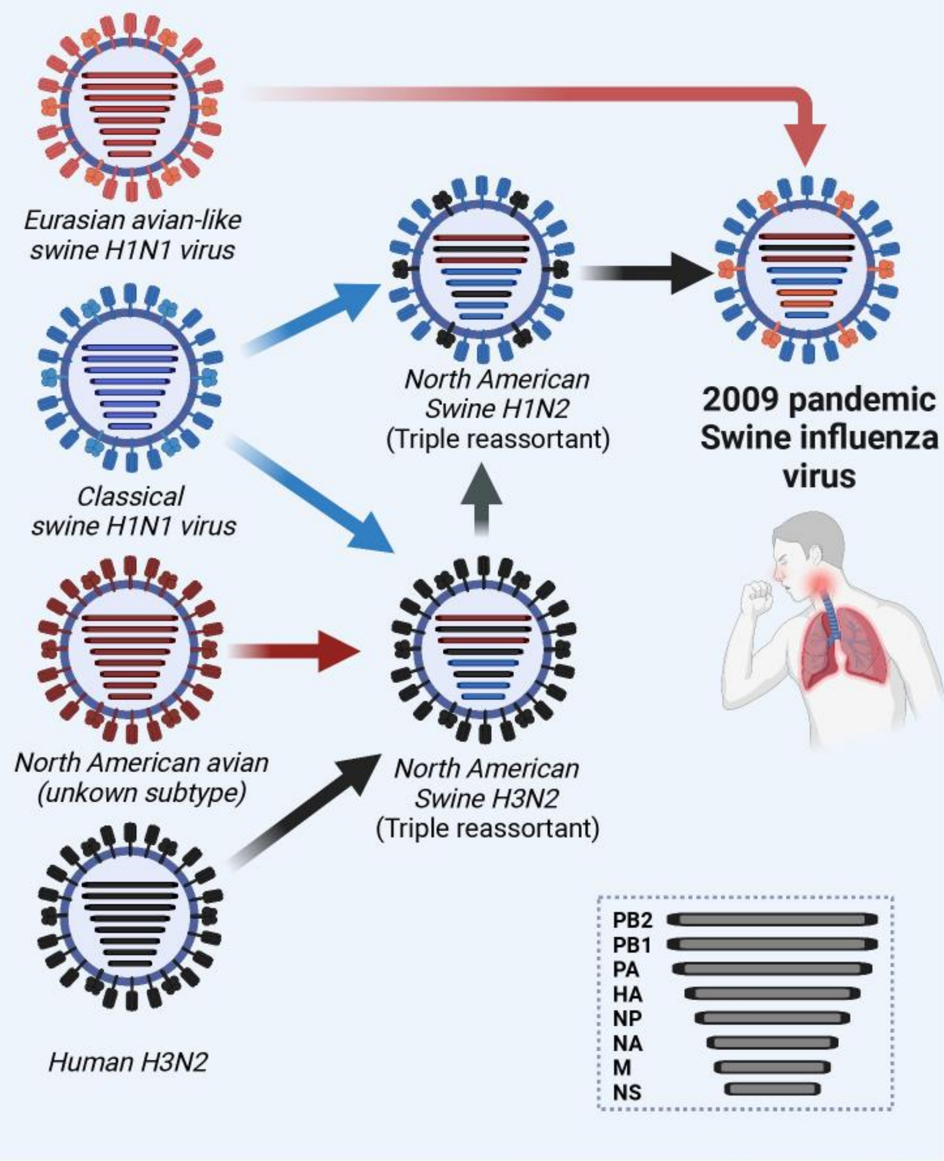
Some viruses

Acquired adaptive changes

in a known intermediate host
domestic birds (IAVs)
or unknown/other intermediate host

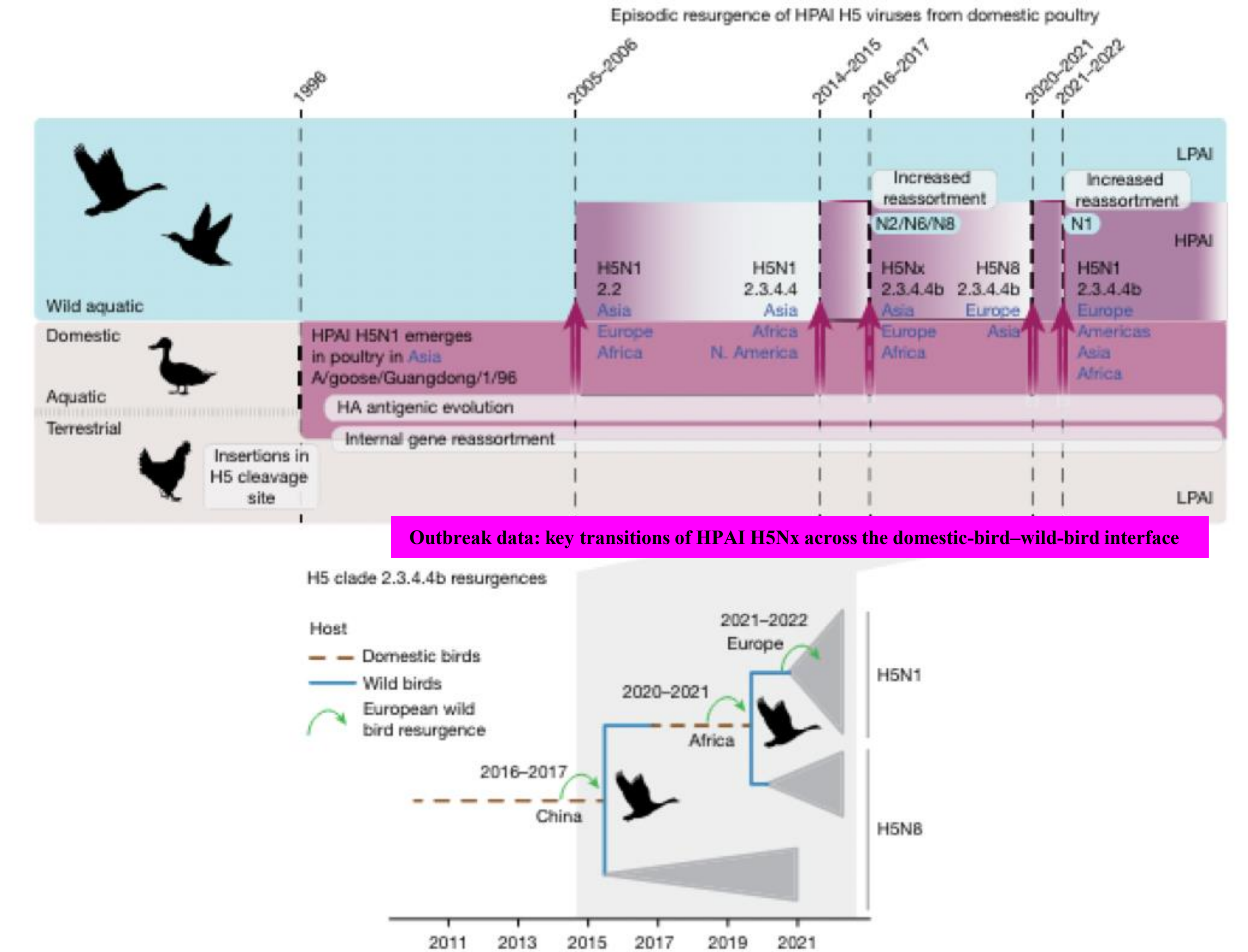
Acquired adaptive substitutions facilitated crossing species barriers by these viruses to infect humans in a phenomenon known as zoonosis

Ecology of influenza A viruses (IAVs) and origin of the 2009 pandemic influenza virus (A/H1N1)

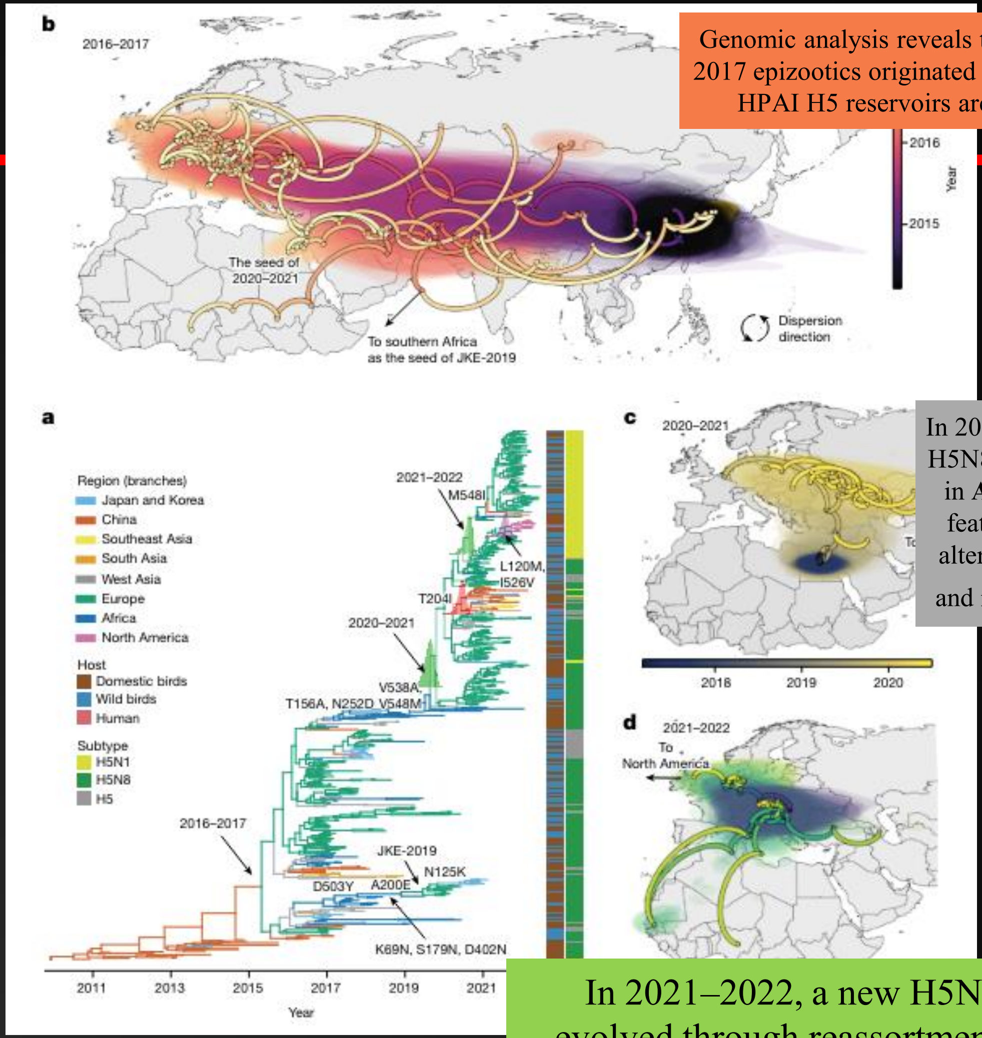


The influenza virus pandemic in 2009 is a paradigm of the genetic reassortment where the genetic segments of IAVs from different sources (human, avian, and swine) mixed in swine to generate the swine-origin IAV (referred to as influenza A/H1N1pdm09 virus) to which humans had no pre-existing immunity

The episodic resurgence of highly pathogenic avian influenza H5 virus



Outbreak data: key transitions of HPAI H5Nx across the domestic-bird–wild-bird interface



Genomic analysis reveals that the 2016–2017 epizootics originated in **Asia**, where HPAI H5 reservoirs are endemic.

In 2020–2021, 2.3.4.4b H5N8 viruses emerged in **African poultry**, featuring mutations altering *HA* structure and receptor binding.

In 2021–2022, a new H5N1 virus evolved through reassortment in **wild birds in Europe**, undergoing further reassortment with low-pathogenic avian influenza in wild and domestic birds during global dissemination.

I virus dell'influenza aviaria ad alta patogenicità (HPAI) evolvono dai LPAI nel pollame acquisendo inserzioni del sito di clivaggio HA che facilitano le infezioni sistemiche

Ruopeng Xie et al., Nature 2023

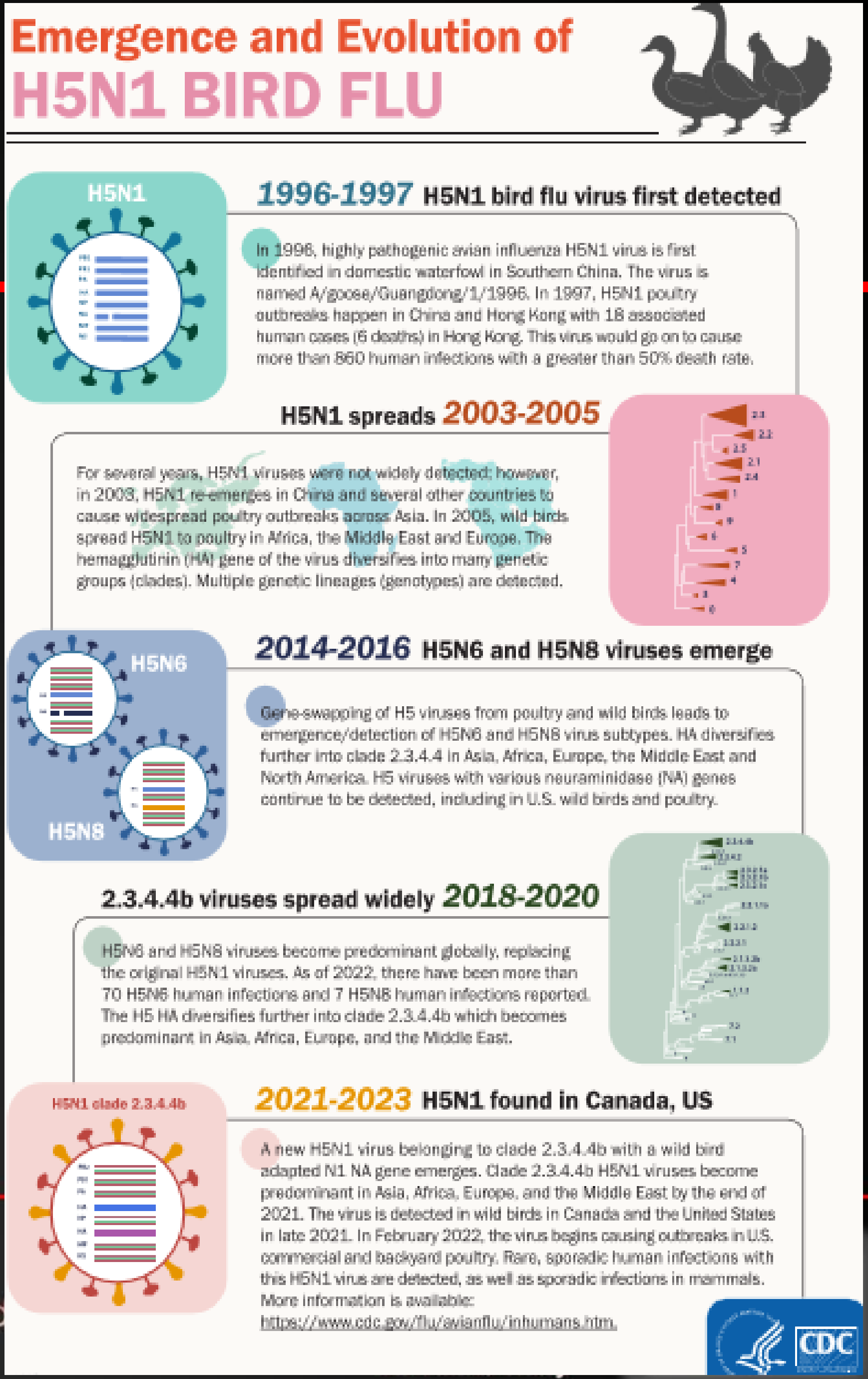
Highly pathogenic avian influenza virus (HPAIV) of the goose/Guangdong/1996 (GS/GD/96) lineage specifically influenza A(H5N1) clade 2.3.4.4, has caused a panzootic in poultry and wild birds

(Katzner TE et al, EID 2025)

1997- Hong Kong
2003-2005 Asia >> Europa e Medio Oriente e Africa
2021-2023 Canada, US
……..

February 8, 2024:

- US Dept Agric declares ongoing HPAI H5N1poultry outbreak



Emergence and Evolution of H5N1 BIRD FLU

1996-1997 H5N1 bird flu virus first detected

In 1996, highly pathogenic avian influenza H5N1 virus is first identified in domestic waterfowl in Southern China. The virus is named A/goose/Guangdong/1/1996. In 1997, H5N1 poultry outbreaks happen in China and Hong Kong with 18 associated human cases (6 deaths) in Hong Kong. This virus would go on to cause more than 860 human infections with a greater than 50% death rate.

H5N1 spreads 2003-2005

For several years, H5N1 viruses were not widely detected; however, in 2003, H5N1 re-emerges in China and several other countries to cause widespread poultry outbreaks across Asia. In 2005, wild birds spread H5N1 to poultry in Africa, the Middle East and Europe. The hemagglutinin (HA) gene of the virus diversifies into many genetic groups (clades). Multiple genetic lineages (genotypes) are detected.

2014-2016 H5N6 and H5N8 viruses emerge

Gene-swapping of H5 viruses from poultry and wild birds leads to emergence/detection of H5N6 and H5N8 virus subtypes. HA diversifies further into clade 2.3.4.4 in Asia, Africa, Europe, the Middle East and North America. H5 viruses with various neuraminidase (NA) genes continue to be detected, including in U.S. wild birds and poultry.

2.3.4.4b viruses spread widely 2018-2020

H5N6 and H5N8 viruses become predominant globally, replacing the original H5N1 viruses. As of 2022, there have been more than 70 H5N6 human infections and 7 H5N8 human infections reported. The H5 HA diversifies further into clade 2.3.4.4b which becomes predominant in Asia, Africa, Europe, and the Middle East.

2021-2023 H5N1 found in Canada, US

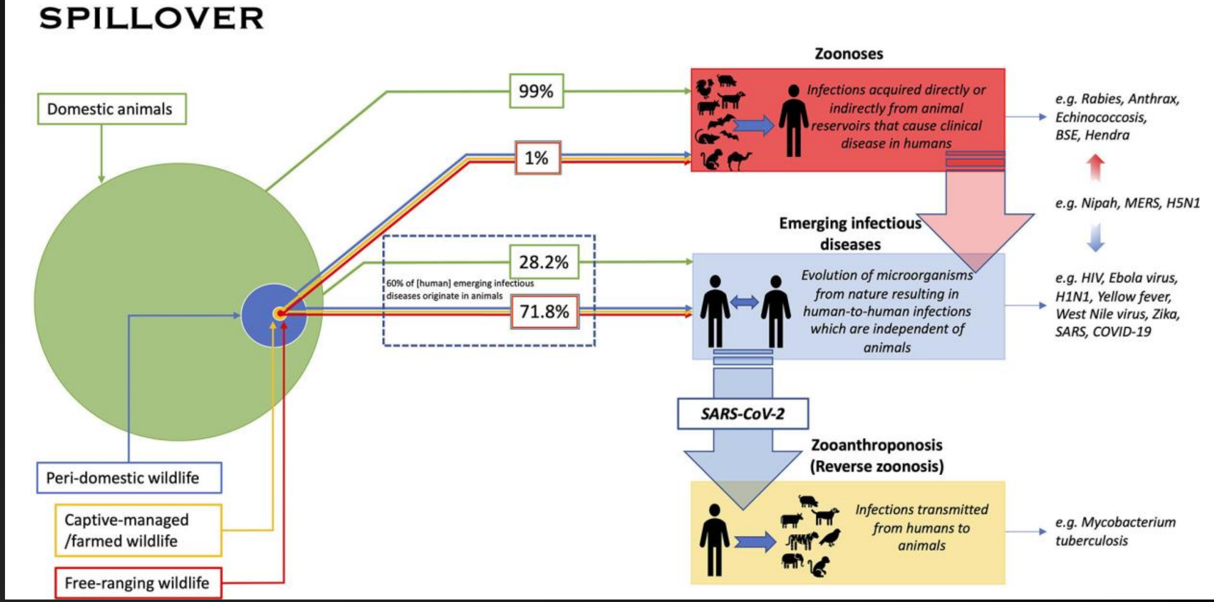
A new H5N1 virus belonging to clade 2.3.4.4b with a wild bird adapted N1 NA gene emerges. Clade 2.3.4.4b H5N1 viruses become predominant in Asia, Africa, Europe, and the Middle East by the end of 2021. The virus is detected in wild birds in Canada and the United States in late 2021. In February 2022, the virus begins causing outbreaks in U.S. commercial and backyard poultry. Rare, sporadic human infections with this H5N1 virus are detected, as well as sporadic infections in mammals. More information is available: https://www.cdc.gov/flu/avianflu/inhumans.htm.

