



HPAI in Europe: update on the genetic characteristics

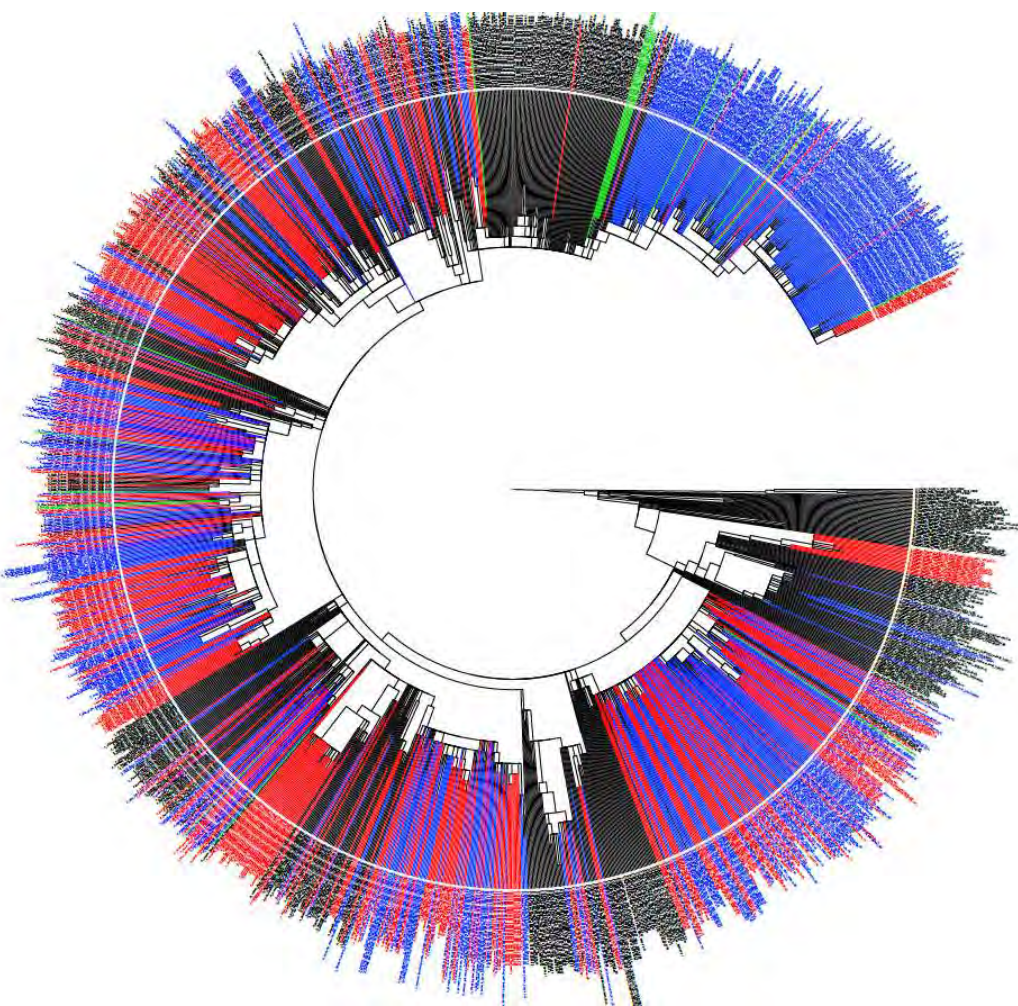
Alice Fusaro on behalf of the EURL Team

Istituto Zooprofilattico Sperimentale delle Venezie (IZSve), Padua, Italy

11 July 2024



2023-2024 epidemiological year in Europe



European H5Nx sequences available for the 2023-2024 epidemiological year (since October 2023):

~ 650 complete genomes

The characterized viruses were collected from **23 European countries** + Russia and Kazakhstan