….And subsequent spillover into some wild mammals

The phenomenon of "*spill-over*" or "*evolutionary jump*" refers to the transmission of a pathogen from a natural animal host to a novel host leading to infection in the new host

March 7, 2024:
- Unknown dairy cattle illness first reported
- March 20, 2024: Samples collected from dairy cattle in Texas

March 25, 2024:
-Texas confirms H5N1 in dairy cattle



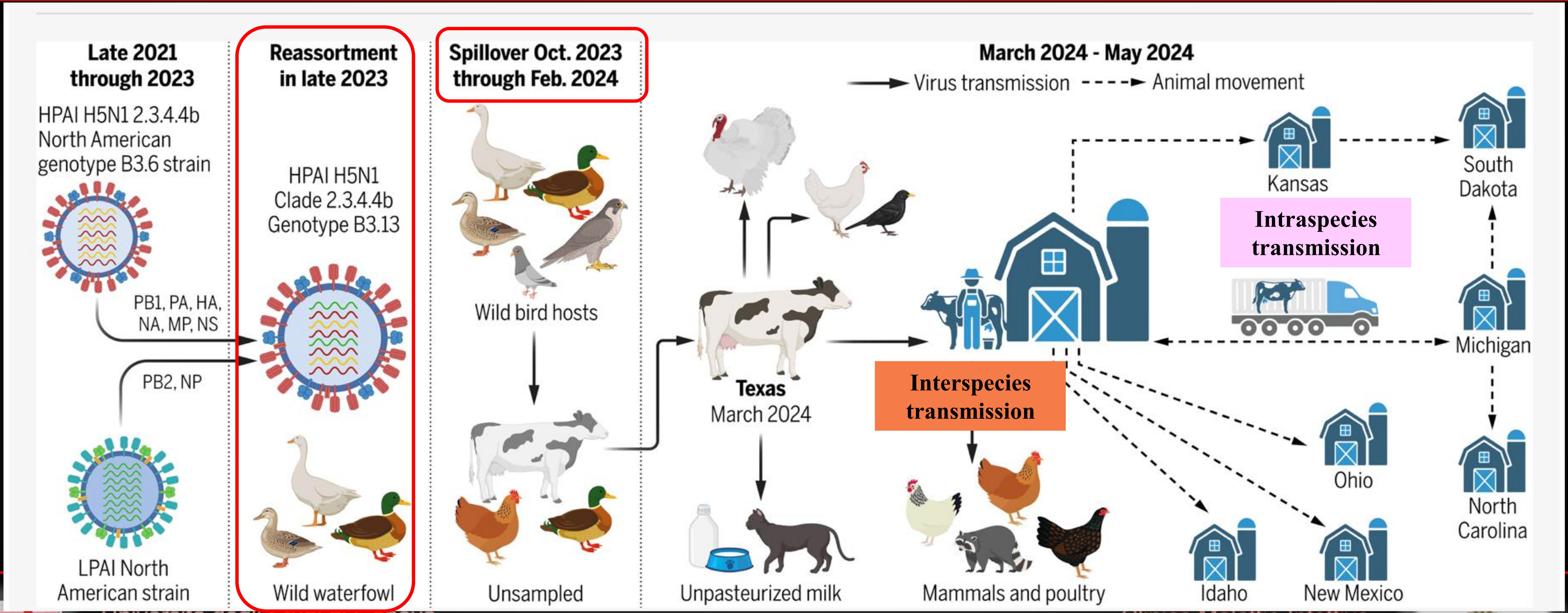
Può avvenire per una nuova esposizione o esposizione ripetuta, o per una modifica genica che consente al patogeno di infettare il nuovo ospite

Heider N, Rothman- Ostrow P et al. Frontiers Public Health 2020

Spillover of highly pathogenic avian influenza H5N1 virus to dairy cattle

The ability of the virus to cross species barriers

H5N1 clade 2.3.4.4b genotype B3.13 influenza A virus

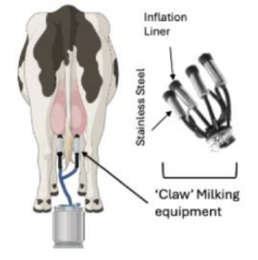


The emergence and spread of highly pathogenic avian influenza virus H5N1 clade 2.3.4.4b in dairy cattle in the US. Highly pathogenic avian influenza (HPAI) H5N1 was detected in North America in late 2021, and epidemiological information and genomic analysis demonstrated a single spillover into dairy cattle by a reassorted HPAI H5N1 genotype B3.13 virus. The virus disseminated across the US through the movement of asymptomatic or presymptomatic animals and was subsequently reintroduced from dairy cattle back into other host species.

Universita degli Studi di Genova

(DISSAL)

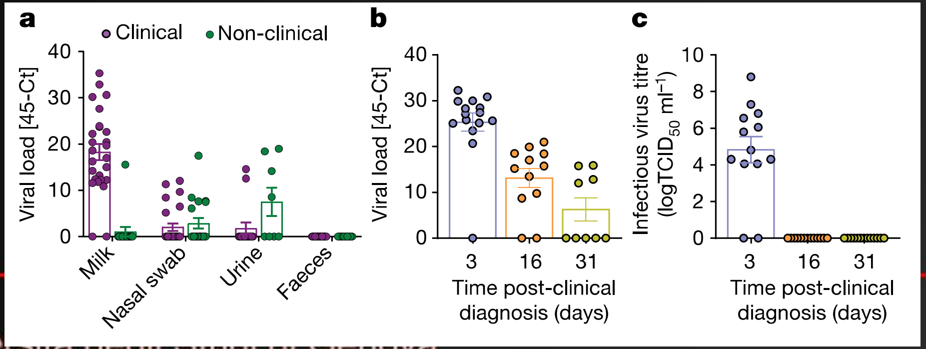
Nguyen T.Q. *et al.*, Science 2025



Clinical presentation of HPAI H5N1 infection in dairy cattle

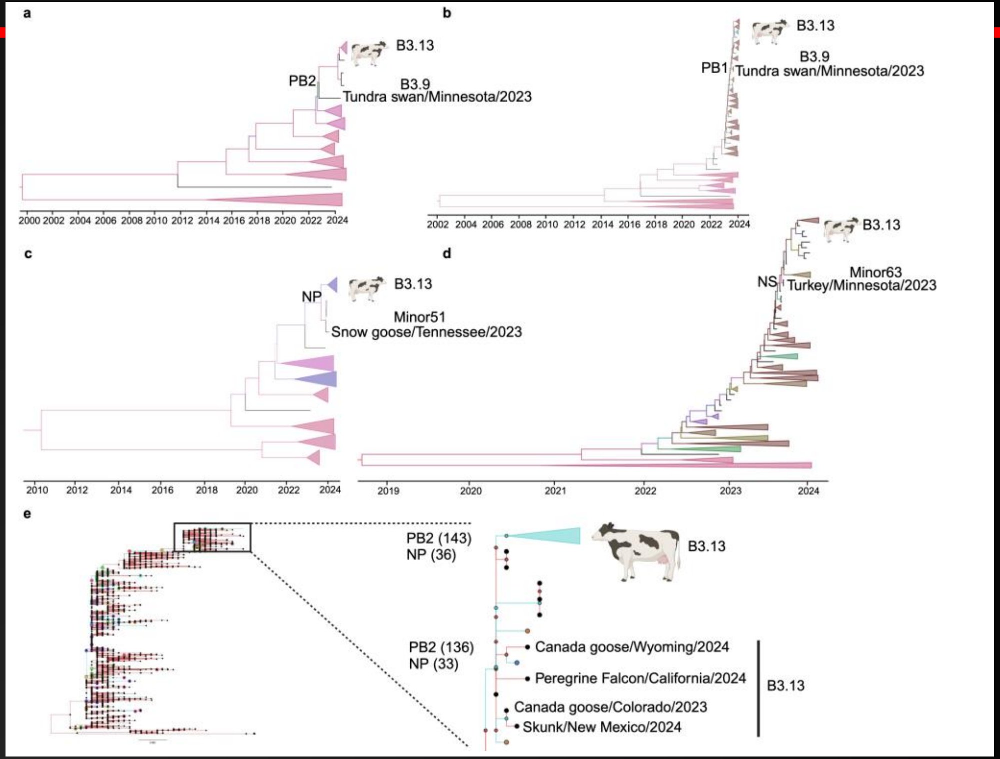
The tropism of HPAI H5N1 for milk-secreting epithelial cells: high expression of sialic acid receptors with an **α2,3** (avian-like receptor) and **α2,6** (human-like receptor) galactose linkage in these cells

Virus shedding patterns



Latte, virus infettante

Phylogenomic and phylogeographical analysis



To estimate the most recent common ancestor (MRCA) for the individual gene fragments

Caserta L.C. *et al*., Nature 2024

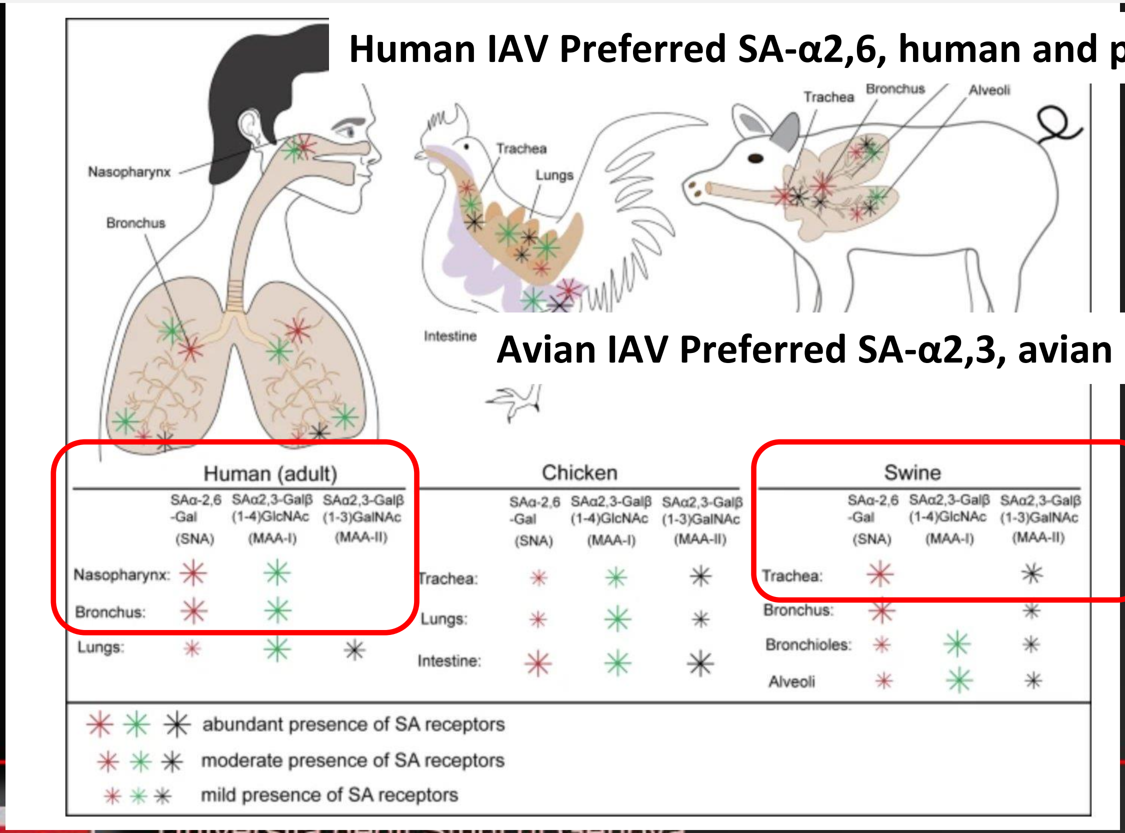
An overview of influenza A virus genes, protein functions

8 segmenti genetici che codificano per 17 proteine

The polymerase genes (PB2, PB1, PA) determinants of pathogenicity and virulence

Adaptive mutations of **glycoprotein—hemagglutinin (HA) and neuraminidase (NA) genes, may facilitate interspecies transmission** and adaptation of IAV.

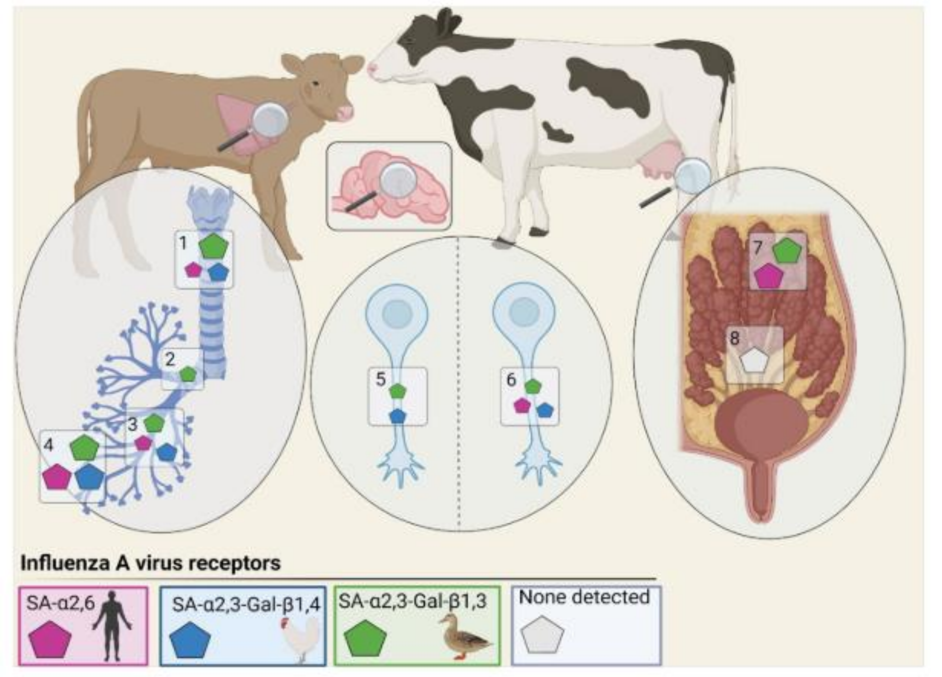
HA binds to sialic acids (SA) terminally attached to glycans facilitating viral endocytosis and membrane fusion



Human IAV Preferred SA-α2,6, human and pig receptor

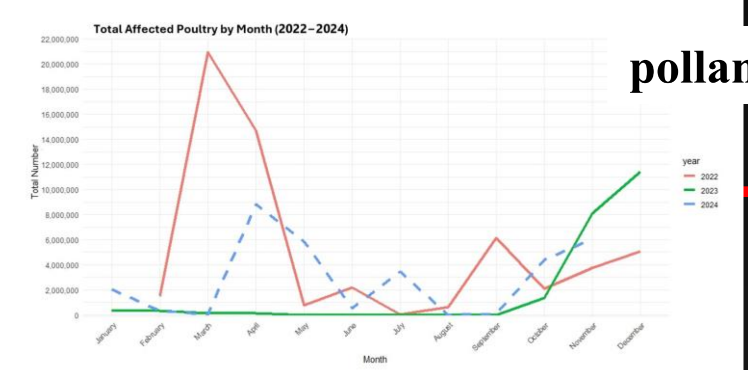
Avian IAV Preferred SA-α2,3, avian receptor

Chauhan et al., Virus Gene 2022

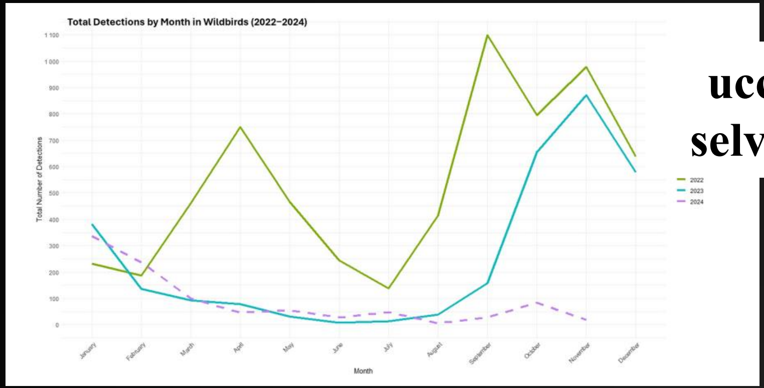


Kristensen C, EID 2024

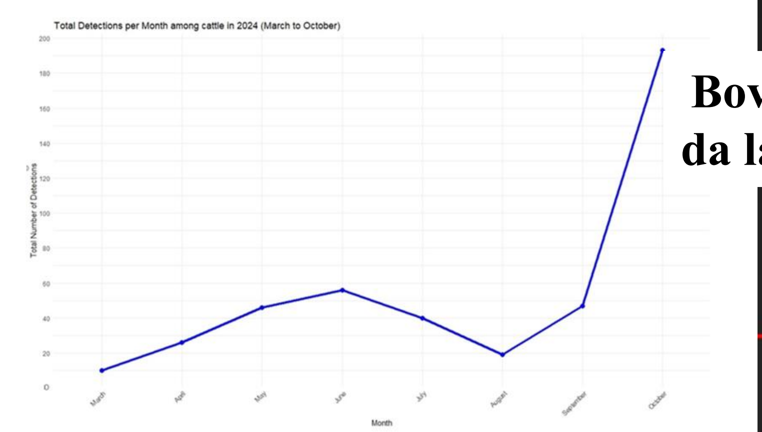
Highly Pathogenic Avian Influenza H5N1 in the United States


Total Affected Poultry by Month (2022–2024)

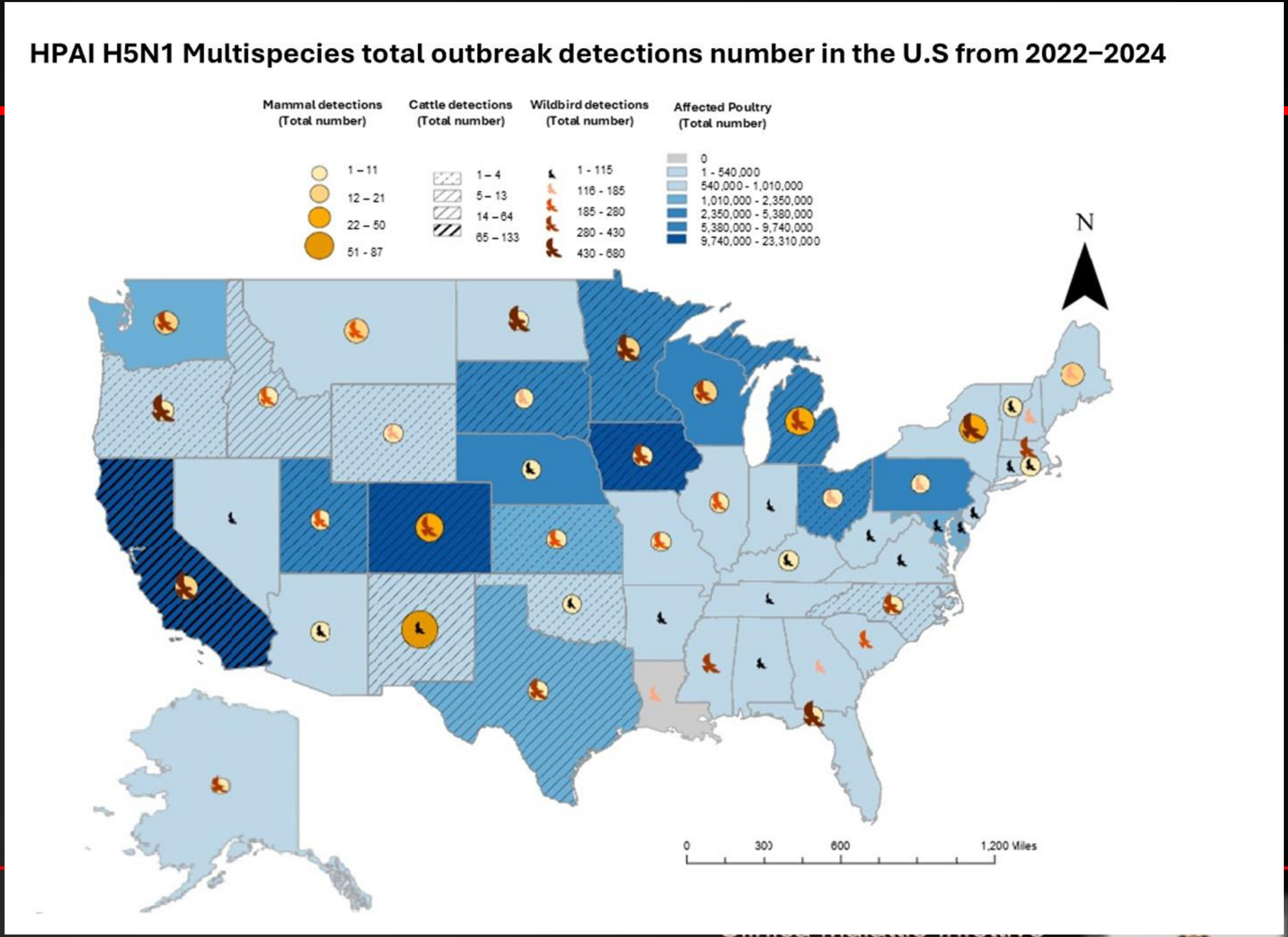
pollame


Total Detections by Month in Wildbirds (2022–2024)

uccelli selvatici


Total Detections per Month among cattle in 2024 (March to October)

Bovini da latte


HPAI H5N1 Multispecies total outbreak detections number in the U.S from 2022–2024

Mena A. *et al.*, Viruses 2025

March 25, 2024:

-Texas confirms H5N1 HPAI A H5N1 clade 2.3.4.4b viruses in dairy cattle and unpastorized milk

March 28, 2024:

- Positive H5N1 specimen collected from human

Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Dairy Farm Worker (Texas)

Figure 1. Conjunctivitis with Subconjunctival Hemorrhage in Both Eyes.

The worker reported wearing gloves when working with cows but did not use any respiratory or eye protection.

March 2024,

A **case of HPAI A(H5N1) virus infection in a dairy farm worker in Texas**.

- an adult dairy farm worker had onset of redness and discomfort in the right eye with subconjunctival hemorrhage and thin, serous drainage.

Vital signs and vital parameters were unremarkable. No history of fever or feverishness, respiratory symptoms, changes in vision, or other symptoms.

The worker reported direct **and close exposure to dairy cows** that appeared to be well and with sick cows that showed the same signs of illness as cows at other dairy farms in the same area of northern Texas with confirmed HPAI A(H5N1) virus infection (e.g., **decreased milk production, reduced appetite, lethargy, fever, and dehydration**).

Home isolation was recommended, and **oral oseltamivir (75 mg twice daily for 5 days) was provided for treatment of the worker and for postexposure prophylaxis for the worker's household contacts** (at the same dose).

Uyeki TM, NEJM May 2024

Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Dairy Farm Worker

Figure 1. Conjunctivitis with Subconjunctival Hemorrhage in Both Eyes.

Complete genome sequences from the conjunctival swab (Ct value, 18) confirmed **clade 2.3.4.4b (genotype B3.13),** with virus isolation from both the conjunctival and nasopharyngeal swabs **yielding identical virus**.

All gene segments were closely related to viruses detected in Texas dairy cattle and other genotype B3.13 viruses detected in peridomestic wild birds in Texas during March 2024

Viral sequences from cattle and from the worker maintained primarily avian genetic characteristics and **lacked changes in the hemagglutinin gene that would affect receptor-binding specificity** (e.g., binding to α2-6–linked sialic acid receptors, primarily located in the human upper respiratory tract) **and transmission risk to humans**.

The virus identified in the worker's specimen had a change (PB2 E627K) that has been associated with viral adaptation to mammalian hosts and detected previously in humans and other mammals infected with HPAI A(H5N1) viruses and other avian influenza A virus subtypes, including A(H7N9) and A(H9N2).

No genetic markers associated with reduced susceptibility to influenza antiviral drugs approved by the Food and Drug Administration were identified

Uyeki TM, NEJM May 2024

CDC Confirms Second Human H5 Bird Flu Case in Michigan; Third Case Tied to Dairy Outbreak

A **second human case** of HPAI A(H5) virus infection has been identified in the state of **Michigan**.

This is the **third human case (Michigan)** associated with an ongoing multistate outbreak of A(H5N1) in U.S. dairy cows.

None of the three cases are associated with the others.

As with **the previous two cases (one in Texas, one in Michigan), the person is a dairy farm worker with exposure to infected cows**, making this another instance of probable cow-to-person spread.

This is the first human case of H5 in the United States to report **more typical symptoms of acute respiratory illness** associated with influenza virus infection, including A(H5N1) viruses.

https://www.cdc.gov/media/releases/2024/p0530-h5-human-case-michigan.html

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Highly Pathogenic Avian Influenza A(H5N1) Virus Infections in Humans

March-October 2024

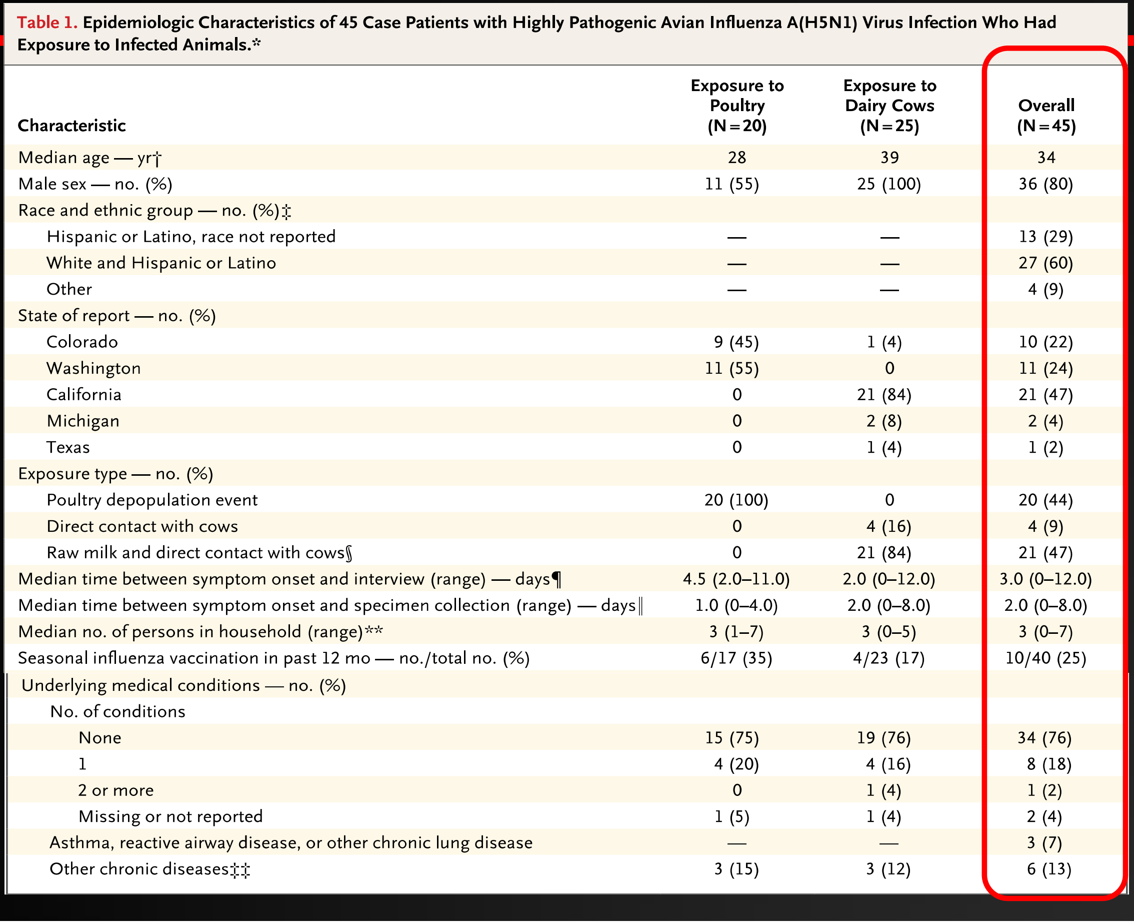


Table 1. Epidemiologic Characteristics of 45 Case Patients with Highly Pathogenic Avian Influenza A(H5N1) Virus Infection Who Had Exposure to Infected Animals.*

Characteristic	Exposure to Poultry (N=20)	Exposure to Dairy Cows (N=25)	Overall (N=45)
Median age — yr†	28	39	34
Male sex — no. (%)	11 (55)	25 (100)	36 (80)
Race and ethnic group — no. (%)‡			
Hispanic or Latino, race not reported	—	—	13 (29)
White and Hispanic or Latino	—	—	27 (60)
Other	—	—	4 (9)
State of report — no. (%)			
Colorado	9 (45)	1 (4)	10 (22)
Washington	11 (55)	0	11 (24)
California	0	21 (84)	21 (47)
Michigan	0	2 (8)	2 (4)
Texas	0	1 (4)	1 (2)
Exposure type — no. (%)			
Poultry depopulation event	20 (100)	0	20 (44)
Direct contact with cows	0	4 (16)	4 (9)
Raw milk and direct contact with cows§	0	21 (84)	21 (47)
Median time between symptom onset and interview (range) — days¶	4.5 (2.0–11.0)	2.0 (0–12.0)	3.0 (0–12.0)
Median time between symptom onset and specimen collection (range) — days‖	1.0 (0–4.0)	2.0 (0–8.0)	2.0 (0–8.0)
Median no. of persons in household (range)**	3 (1–7)	3 (0–5)	3 (0–7)
Seasonal influenza vaccination in past 12 mo — no./total no. (%)	6/17 (35)	4/23 (17)	10/40 (25)
Underlying medical conditions — no. (%)			
No. of conditions			
None	15 (75)	19 (76)	34 (76)
1	4 (20)	4 (16)	8 (18)
2 or more	0	1 (4)	1 (2)
Missing or not reported	1 (5)	1 (4)	2 (4)
Asthma, reactive airway disease, or other chronic lung disease	—	—	3 (7)
Other chronic diseases‡‡	3 (15)	3 (12)	6 (13)

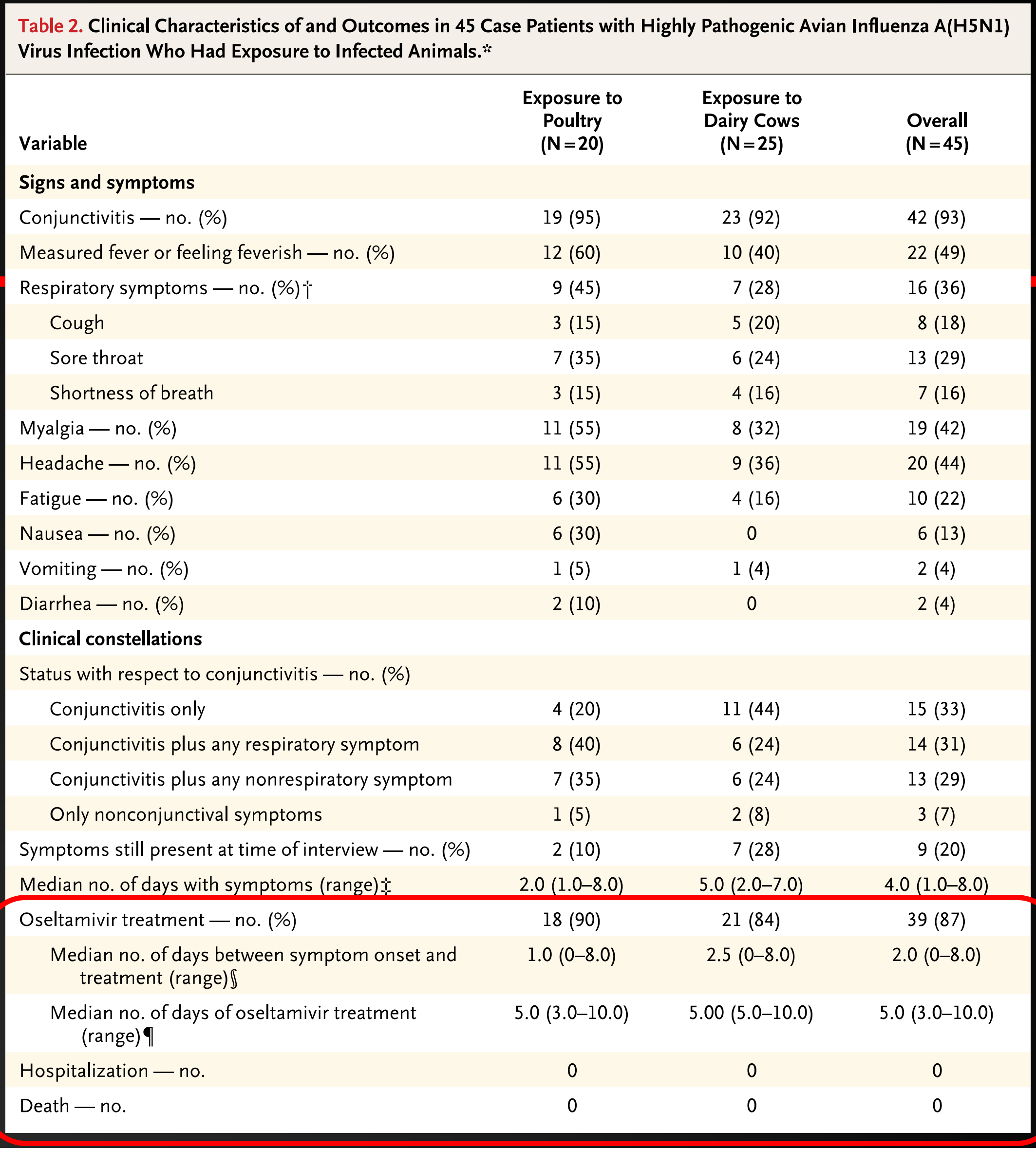


Table 2. Clinical Characteristics of and Outcomes in 45 Case Patients with Highly Pathogenic Avian Influenza A(H5N1) Virus Infection Who Had Exposure to Infected Animals.*

Variable	Exposure to Poultry (N=20)	Exposure to Dairy Cows (N=25)	Overall (N=45)
Signs and symptoms			
Conjunctivitis — no. (%)	19 (95)	23 (92)	42 (93)
Measured fever or feeling feverish — no. (%)	12 (60)	10 (40)	22 (49)
Respiratory symptoms — no. (%)†	9 (45)	7 (28)	16 (36)
Cough	3 (15)	5 (20)	8 (18)
Sore throat	7 (35)	6 (24)	13 (29)
Shortness of breath	3 (15)	4 (16)	7 (16)
Myalgia — no. (%)	11 (55)	8 (32)	19 (42)
Headache — no. (%)	11 (55)	9 (36)	20 (44)
Fatigue — no. (%)	6 (30)	4 (16)	10 (22)
Nausea — no. (%)	6 (30)	0	6 (13)
Vomiting — no. (%)	1 (5)	1 (4)	2 (4)
Diarrhea — no. (%)	2 (10)	0	2 (4)
Clinical constellations			
Status with respect to conjunctivitis — no. (%)			
Conjunctivitis only	4 (20)	11 (44)	15 (33)
Conjunctivitis plus any respiratory symptom	8 (40)	6 (24)	14 (31)
Conjunctivitis plus any nonrespiratory symptom	7 (35)	6 (24)	13 (29)
Only nonconjunctival symptoms	1 (5)	2 (8)	3 (7)
Symptoms still present at time of interview — no. (%)	2 (10)	7 (28)	9 (20)
Median no. of days with symptoms (range)‡	2.0 (1.0–8.0)	5.0 (2.0–7.0)	4.0 (1.0–8.0)
Oseltamivir treatment — no. (%)	18 (90)	21 (84)	39 (87)
Median no. of days between symptom onset and treatment (range)§	1.0 (0–8.0)	2.5 (0–8.0)	2.0 (0–8.0)
Median no. of days of oseltamivir treatment (range)¶	5.0 (3.0–10.0)	5.00 (5.0–10.0)	5.0 (3.0–10.0)
Hospitalization — no.	0	0	0
Death — no.	0	0	0

Except for one case patient with an undetermined exposure source (not in the table) all case patients had occupational exposure to infected animals.

No additional cases were identified among the 97 household contacts of case patients with animal exposures

Garg S. et al., NEJM Dec 2024

HPAI H5N1 nell’uomo

- Periodo di incubazione: media da 2 a 5 giorni e fino a 17 giorni
- Sintomi: febbre, astenia, tosse, faringodinia, mialgie, sintomi gastrointestinali (nausea, vomito, diarrea) e congiuntivite
- infezione respiratoria grave, >>SARI e ARDS

The NEW ENGLAND JOURNAL of MEDICINE

CORRESPONDENCE

Critical Illness in an Adolescent with Influenza A(H5N1) Virus Infection

British Columbia-Canada

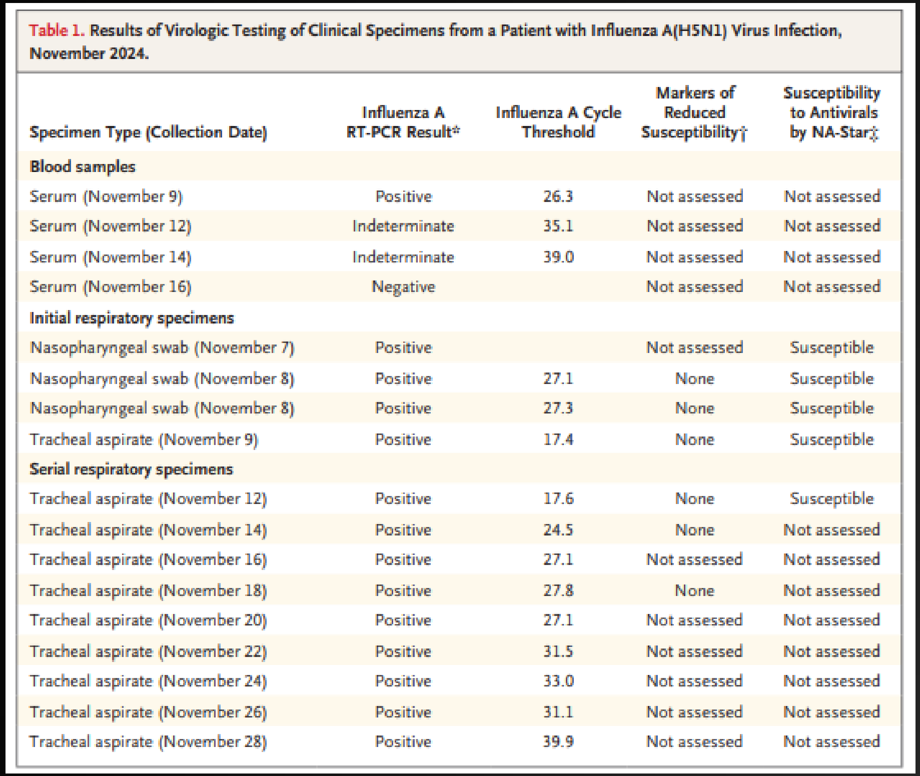


Table 1. Results of Virologic Testing of Clinical Specimens from a Patient with Influenza A(H5N1) Virus Infection, November 2024.