Genetic diversity, 2023-2024

Genotype	PB2	PB1	PA	HA	NP	NA	MP	NS	N. seq	Reference	GISAID seq ID
DA	4	52	3	20	38	1	20	27	170	DA (H5N1-A/mute_swan/Slovenia/PER1486-23TA_23VIR10323-22/2023-like)	EPI_ISL_18612233
AB	31	1	3	20	38	1	20	1	150	AB (H5N1-A/duck/Saratov/29-02V/2021-like)	EPI_ISL_5463797
DI	14	14	3	20	38	1	20	27	134	DI (H5N1-A/mute_swan/Poland/MB008-1/2024-like)	EPI_ISL_18787976
DG	57	1	14	20	38	1	20	1	51	DG (H5N1-A/Gallus_gallus/Belgium/11307_0002/2023-like)	EPI_ISL_18607170
DB	31	53	3	20	38	1	20	1	39	DB (H5N1- A/herring_gull/Germany-NI/2023AI08764/2023-like)	EPI_ISL_18526630
BB	31	1	43	20	43	1	20	43	33	BB (H5N1-A/Herring_gull/France/22P015977/2022-like)	EPI_ISL_13519451
I	25	14	25	20	26	13	20	28	19	I (H5N5-A/whooper_swan/Romania/10123_21VIR849-1/2021-like)	EPI_ISL_1665268
DJ	31	52	3	20	26	1	20	58	13	DJ (H5N1 A/Barnacle_Goose/Netherlands/24000825-002/2024-like)	EPI_ISL_18918831
CK	4	1	3	20	38	1	20	1	8	CK (H5N1 A/Cormorants/Sweden/SVA240102SZ0114/FB00004/M-2023-like)	EPI_ISL_18815224
AF	12	6	1	20	50	1	20	29	3	AF (H5N1-A/chicken/Italy/IZSLT-122448_21VIR9218-1/2021-like)	EPI_ISL_7733644
DE	41	53	3	20	26	1	20	56	3	DE (H5N1-A/Chicken/Scotland/114176/2023-like)	EPI_ISL_18538402
DM	31	52	3	20	11	1	20	27	3	DM (H5N1-A/cygnus-olor/Romania/16868_24VIR1002-1/2023-like)	EPI_ISL_18956171
DP	31	1	65	20	26	1	20	1	3	DP (H5N1 A/turkey/Poland/H40-T2/2024-like)	EPI_ISL_19033547
DR	57	53	3	20	16	1	20	27	3	DR (H5N1_A/Red_Knot/Germany-SH/2024AI01285/2024-like)	EPI_ISL_19014084
DT	31	43	43	20	43	1	20	43	3	DT (H5N1-A/gull/Spain/5061-23_24VIR4860-8/2023-like)	EPI_ISL_19207490
DL	31	1	1	20	38	1	20	1	2	DL (H5N1-A/Chicken/England/005435/2024-like)	EPI_ISL_18927384
DQ	31	1	14	20	38	1	20	1	2	DQ (H5N1_A/chicken/Germany-MV/2024AI00860/2024-like)	EPI_ISL_19014079
CH	31	1	3	20	26	1	20	1	1	CH (H5N1-A/Eurasian_Wigeon/Netherlands/3/2022-like)	EPI_ISL_15925882
DC	41	53	32	20	36	1	20	1	1	DC (H5N1-A/Common_Buzzard/Netherlands/23023642-002/2023-like)	EPI_ISL_18506031
DF	4	52	3	20	50	1	20	27	1	DF (H5N1_A/hens/Bulgaria/309_24VIR2991-20/2024-like)	\
DH	4	52	3	20	11	1	20	27	1	DH (H5N1-A/teal/Italy/23VIR11492-4/2023-like)	EPI_ISL_18812084
DK	4	1	12	20	26	1	20	1	1	DK (H5N1-A/barnacle_goose/Denmark/09539-1.02/2023-like)	\
DN	4	60	3	20	26	1	20	27	1	DN (H5N1-A/peregrine-falcon/Cyprus/24VIR1053/2024-like)	EPI_ISL_18956184
DO	57	1	14	20	26	1	20	1	1	DO (H5N1 A/fox/Germany-BW/2024AI00417/2024-like)	EPI_ISL_18937337
DS	57	53	3	20	16	66	20	27	1	DS (H5N8_A/Red_Knot/Germany-SH/2024AI01485/2024-like)	EPI_ISL_19030161
DD	41	1	3	20	26	1	20	56	0	DD (H5N1-A/Pheasant/England/113705/2023-like)	EPI_ISL_18538399