Specimen Type (Collection Date)	Influenza A RT-PCR Result*	Influenza A Cycle Threshold	Markers of Reduced Susceptibility†	Susceptibility to Antivirals by NA-Star‡
Blood samples				
Serum (November 9)	Positive	26.3	Not assessed	Not assessed
Serum (November 12)	Indeterminate	35.1	Not assessed	Not assessed
Serum (November 14)	Indeterminate	39.0	Not assessed	Not assessed
Serum (November 16)	Negative		Not assessed	Not assessed
Initial respiratory specimens				
Nasopharyngeal swab (November 7)	Positive		Not assessed	Susceptible
Nasopharyngeal swab (November 8)	Positive	27.1	None	Susceptible
Nasopharyngeal swab (November 8)	Positive	27.3	None	Susceptible
Tracheal aspirate (November 9)	Positive	17.4	None	Susceptible
Serial respiratory specimens				
Tracheal aspirate (November 12)	Positive	17.6	None	Susceptible
Tracheal aspirate (November 14)	Positive	24.5	None	Not assessed
Tracheal aspirate (November 16)	Positive	27.1	Not assessed	Not assessed
Tracheal aspirate (November 18)	Positive	27.8	None	Not assessed
Tracheal aspirate (November 20)	Positive	27.1	Not assessed	Not assessed
Tracheal aspirate (November 22)	Positive	31.5	Not assessed	Not assessed
Tracheal aspirate (November 24)	Positive	33.0	Not assessed	Not assessed
Tracheal aspirate (November 26)	Positive	31.1	Not assessed	Not assessed
Tracheal aspirate (November 28)	Positive	39.9	Not assessed	Not assessed

November 4, 2024

13-y-o girl with mild asthma >35 BMI to ER in BC with a 2-day febrile conjunctivitis - discharged

7.11 SARI and hemodynamic instability, **NF swab positive H5N1**

8.11, transferred in P-ICU with ARDS, pneumonia in the left lower lobe, bilevel ventilation, acute kidney injury, thrombocytopenia, and leukopenia

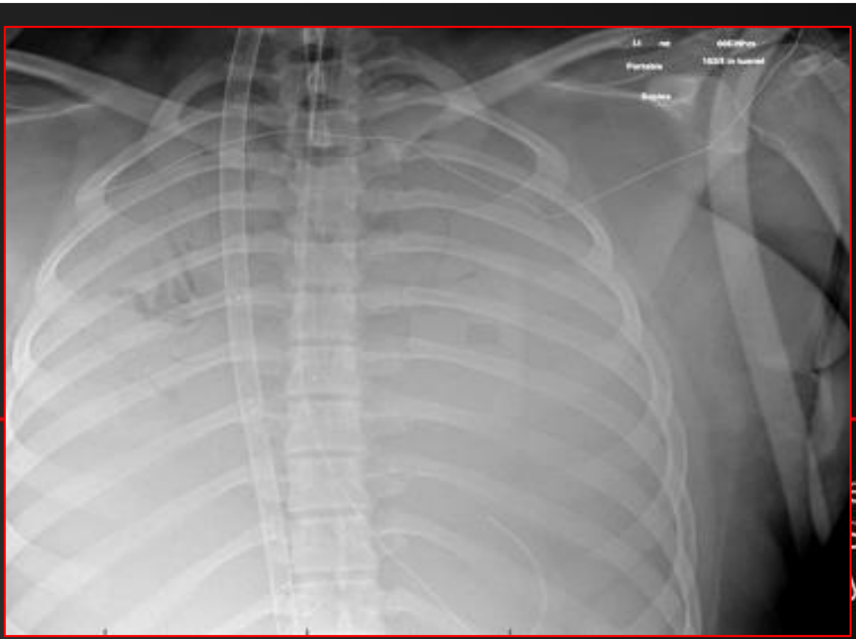
8.11 oseltamivir (, 75 x 2 than 150 x2), **9.11** amantadine (100 x 2) and

11.11 baloxavir (**11.11** 80 mg every 48hrs); **Nov 8-28** Intubated;

Nov 9-22 ECMO e CVVHD

H5N1 was **cultured between 8-12.11** but not thereafter.

No evidence of reduced susceptibility to any of the three antiviral agents used in treatment was observed in serial respiratory specimens.



8.11

Jassem AN, *et al.*, NEJM 2024

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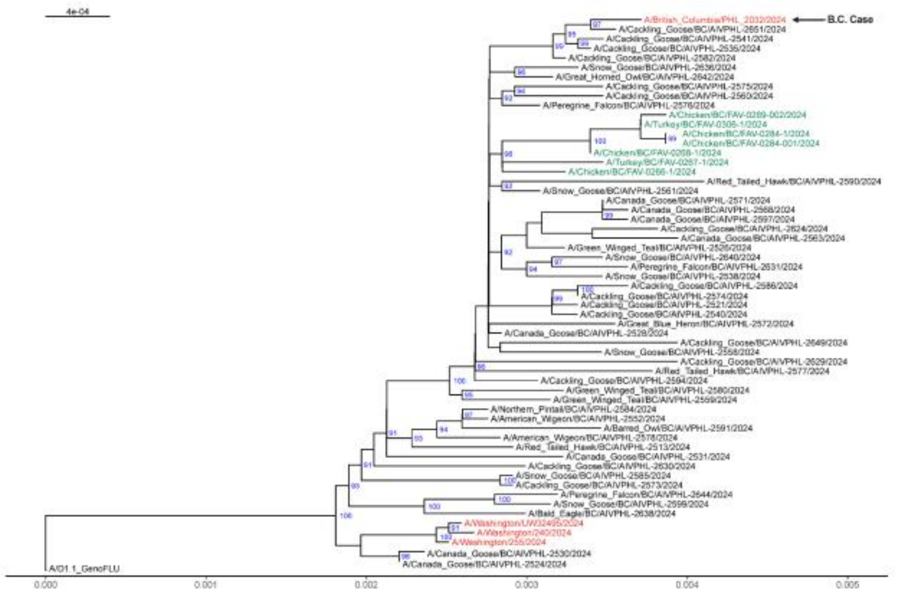
The virus was typed as clade 2.3.4.4b, genotype D1.1, most closely related to viruses detected in wild birds in British Columbia around the same time

Markers of adaptation to humans were detected:

- **E627K mutation was detected in the polymerase basic 2 (PB2) gene (52% allele frequency)**
- **H5 HA yielded ambiguous calls in E186 and Q222 (28-35% allele frequency), linked** to **increase binding to α2-6–linked sialic acids**, which act as receptors that facilitate viral entry into cells in the human respiratory tract and enable viral replication

Supplementary Figure 2. Concatenated whole genome phylogeny of HPAI A(H5N1) clade 2.3.4.4b, genotype D1.1 viruses from human cases identified in British Columbia, Canada and Washington state, United states (red), contextualized by B.C wild bird (black) and poultry (green) detections collected between September 23rd and November 8th, 2024. Bootstrap values over 90% are displayed on the nodes. Scale bar is substitutions per site.



Jassem AN, *et al.*, NEJM 2024

December 26, 20204: Genetic Sequences of Highly Pathogenic Avian Influenza A(H5N1) Viruses Identified in a Person in Louisiana

- Genetic sequences from the severely ill patients (> 65 y, underlying medical condition >> dead) with HPAI A(H5N1) were identified as the **D1.1 genotype** different from that of dairy cows

The analysis identified low frequency mutations in the HA gene (A134V, N182K, **E186D**) resulting in **increased virus binding to α2-6 cell receptors** in human upper respiratory tract from the patient, **not found in sequences from poultry samples on the patient's property**, suggesting **the changes emerged in the patient after infection**.

- **No PB2 E627K** change or others in polymerase genes associated with adaptation to mammals and no evidence of low frequency changes at critical positions.

https://www.cdc.gov/bird-flu/spotlights/h5n1-response-12232024.html Dec 26, 2024

2025 , 19 Feb Wyoming >>> backyard pultry exposure
21 Feb 2025 Ohio >> commercial poultry farm
California < 18 aa >> no known exposure to infected animals

27 January 2025, UK

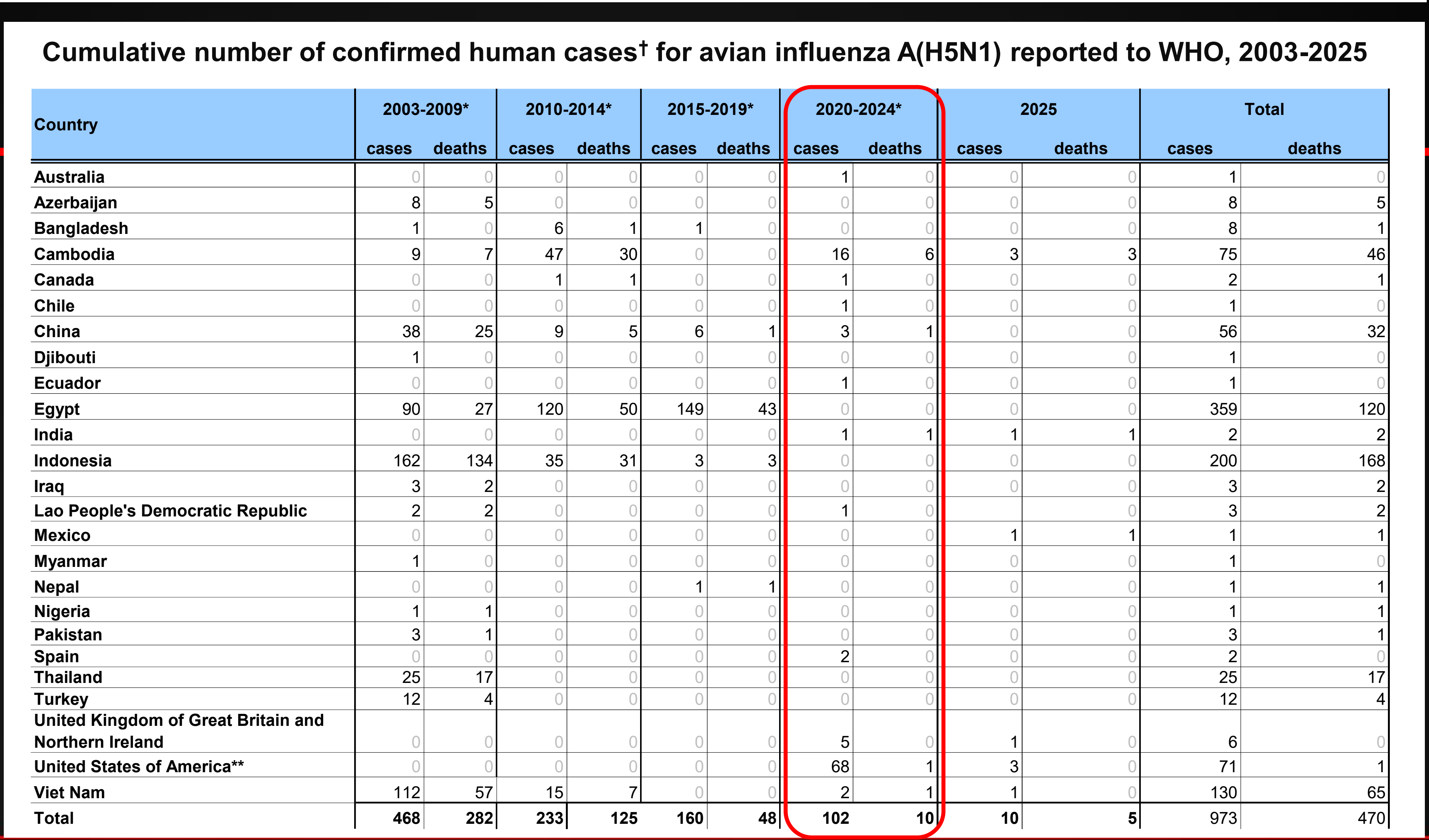
A human case of A(H5N1) in the West Midlands region >>> to close and prolonged occupational exposure to a large number of infected birds on a farm.

The individual experienced **mild** respiratory symptoms and eye irritation.

The sequenced strain, A/England/0480160/2025, **genotype EA-2024-DI.2, currently common in Europe, and had change I292V in the PB2 segment**.

This change is associated with **increased polymerase activity in mammalian cell line and increased virulence in mice** (tested on subtypes H10N8 and H9N2) (Suttie et al., 2019).
The HA segment of the strain is nearly identical to that of a strain collected on 18 January 2025 from a chicken in the United Kingdom.

WHO cumulative data on H5N1 cases worldwide 2003- May 30, 2025



Cumulative number of confirmed human cases† for avian influenza A(H5N1) reported to WHO, 2003-2025

Country	2003-2009*		2010-2014*		2015-2019*		2020-2024*		2025		Total	
	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths	cases	deaths
Australia	0	0	0	0	0	0	1	0	0	0	1	0
Azerbaijan	8	5	0	0	0	0	0	0	0	0	8	5
Bangladesh	1	0	6	1	1	0	0	0	0	0	8	1
Cambodia	9	7	47	30	0	0	16	6	3	3	75	46
Canada	0	0	1	1	0	0	1	0	0	0	2	1
Chile	0	0	0	0	0	0	1	0	0	0	1	0
China	38	25	9	5	6	1	3	1	0	0	56	32
Djibouti	1	0	0	0	0	0	0	0	0	0	1	0
Ecuador	0	0	0	0	0	0	1	0	0	0	1	0
Egypt	90	27	120	50	149	43	0	0	0	0	359	120
India	0	0	0	0	0	0	1	1	1	1	2	2
Indonesia	162	134	35	31	3	3	0	0	0	0	200	168
Iraq	3	2	0	0	0	0	0	0	0	0	3	2
Lao People's Democratic Republic	2	2	0	0	0	0	1	0		0	3	2
Mexico	0	0	0	0	0	0	0	0	1	1	1	1
Myanmar	1	0	0	0	0	0	0	0	0	0	1	0
Nepal	0	0	0	0	1	1	0	0	0	0	1	1
Nigeria	1	1	0	0	0	0	0	0	0	0	1	1
Pakistan	3	1	0	0	0	0	0	0	0	0	3	1
Spain	0	0	0	0	0	0	2	0	0	0	2	0
Thailand	25	17	0	0	0	0	0	0	0	0	25	17
Turkey	12	4	0	0	0	0	0	0	0	0	12	4
United Kingdom of Great Britain and Northern Ireland	0	0	0	0	0	0	5	0	1	0	6	0
United States of America**	0	0	0	0	0	0	68	1	3	0	71	1
Viet Nam	112	57	15	7	0	0	2	1	1	0	130	65
Total	**468**	**282**	**233**	**125**	**160**	**48**	**102**	**10**	**10**	**5**	973	470

Avian Influenza Weekly Update May 2025

973 casi dal 2003

case fatality ratio del 48% (n=470)

PAHO

Pan American Health Organization

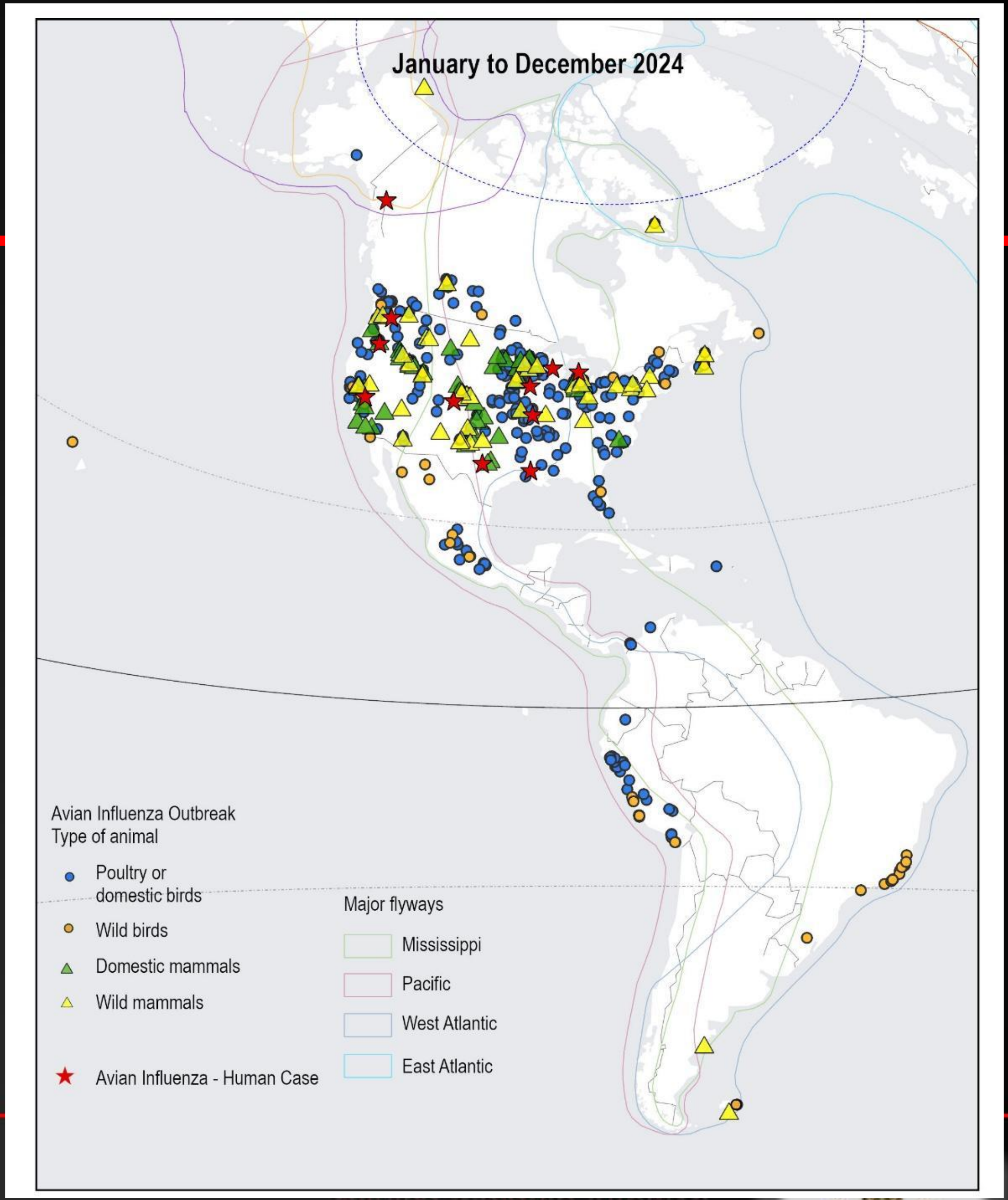
World Health Organization

Americas Region

Epidemiological Update
Avian Influenza A(H5N1)
in the Americas Region

24 January 2025

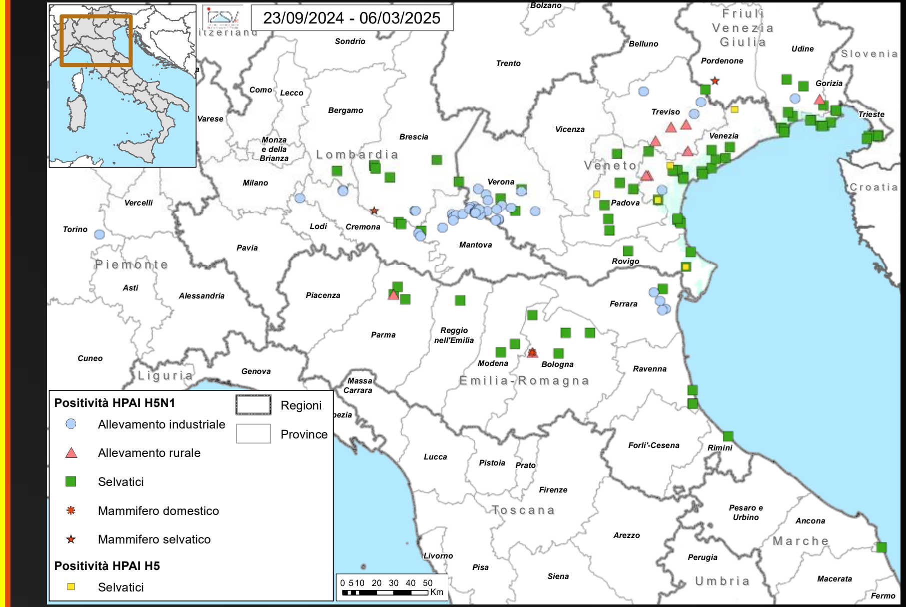
History of avian influenza outbreaks between January and December 2024 by species and main migratory routes of wild birds in the Americas Region



Influenza aviaria (H5N1): situazione epidemiologica in Italia – HPAI

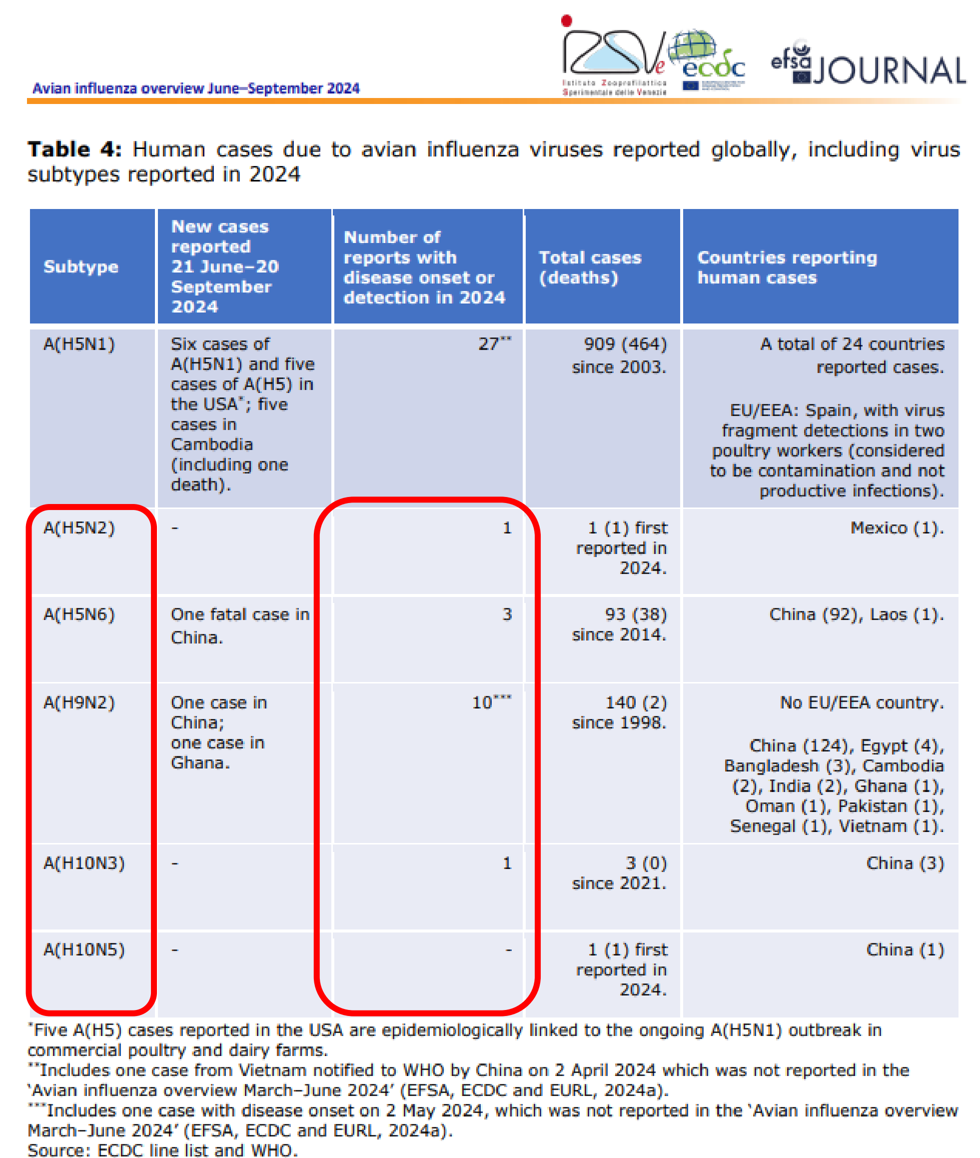
Influenza Aviaria in Italia, i numeri (2024-25)

- **76** **focolai nei volatili selvatici**
- **51** **focolai negli allevamenti di pollame**
- **5** regioni interessate (Veneto, Lombardia, Emilia-Romagna, Friuli-Venezia Giulia e Marche)



https://www.izsvenezie.it/documenti/temi/influenza-aviaria/situazione-epidemiologica-HPAI/HPAI-mappe

Avian influenza - virus subtypes overview 2024-2025



Avian influenza overview June–September 2024

Table 4: Human cases due to avian influenza viruses reported globally, including virus subtypes reported in 2024

Subtype	New cases reported 21 June–20 September 2024	Number of reports with disease onset or detection in 2024	Total cases (deaths)	Countries reporting human cases
A(H5N1)	Six cases of A(H5N1) and five cases of A(H5) in the USA[*]; five cases in Cambodia (including one death).	27[**]	909 (464) since 2003.	A total of 24 countries reported cases. EU/EEA: Spain, with virus fragment detections in two poultry workers (considered to be contamination and not productive infections).
A(H5N2)	-	1	1 (1) first reported in 2024.	Mexico (1).
A(H5N6)	One fatal case in China.	3	93 (38) since 2014.	China (92), Laos (1).
A(H9N2)	One case in China; one case in Ghana.	10[***]	140 (2) since 1998.	No EU/EEA country. China (124), Egypt (4), Bangladesh (3), Cambodia (2), India (2), Ghana (1), Oman (1), Pakistan (1), Senegal (1), Vietnam (1).
A(H10N3)	-	1	3 (0) since 2021.	China (3)
A(H10N5)	-	-	1 (1) first reported in 2024.	China (1)

[*] Five A(H5) cases reported in the USA are epidemiologically linked to the ongoing A(H5N1) outbreak in commercial poultry and dairy farms.

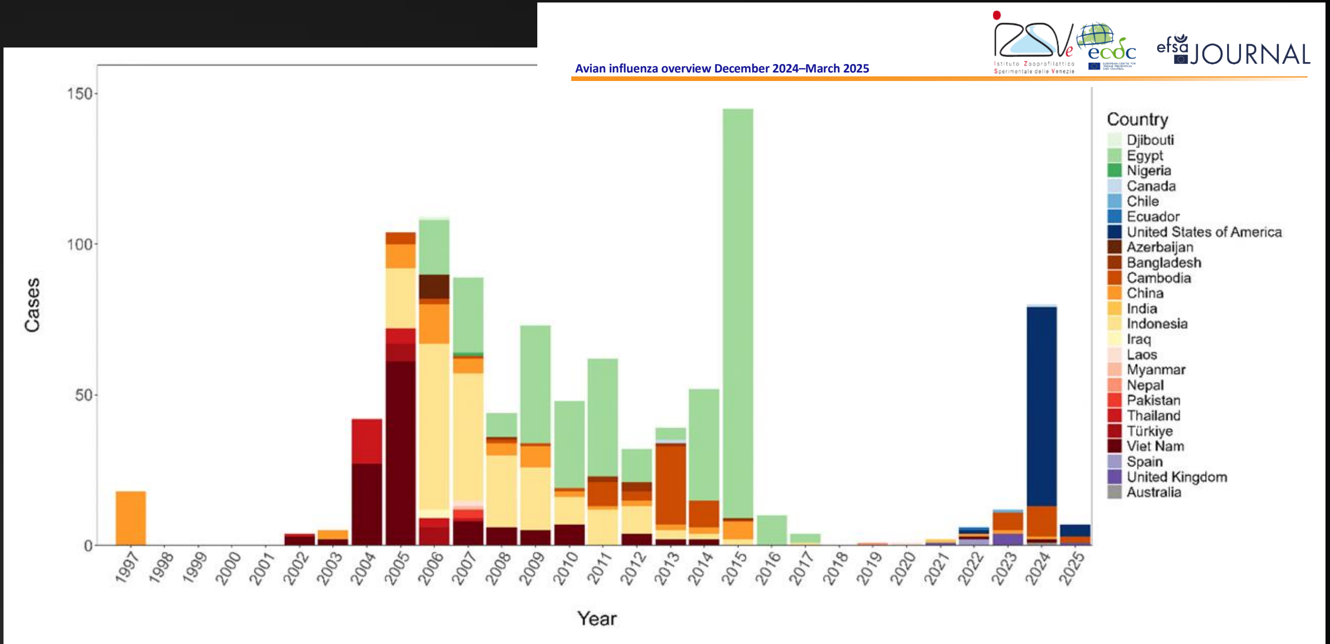
[**] Includes one case from Vietnam notified to WHO by China on 2 April 2024 which was not reported in the 'Avian influenza overview March–June 2024' (EFSA, ECDC and EURL, 2024a).

[***] Includes one case with disease onset on 2 May 2024, which was not reported in the 'Avian influenza overview March–June 2024' (EFSA, ECDC and EURL, 2024a).

Source: ECDC line list and WHO.

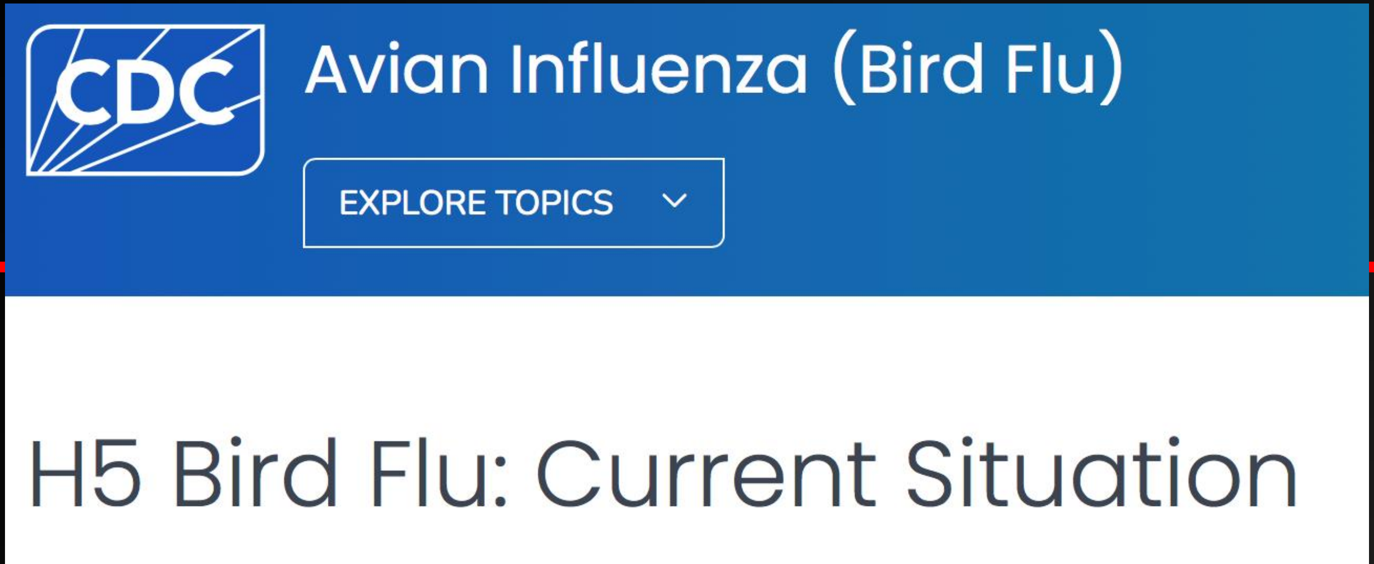
In Germany, HPAI A(H7N5) virus emerged in a poultry establishment near the border with the Netherlands.

Mexico one (H5N2), China (one fatal A(H5N6) case and one A(H9N2) case), and Ghana (one A(H9N2) case), China (one A(H10N3) and one A(H10N5)



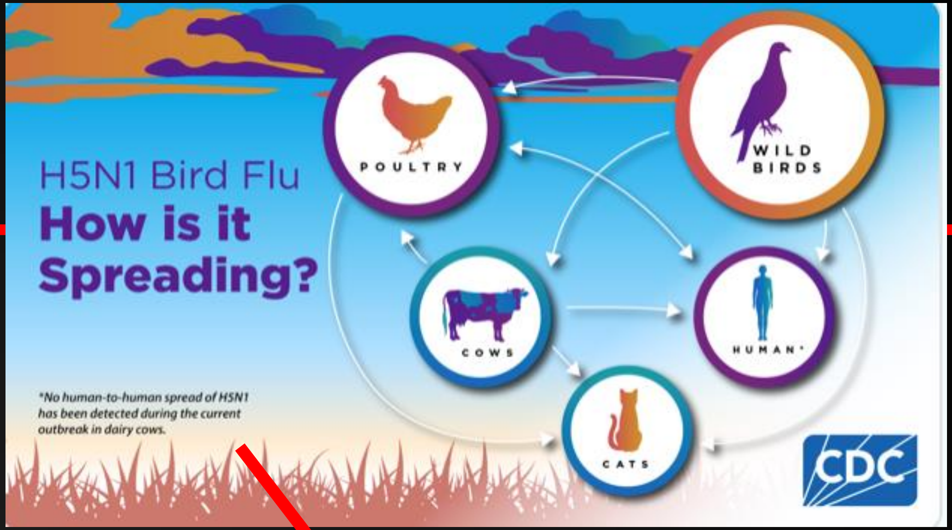
The risk of infection with currently circulating avian A(H5) influenza viruses of clade 2.3.4.4b in Europe remains rare for the general public EU/EEA.

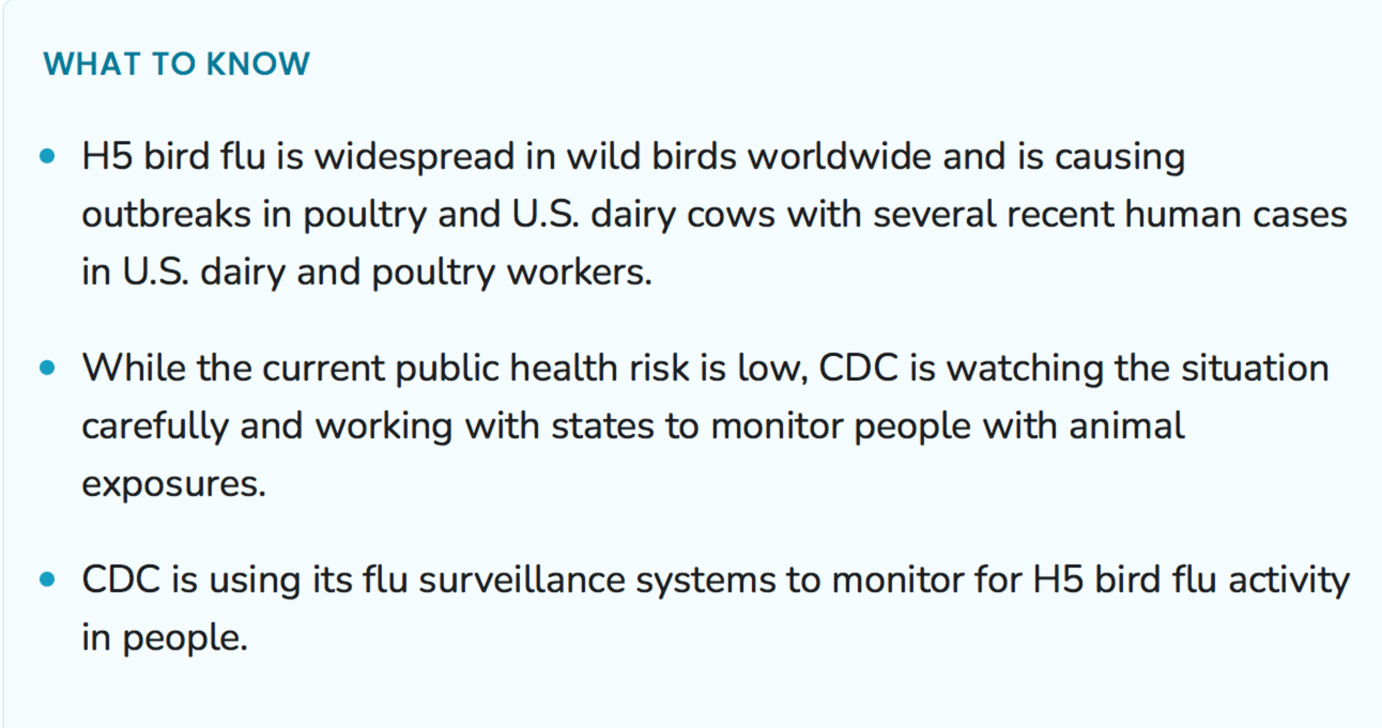
The risk of infection remains low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.



Avian Influenza (Bird Flu)

H5 Bird Flu: Current Situation





WHAT TO KNOW

- H5 bird flu is widespread in wild birds worldwide and is causing outbreaks in poultry and U.S. dairy cows with several recent human cases in U.S. dairy and poultry workers.
- While the current public health risk is low, CDC is watching the situation carefully and working with states to monitor people with animal exposures.
- CDC is using its flu surveillance systems to monitor for H5 bird flu activity in people.

Durante l'attuale focolaio
nei bovini da latte
NON è stata rilevata alcuna diffusione da uomo a uomo

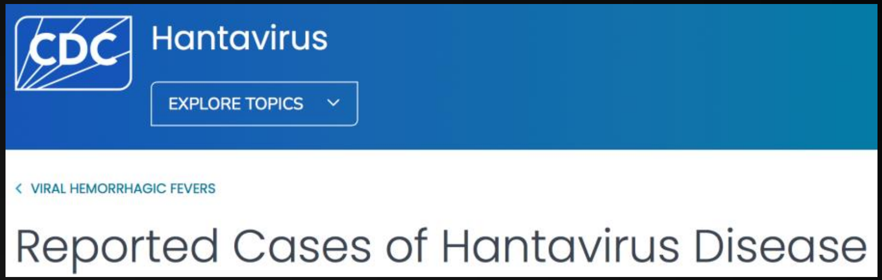
CDC, June 2025

……e
le altre zoonosi respiratorie potenzialmente patogene per l’uomo

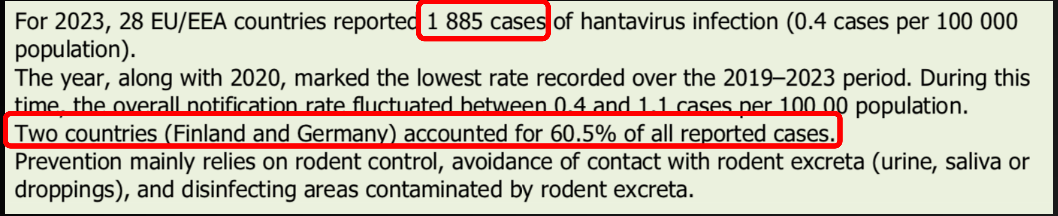

SURVEILLANCE

Hantavirus infection

Annual Epidemiological Report for 2023



Reported Cases of Hantavirus Disease

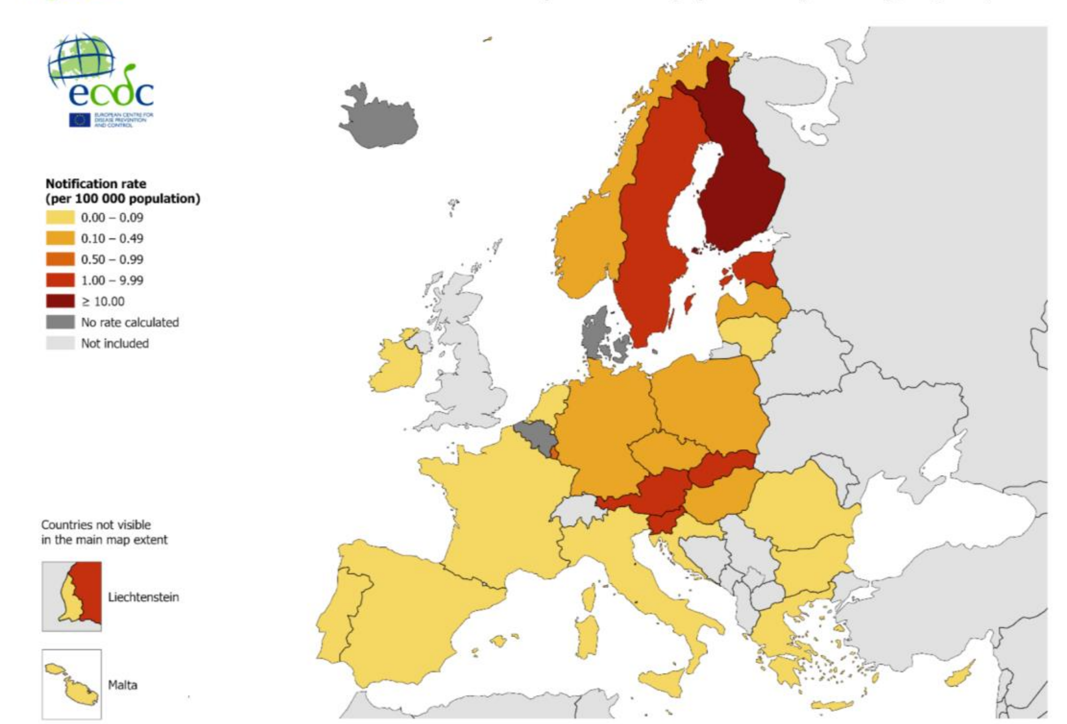

For 2023, 28 EU/EEA countries reported 1 885 cases of hantavirus infection (0.4 cases per 100 000 population).

The year, along with 2020, marked the lowest rate recorded over the 2019–2023 period. During this time, the overall notification rate fluctuated between 0.4 and 1.1 cases per 100 00 population.

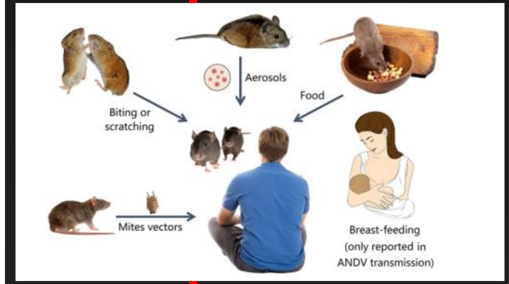
Two countries (Finland and Germany) accounted for 60.5% of all reported cases.