Fusaro A., Zecchin B., et al. High pathogenic avian influenza A(H5) viruses of clade 2.3.4.4b in Europe – why trends of virus evolution are more difficult to predict, *Virus Evolution*, 2024; <https://doi.org/10.1093/ve/veae027>

Genetic diversity, 2023-2024

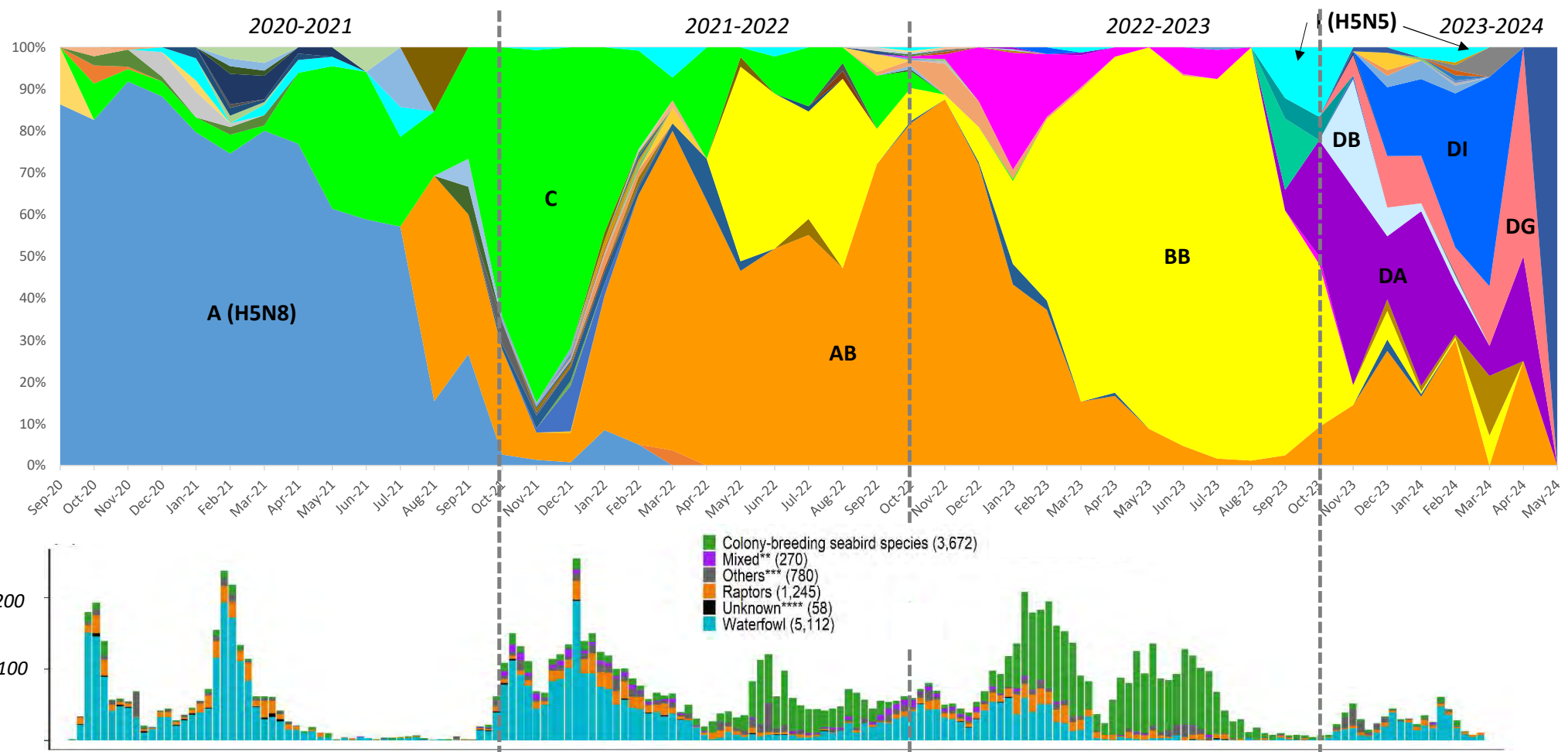
92%

Genotype	PB2	PB1	PA	HA	NP	NA	MP	NS	N. seq	Reference	GISAID seq ID
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DL	31	1									EPI_ISL_18927384
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CH	31	1									EPI_ISL_15925882