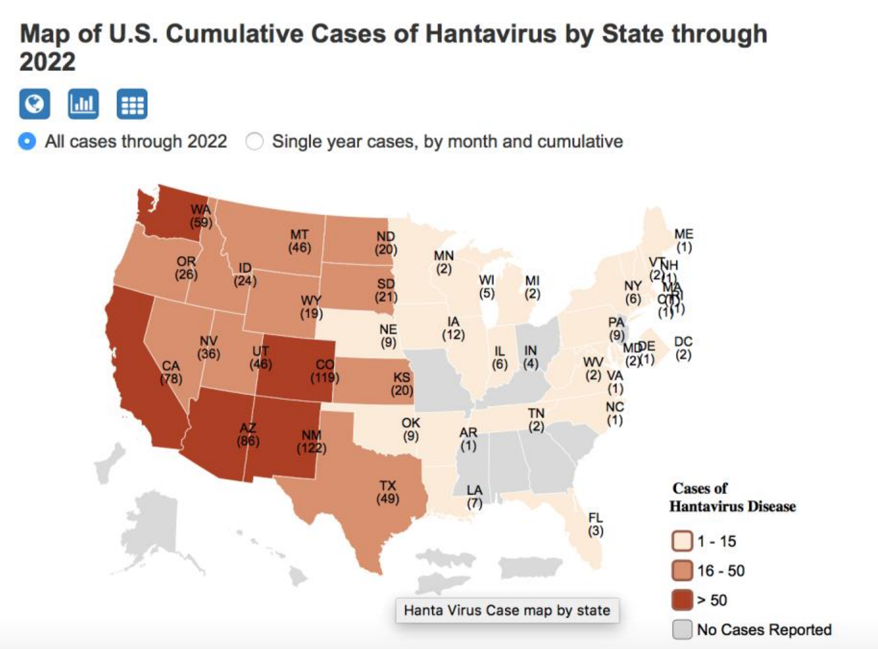
Prevention mainly relies on rodent control, avoidance of contact with rodent excreta (urine, saliva or droppings), and disinfecting areas contaminated by rodent excreta.

Figure 1. Distribution of hantavirus infection rates per 100 000 population by country, EU/EEA, 2023



Administrative boundaries: © EuroGeographics. The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union. Map produced by ECDC on 23 January 2025



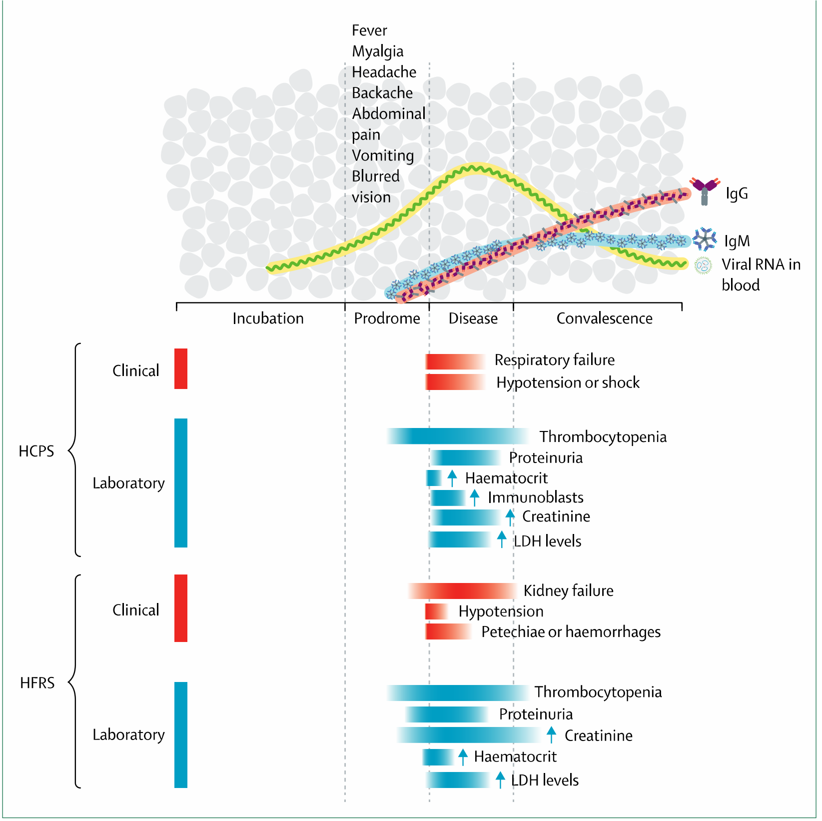

Map of U.S. Cumulative Cases of Hantavirus by State through 2022

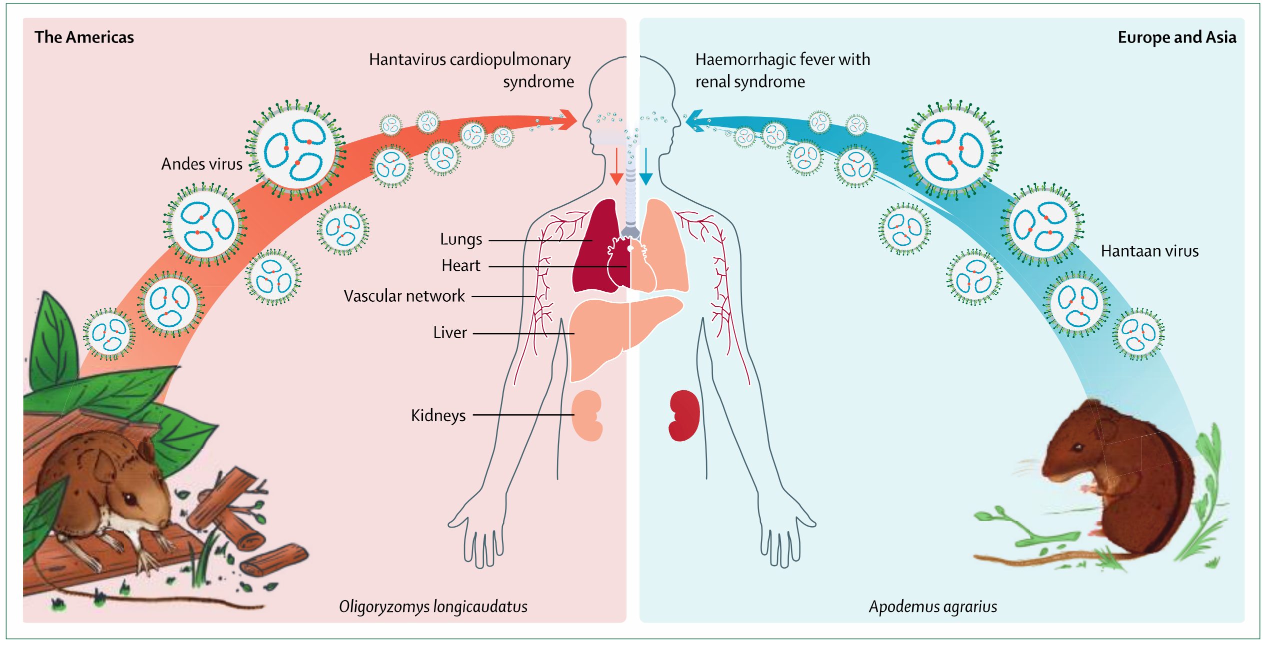
● All cases through 2022 ○ Single year cases, by month and cumulative

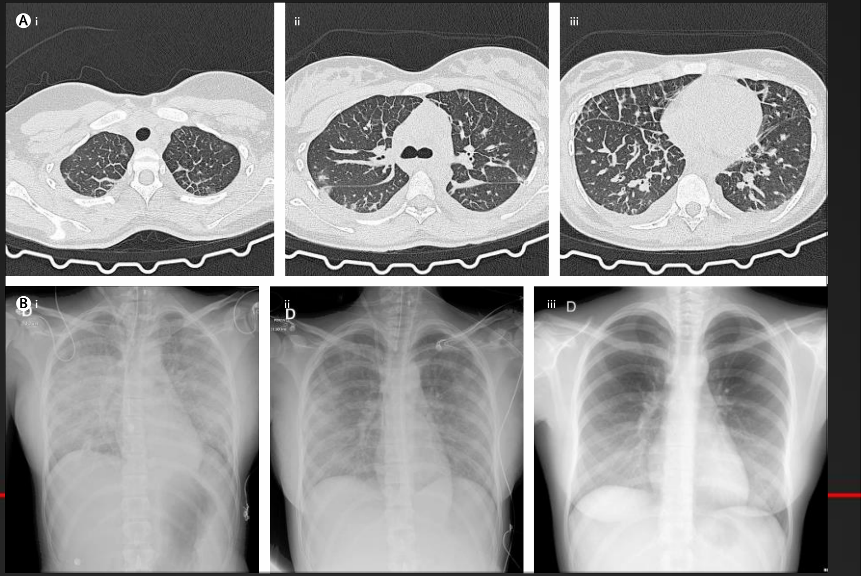
As of the end of **2022**, **864 cases** of hantavirus disease were reported in the United States since surveillance began in 1993. These were all laboratory-confirmed cases and included HPS and non-pulmonary hantavirus infection.

Hantavirus in humans: a review of clinical aspects and management

Main clinical syndromes associated:
- Haemorrhagic fever with renal syndrome (HFRS) (Europe and Asia)
- Hantavirus cardiopulmonary syndrome (HCPS), (Americas)
- Nephropatia Epidemica: kidneys disease (Europe)





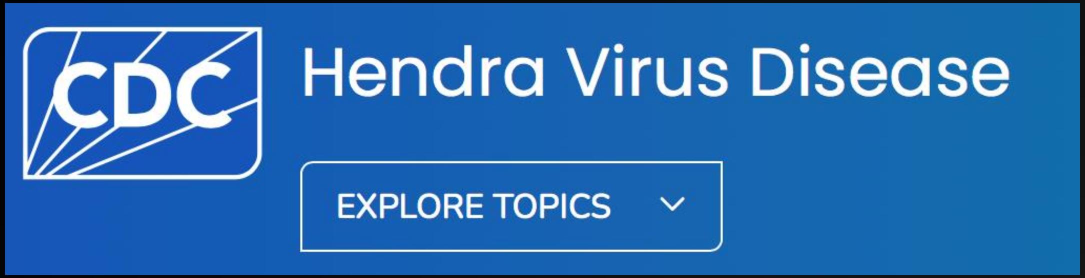


Therapy:

- Ribavirina?
- Metilprednisolone NO
- Favipiravir (pre-viraemic phase/animal model)
- icatibant acetate, a bradykinin receptor antagonist
- mAb in vitro efficacy
- CP non RCT in Chile < mortality

Supportive therapy with ECMO

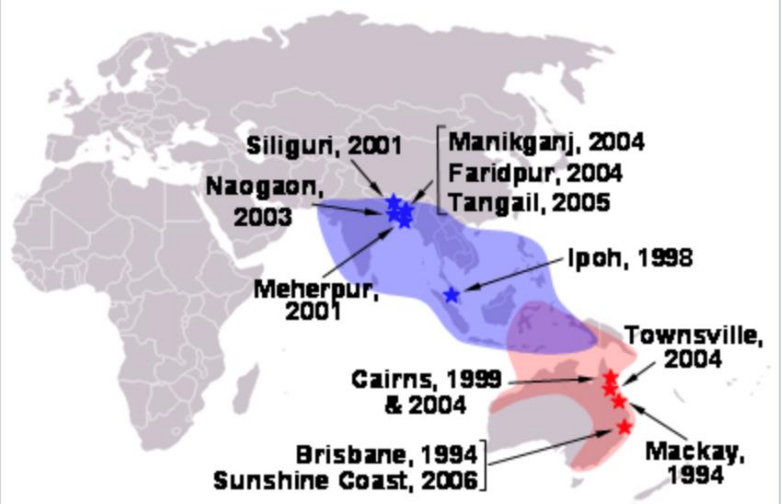
Vial Pablo A,et al., Lancet infect Dis 2023


Hendra Virus Disease

- Famiglia
  - *Paramyxoviridae*
- Sottofamiglia
  - *Paramyxovirinae*
- Genere
  - *Henipavirus*
- Specie
  - *Hendra virus (cavallo)*
  - *Nipah virus (suino)*

Malattia da virus Hendra: rara, segnalata nell'uomo e nei cavalli (outbreak sintomi polmonari e encefalitici nel 1994, Australia Queensland and New South Wales)

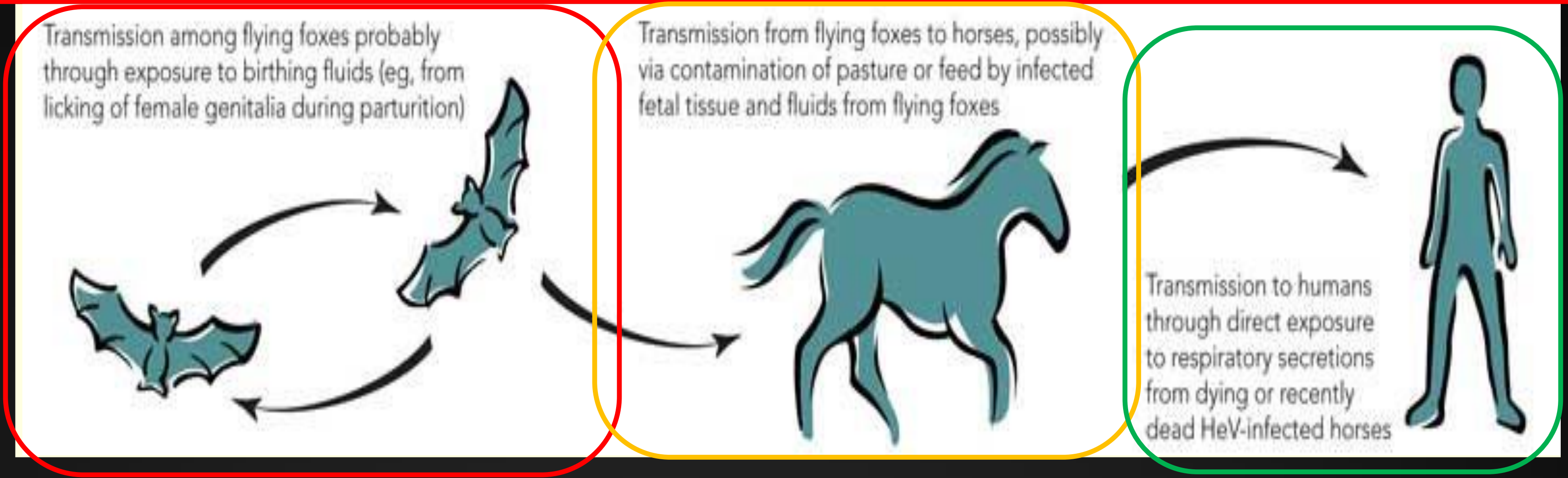
Uomo si può infettare con contatto con cavalli infetti
(**Solo 7 casi segnalati nell'uomo)**



Area di *Pteropus scapulatus* e *Pteropus Alecto* serbatoi naturali di Hendra virus.

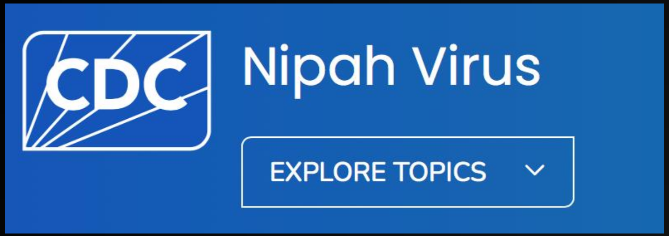
Area di Pteropus lylei, serbatorio naturale di Nipah virus

Cavalli si ammalano dopo contatto con pipistrelli –volpi volanti australiani (morso) o con loro fluidi (urine, saliva, fetal fluid).
4 specie di flying fox bats



Sintomi nell'uomo: dopo 9-16 gg contatto con cavallo infetto.
Severe Flu-like Symptoms e raro encefalite
57% mortalità

Terapia: ribavirina (studi in vitro)
mAb in Australia (per esposti che sviluppano sintomi)



Virus Nipah trasmesso dal pipistrello della frutta

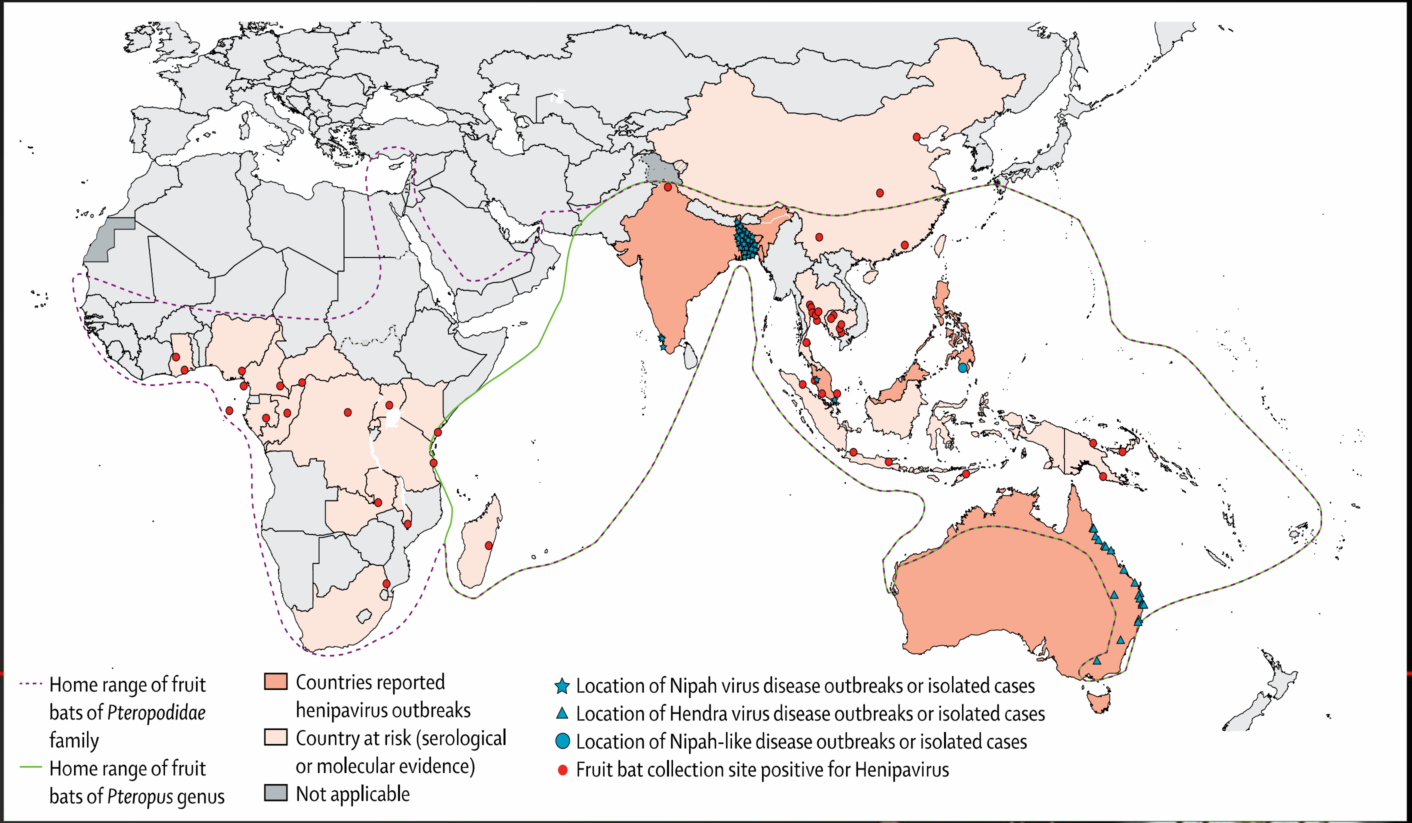
Mortalità: 40-75%

Focolai in Malesia, Singapore, Bangladesh e India dal 1998

Nel maggio 2018, è stato segnalato un focolaio nel Kerala (India). 21 decessi/23 casi.