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DD	41	1	3	20	26	1	20	56	0	DD (H5N1-A/Pheasant/England/113705/2023-like)	EPI_ISL_18538399

>90% of the characterized viruses during the 2023-2024 epidemiological year belong to seven major genotypes:

- 3 genotypes persistently circulating in Europe from previous epidemiological years (AB, BB, I)
- 4 new genotypes, which emerged in 2023-2024 from reassortment events (DA, DI, DG, DB)

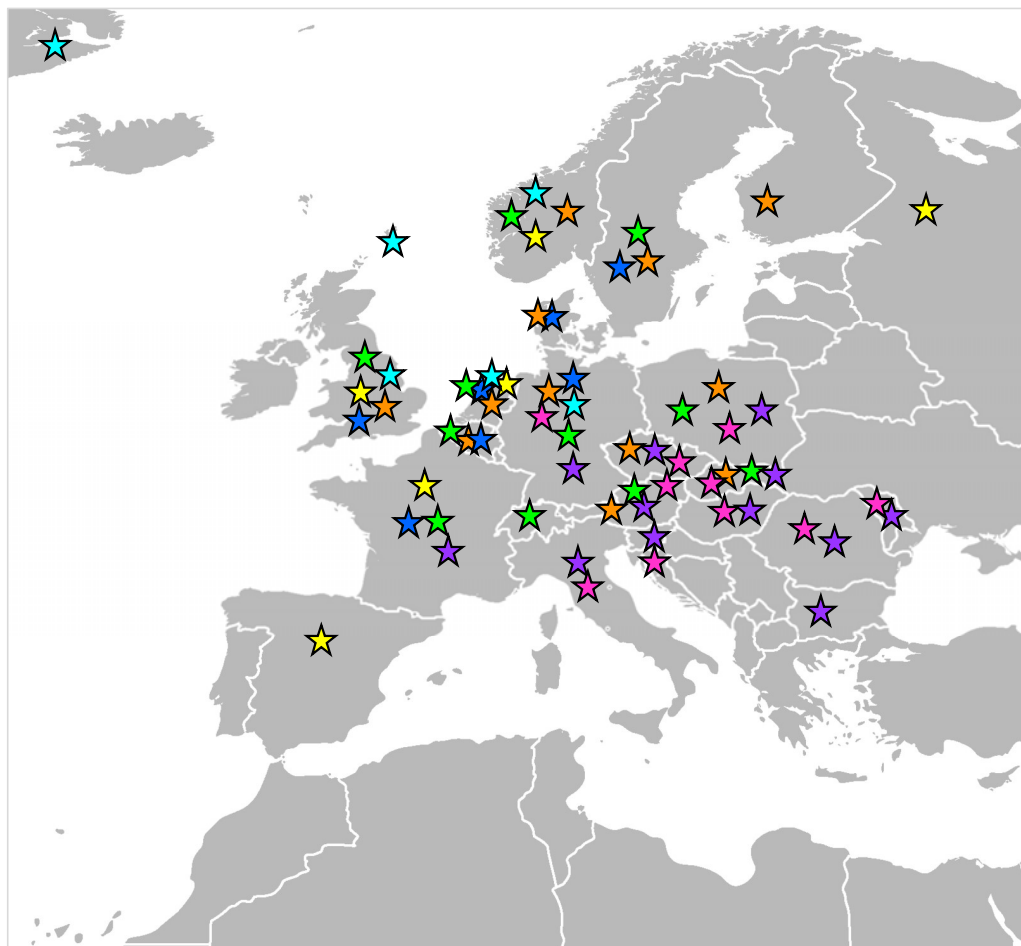
Temporal dynamics of the virus genotypes in Europe: 2020-2024