Soggetti a rischio per infezione da Nipah virus:

- Persone a stretto contatto con suini infetti
- Caregivers di persone con Nipah virus
- Persone esposte a cibi o bevande contaminate da animali infetti

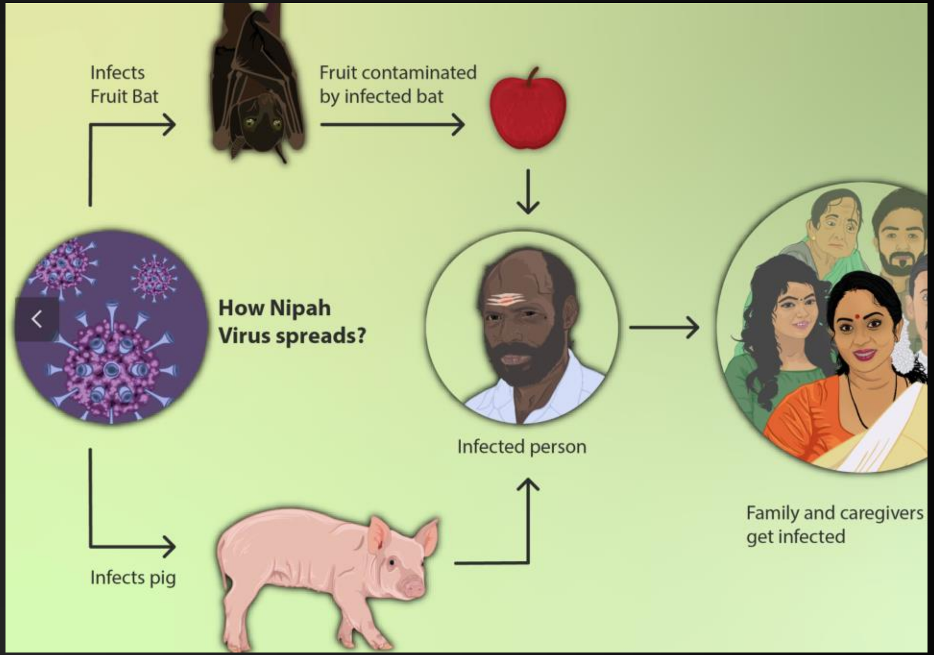


Moore KA et al, Lancet Infect Dis 2024

Sintomi: 4-14 giorni dopo esposizione a virus (riportati casi dopo mesi o anni).
Malattia da lieve a grave.
Febbre, cefalea, tosse, faringodinia e dispnea.
Stadi più avanzati di malattia: encefalite, coma

Kerala 2018:
allevamento intensivo suini/alberi da frutto: interfaccia che ha permesso lo spillover del virus Nipah dai pipistrelli che si nutrono degli alberi da frutto ai suini alloggiati in basso

Vaccini:
Phase 1 clinical trials:
soluble glycoprotein vaccine (Hendra virus-sG-V; NCT04199169),
mRNA vaccine (NCT05398796),
recombinant VSV-vectored live attenuated vaccine (NCT05178901),
chimpanzee adenovirus-vectored vaccine (ChAdOx1 NipahB vaccine; ISRCTN87634044).



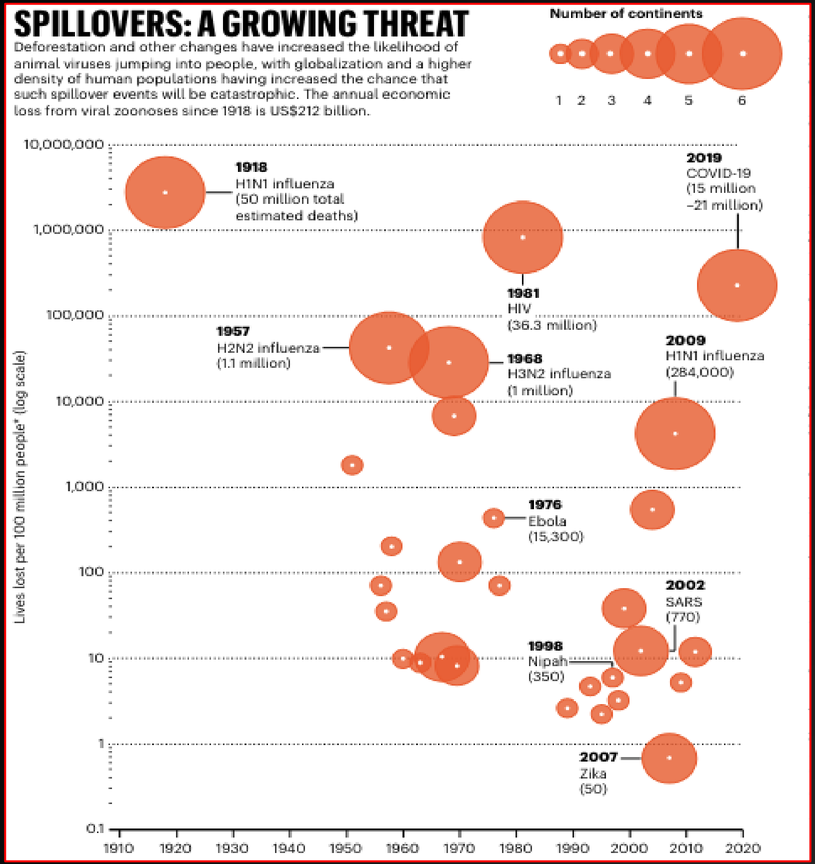
Terapia:
- m102.4, mAb early therapy, PEP, terminato fase 1
- Remdesivir post esposizione in nonhuman primates
- Favipiravir
- Ribavirin utilizzata nel 1999 Malaysian Nipah outbreak, efficacia unclear

Moore KA et al, Lancet Infect Dis 2024

Si vuole prevenire le pandemie?

Stop spillovers

Lo spillover , salto di specie, è la fuoriuscita di un virus da una specie "serbatoio", in cui esso abitualmente circola, verso una nuova specie "ospite" in cui esso può morire oppure adattarsi fino a innescare epidemie

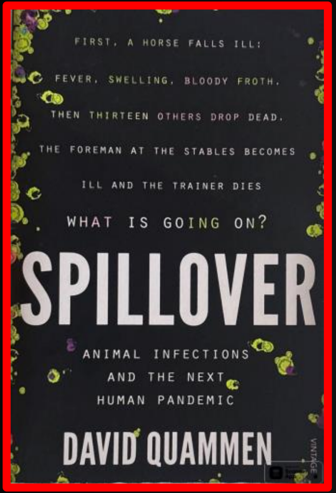


SPILLOVERS: A GROWING THREAT

Deforestation and other changes have increased the likelihood of animal viruses jumping into people, with globalization and a higher density of human populations having increased the chance that such spillover events will be catastrophic. The annual economic loss from viral zoonoses since 1918 is US$212 billion.

Neil M. Vora Nature May 2022

Cosa si può fare?

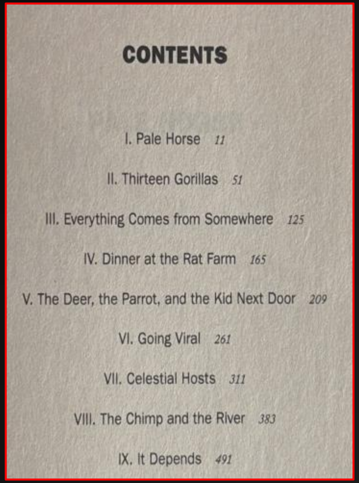


FIRST, A HORSE FALLS ILL:
FEVER, SWELLING, BLOODY FROTH.
THEN THIRTEEN OTHERS DROP DEAD.
THE FOREMAN AT THE STABLES BECOMES
ILL AND THE TRAINER DIES
WHAT IS GOING ON?

SPILLOVER

ANIMAL INFECTIONS
AND THE NEXT
HUMAN PANDEMIC

DAVID QUAMMEN

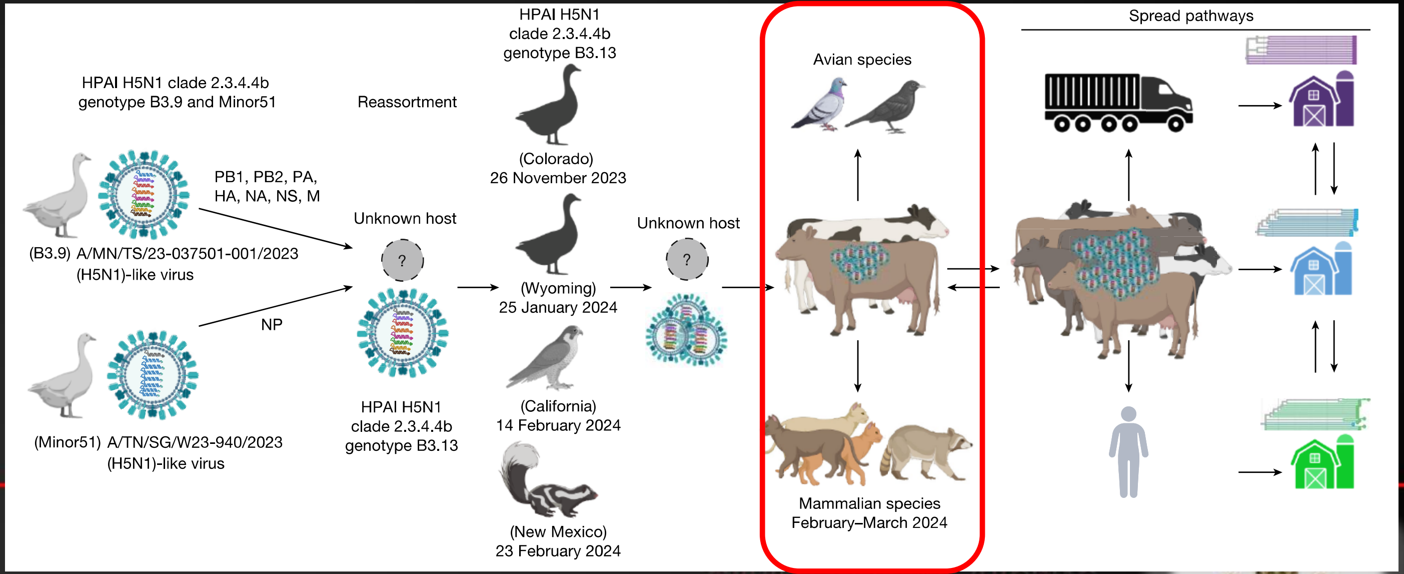


CONTENTS

Ogni capitolo è una storia di evoluzione e diffusione delle malattie infettive. **Racconta le epidemie, comprendere meccanismi e cause e cercare di individuare lo *spillover*.**

Ridurre la possibilità di Spillover:
Conoscere per prevenire

The ability of the virus to cross species barriers



Caserta L.C. *et al*., Nature 2024

A provocare il prossimo *Big One* – la prossima grande epidemia – potrà essere un'altra entità ancora innominata- Disease X

WHO 2020

Le uniche incertezze sulle epidemie
Sono il momento e la gravità

Cosa si può fare?

Ridurre la possibilità di Spillover:
Meno Ego….

Oms, accordo pandemico adottato. L'Italia si è astenuta con altri dieci Stati. I sì sono stati 124

Tedros Adhanom Ghebreyesus: «L' Accordo pandemico dell'Oms non deve essere interpretato nel senso di conferire al Segretariato dell'Oms, alcuna autorità per dirigere, ordinare, modificare o altrimenti prescrivere la legislazione nazionale e/o interna, a seconda dei casi, o le politiche di qualsiasi Parte, o per rendere obbligatorio o altrimenti imporre qualsiasi requisito affinché le Parti intraprendano azioni specifiche, come vietare o accettare viaggiatori, imporre mandati di vaccinazione o misure terapeutiche o diagnostiche o attuare lockdown»


Viewpoint

May 27, 2025

The WHO Pandemic Agreement
The World Together Equitably

Il 20 Maggio 2025 OMS ha adottato uno storico accordo sulle pandemie.

A seguito al ritiro del Presidente Trump dall'OMS,
gli Stati Uniti non ne trarranno benefici.

Visione d'accordo di cooperazione internazionale universale
ed equità ?

Gostin L.O., et al. JAMA, May 2025

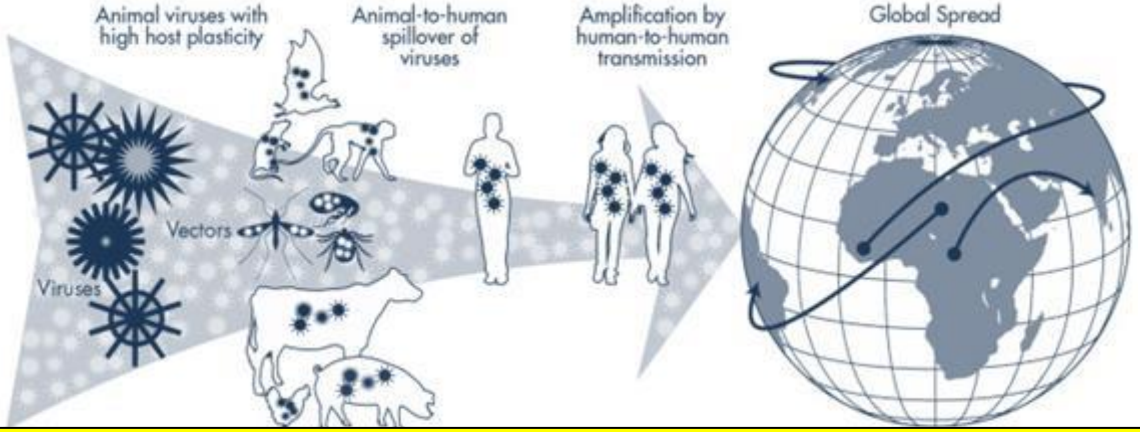
Cosa si deve fare?

Ridurre la possibilità di Spillover: **Meno Ego….Più Eco**

Modificata da E. Nicastri

The rationale for One Health

- 70-80% of (re-) emerging infectious diseases are known to be of zoonotic origin



The anthropogenic nature of drivers of EZDs (increased human population, globalization, climate change)

- Drivers – changes at the human-animal-environment interface

Deforestation Biodiversity loss Climate change

Intensive farming and agriculture Pollution

Urbanization Migration Global mobility

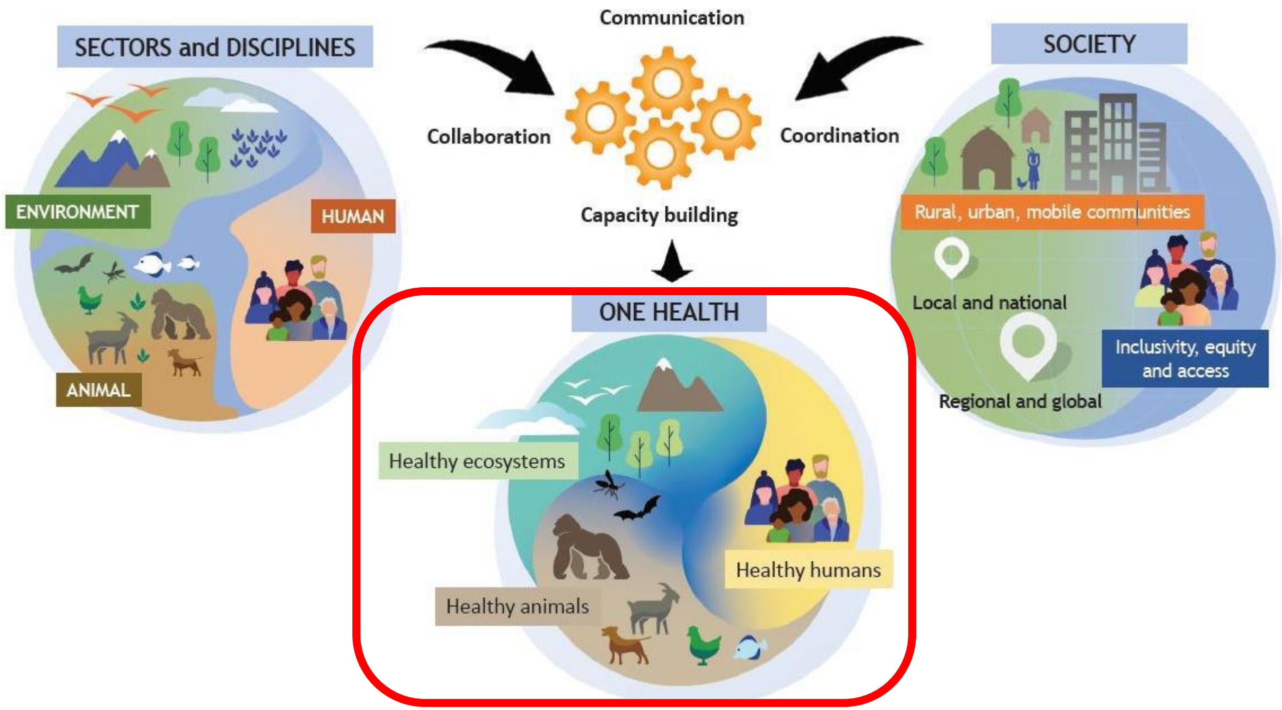
WHO 2023

Gostin L.O. Nat Med 2024

What is the One Health approach?

To improve environmental balance and human and animal welfare

Definition by the One Health High Level Expert Panel:



One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems.

It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and inter-dependent.

WHO 2023

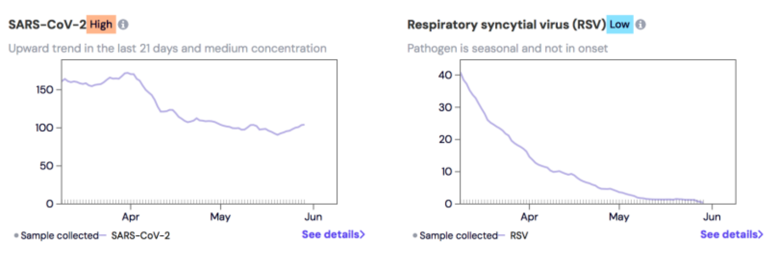
Adisasmito WB, et al. Plos Path 2022

Cosa si deve fare?

Rete con IZP per aggiornamenti costanti su sorveglianza animale e **ISS** su acque reflue

ECDC/WHO: Surveillance from wastewater for respiratory viruses including H5N1 to early detect viral community circulation

WastewaterSCAN Dashboard

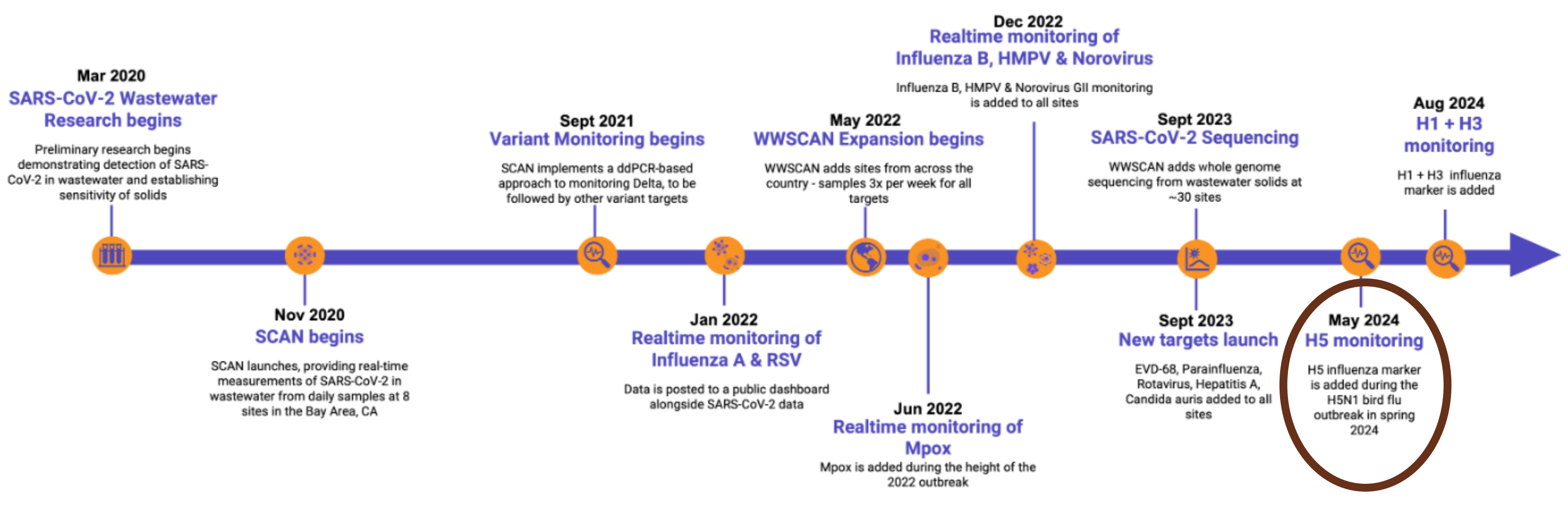


SARS-CoV-2 High

Upward trend in the last 21 days and medium concentration

Respiratory syncytial virus (RSV) Low

Pathogen is seasonal and not in onset



Mar 2020
SARS-CoV-2 Wastewater Research begins
Preliminary research begins demonstrating detection of SARS-CoV-2 in wastewater and establishing sensitivity of solids

Nov 2020
SCAN begins
SCAN launches, providing real-time measurements of SARS-CoV-2 in wastewater from daily samples at 8 sites in the Bay Area, CA

Sept 2021
Variant Monitoring begins
SCAN implements a ddPCR-based approach to monitoring Delta, to be followed by other variant targets

Jan 2022
Realtime monitoring of Influenza A & RSV
Data is posted to a public dashboard alongside SARS-CoV-2 data

May 2022
WWSCAN Expansion begins
WWSCAN adds sites from across the country - samples 3x per week for all targets

Jun 2022
Realtime monitoring of Mpox
Mpox is added during the height of the 2022 outbreak

Dec 2022
Realtime monitoring of Influenza B, HMPV & Norovirus
Influenza B, HMPV & Norovirus GII monitoring is added to all sites

Sept 2023
SARS-CoV-2 Sequencing
WWSCAN adds whole genome sequencing from wastewater solids at ~30 sites

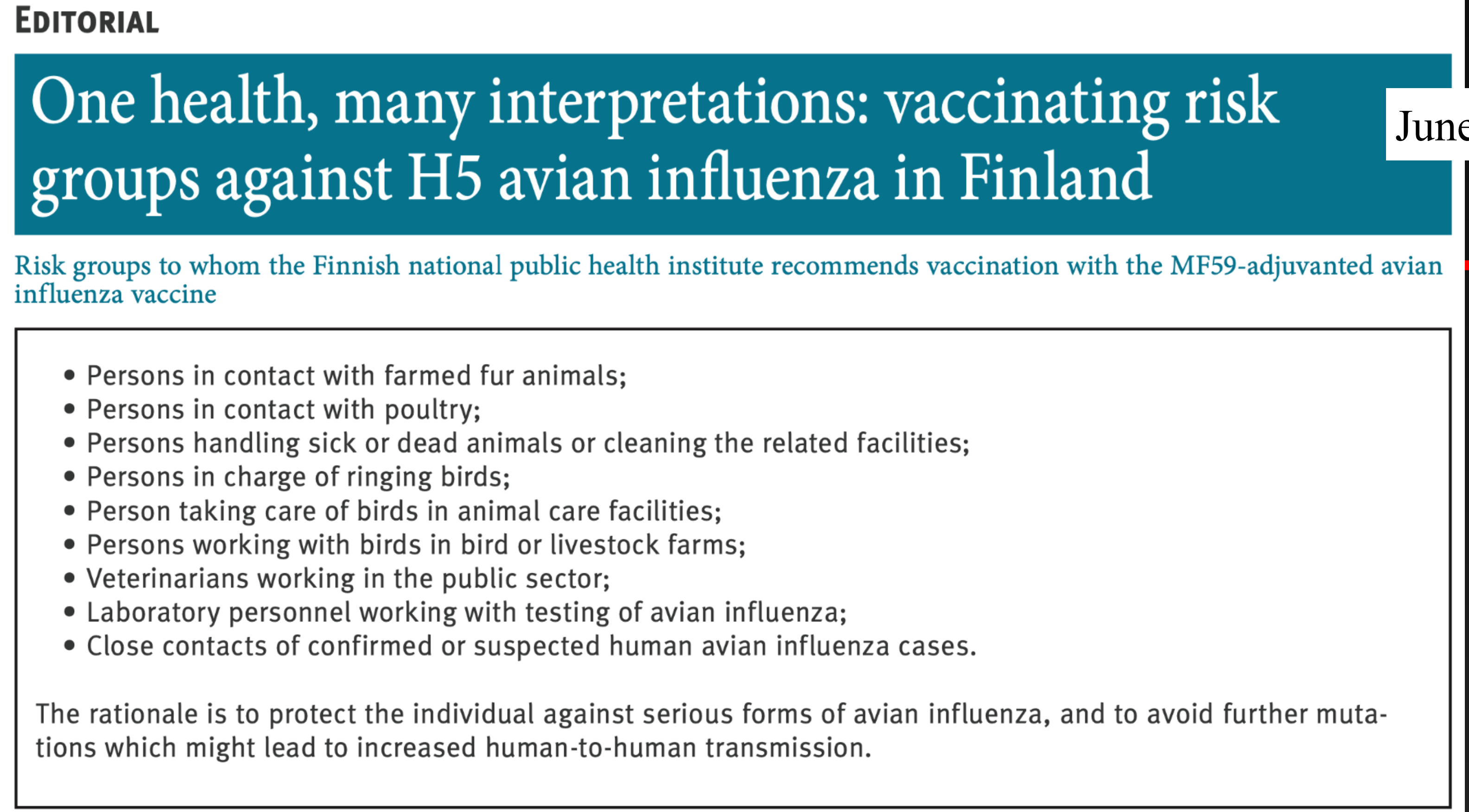
Sept 2023
New targets launch
EVD-68, Parainfluenza, Rotavirus, Hepatitis A, Candida auris added to all sites

May 2024
H5 monitoring
H5 influenza marker is added during the H5N1 bird flu outbreak in spring 2024

Aug 2024
H1 + H3 monitoring
H1 + H3 influenza marker is added

Cosa si deve fare?

Promozione **vaccinazione influenzale tradizionale e H5N1** in tutti gli operatori del settore dell'allevamento animale esposti a focolai



Editorial

One health, many interpretations: vaccinating risk groups against H5 avian influenza in Finland

Risk groups to whom the Finnish national public health institute recommends vaccination with the MF59-adjuvanted avian influenza vaccine

- Persons in contact with farmed fur animals;
- Persons in contact with poultry;
- Persons handling sick or dead animals or cleaning the related facilities;
- Persons in charge of ringing birds;
- Person taking care of birds in animal care facilities;
- Persons working with birds in bird or livestock farms;
- Veterinarians working in the public sector;
- Laboratory personnel working with testing of avian influenza;
- Close contacts of confirmed or suspected human avian influenza cases.

The rationale is to protect the individual against serious forms of avian influenza, and to avoid further mutations which might lead to increased human-to-human transmission.

June 2024

Same group >> Seasonal influenza vaccine during autumn 2023
-- **cross protection against HPAI**
-- **slow down potential reassortment** simultaneous infection of seasonal and HPAI occur in the same individual

Authorised by EMA under the brand name **Zoonotic influenza vaccine, Seqirus**
 - Zoonotic influenza vaccine Seqirus is based on A/ Astrakhan/3212/2020 (H5N8)-like strain (CBER-RG8A) (clade 2.3.4.4b) and is expected to provide protection against clade 2.3.4.4b avian influenza viruses

Nohynek H, Helve O. Euro Surveill 2024

EMA
Committee for Medicinal Products for Human Use (CHMP)
February 2024

CHMP adopted positive opinions for **two vaccines intended for active immunisation against the H5N1** subtype of influenza A virus, both produced **by Seqirus**

-- **Prepandemic - Celldemic** (zoonotic influenza vaccine (H5N1)(surface antigen, **inactivated, adjuvanted, prepared in cell cultures**)), is intended for immunisation during outbreaks of influenza coming from animals, including when public health authorities anticipate a possible pandemic.

--**Pandemic - Incellipan** (pandemic influenza vaccine (H5N1) (surface antigen, **inactivated, adjuvanted, prepared in cell cultures)),** is a pandemic preparedness vaccine intended for use only if a flu pandemic has been officially declared.

EMA 23 February 2024

Cosa si deve fare?

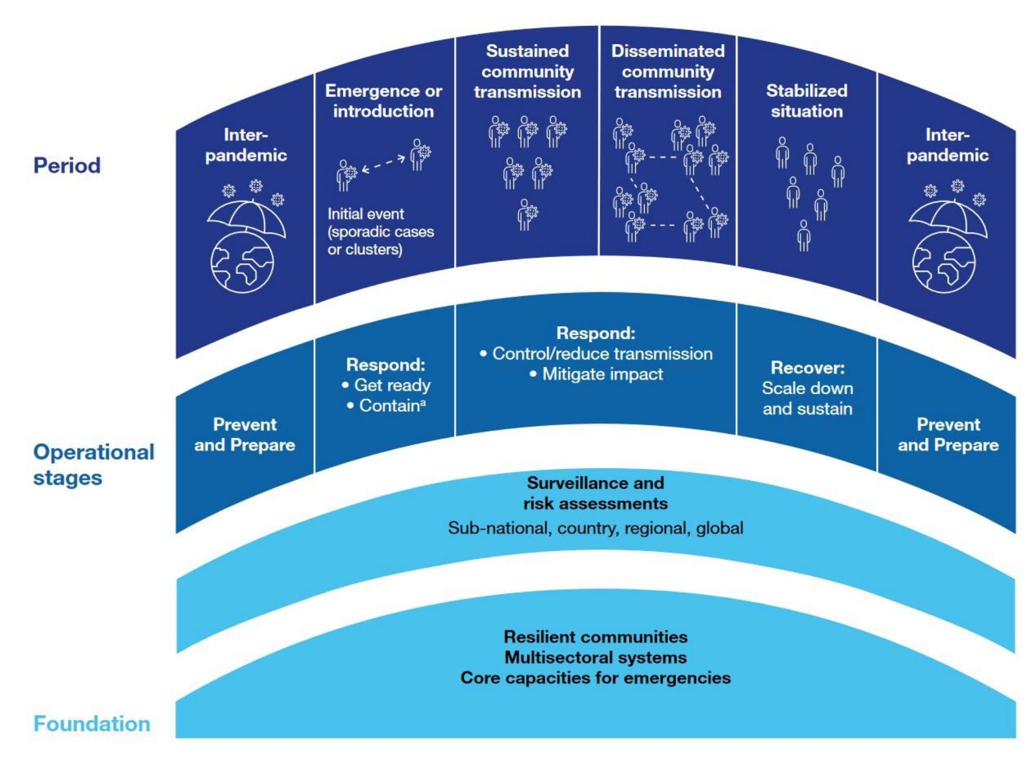
Promozione di **sorveglianza su casi umani di influenza A** non tipizzata con **link epidemiologico** con animali

ECDC/WHO: Surveillance in health care sentinel sites of biological samples from patients with respiratory tract infections is a priority to early detect A(H5N1) first cases.

Italia: Piano strategico operativo di preparazione e risposta ad una pandemia da patogeni a trasmissione respiratoria a maggiore potenziale pandemico 2025-2029 (bozza gennaio 2025)

Modello di corrispondenza tra le fasi pandemiche e le fasi operative proposto dall'OMS

Documento OMS "Preparedness and Resilience for Emerging Threats Module 1: Planning for respiratory pathogen pandemics Version 1.0"



- **Prevent and Prepare,**
- **Get ready,**
- **Contain,**
- **Control/reduce transmission,**
- **Mitigate,**
- **Scale down and Sustain**

Italia: Piano strategico operativo di preparazione e risposta ad una pandemia da patogeni a trasmissione respiratoria a maggiore potenziale pandemico 2025-2029 (bozza gennaio 2025)

Si richiamano:

- Piano Nazionale della Prevenzione (PNP) 2020-2025
- Piano Nazionale della Prevenzione Vaccinale (PNPV) 2023-2025
- Piano Nazionale di Contrasto all’Antibiotico-Resistenza (PNCAR) 2022-2025

- **Obiettivo 1: ridurre gli effetti di una pandemia da patogeni a trasmissione respiratoria sulla salute della popolazione, riducendone la trasmissione, la morbilità e la mortalità.**

- **Obiettivo 2:** consentire azioni appropriate e tempestive per il coordinamento a livello nazionale e locale delle emergenze, ovvero negli ambiti della sorveglianza integrata, della protezione della comunità, dei servizi sanitari, dell'accesso alle contromisure e del personale sanitario.

- **Obiettivo 3:** ridurre l’impatto della pandemia sui servizi sanitari e sociali e garantire la continuità dei servizi essenziali.

- **Obiettivo 4:** tutelare la salute degli operatori sanitari e del personale coinvolto nella gestione dell’emergenza.

- **Obiettivo 5:** informare, coinvolgere e responsabilizzare la comunità nella risposta ad una pandemia da agenti patogeni respiratori.

Rete italiana di preparedness pandemica

Reti istituite nell'ambito del PanFlu 2021- 2023 e aggiornate in relazione alle finalità e al perimetro di questo Piano

Rete italiana di *preparedness* pandemica

MiRiK:

valutazione microbiologica del rischio pandemico

DISPATCH:

scenari pandemici e valutazione del rischio epidemiologico. Valutazioni di impatto sulla salute e sui servizi sanitari

Protocollo *First Few cases* (FFX)

Comprensione dei principali aspetti clinici, epidemiologici e virologici dei primi casi di infezione dal nuovo patogeno

World Health Organization

Sfide nella gestione delle zoonosi emergenti e rimergenti

Livello Organizzativo

(i) Poor level of awareness among policy and decision-makers about the serious nature of the disease;

(ii) Insufficient information on the burden , trend and risks of zoonotic diseases;

(iii) Inadequate resources and skilled manpower for control of zoonotic diseases;

(iv) Presence of other competitive health priorities often taking precedence;

(v) Lack of transparency of the countries to report emergence or occurrence of zoonotic disease for fear of repercussions;

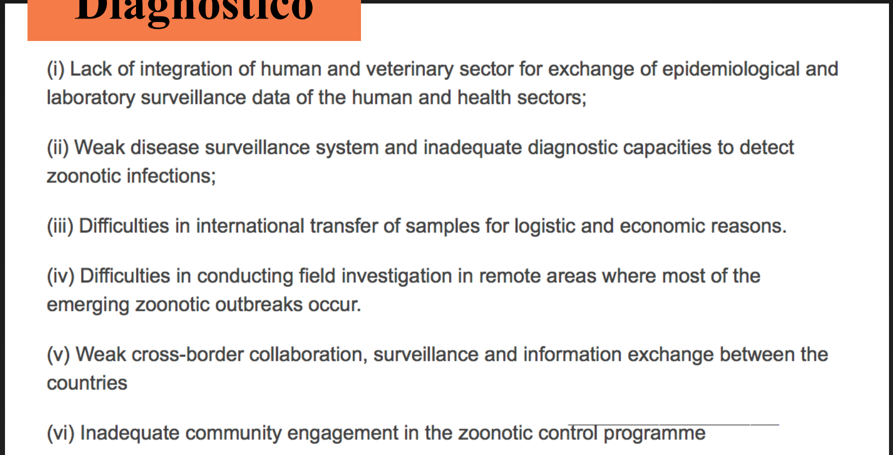
(vi) Weakness or absence of collaboration and cooperation between the public health , veterinary, agriculture and wildlife sectors;

(vii) Inadequate collaboration and partnerships to harness resources to support the prevention and control programme of zoonotic diseases

(viii) Absence of cross-talk within the health sector between the surveillance, clinical services and laboratory services departments.

(ix) Breakdown of weakness of health infrastructures specially in countries with complex emergencies;

Livello Diagnostico



(i) Lack of integration of human and veterinary sector for exchange of epidemiological and laboratory surveillance data of the human and health sectors;

(ii) Weak disease surveillance system and inadequate diagnostic capacities to detect zoonotic infections;

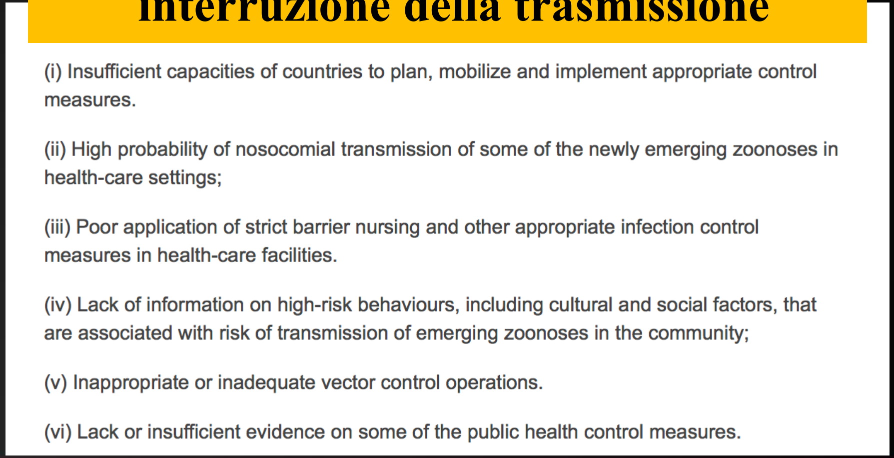
(iii) Difficulties in international transfer of samples for logistic and economic reasons.

(iv) Difficulties in conducting field investigation in remote areas where most of the emerging zoonotic outbreaks occur.

(v) Weak cross-border collaboration, surveillance and information exchange between the countries

(vi) Inadequate community engagement in the zoonotic control programme

Livello di Controllo e interruzione della trasmissione



(i) Insufficient capacities of countries to plan, mobilize and implement appropriate control measures.

(ii) High probability of nosocomial transmission of some of the newly emerging zoonoses in health-care settings;

(iii) Poor application of strict barrier nursing and other appropriate infection control measures in health-care facilities.

(iv) Lack of information on high-risk behaviours, including cultural and social factors, that are associated with risk of transmission of emerging zoonoses in the community;

(v) Inappropriate or inadequate vector control operations.

(vi) Lack or insufficient evidence on some of the public health control measures.

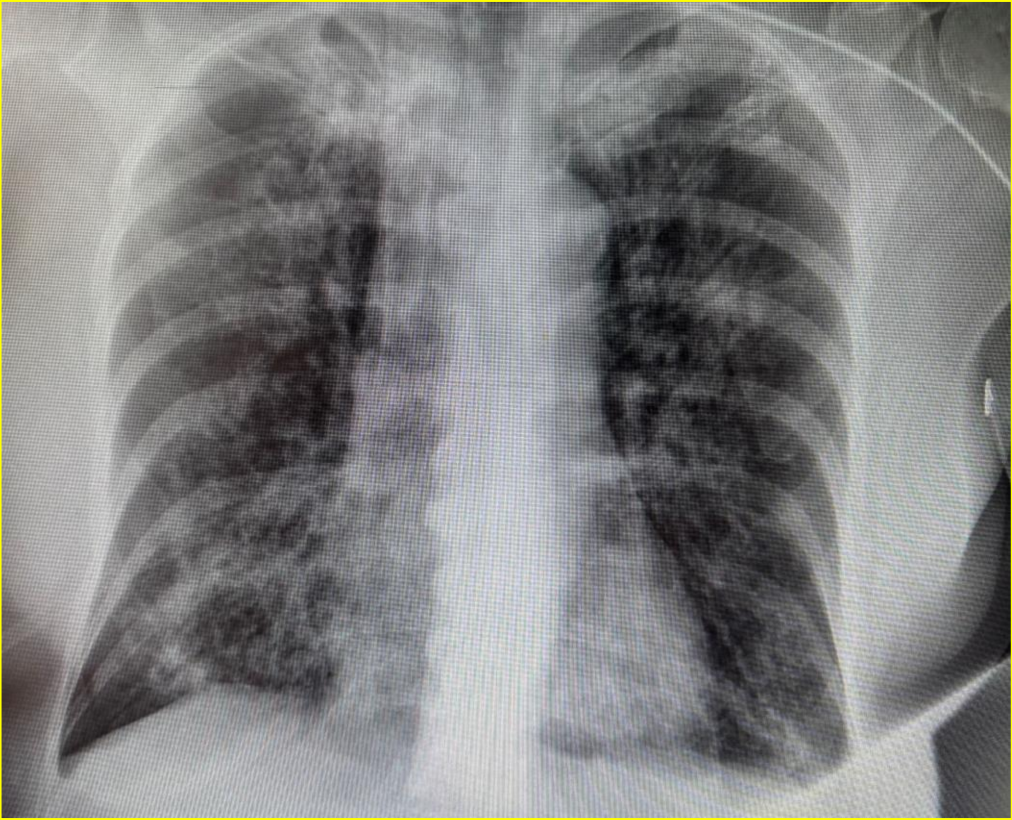
Cosa si deve fare?

Gestione in collaborazione con gli specialisti (pneumologi, rianimatori, medicina d’urgenza) dei casi clinici gravi (SARI) con link epidemiologico

Personal opinion

13 anni, femmina,
British Columbia, Canada,
BMI > 35, NF: H5N1

Maggio 2025, IRCCS Policlinico San Martino
66 anni, femmina, in crociera, proveniente da Ottawa, Canada, BMI > 30, BAL: SARS-CoV-2 LP.8.1.1 variante omicron



Jassem AN, *et al.*, NEJM 2024

Grazie per l'attenzione