Source: Scientific report: Avian influenza overview December 2023 – March 2024. EFSA Journal 2024; doi:<https://doi.org/10.2903/j.efsa.2024.8754>

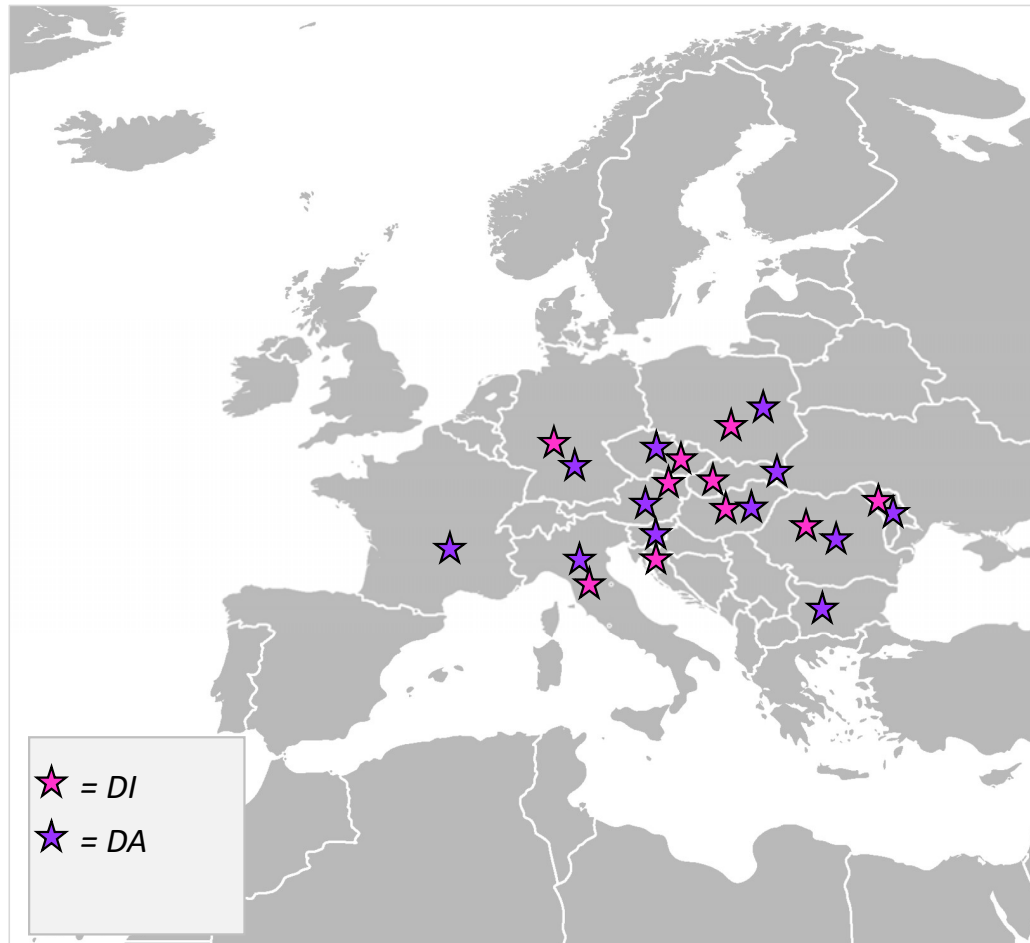
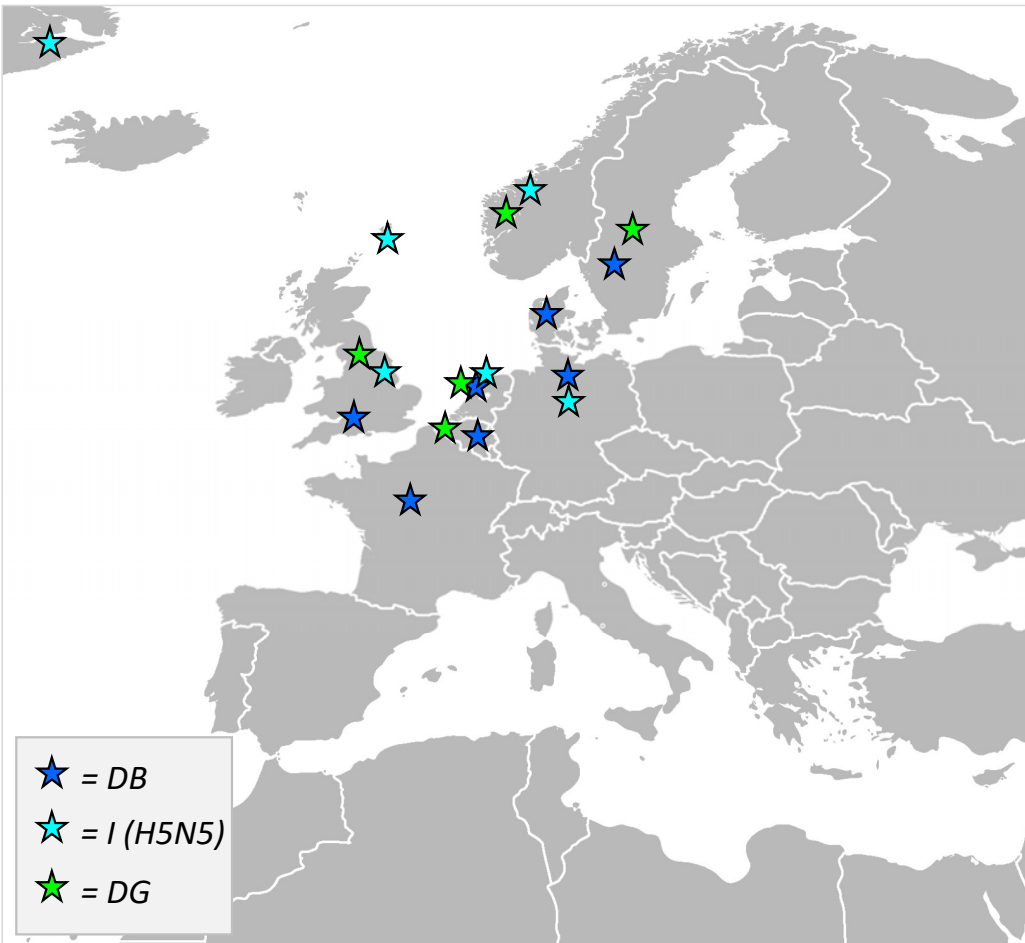
● The genotype distribution in birds in Europe, 2023-2024

- High genetic diversity among the viruses circulating in Northern and Central Europe



- ★ = AB
- ★ = DB
- ★ = I (H5N5)
- ★ = BB
- ★ = DG
- ★ = DI
- ★ = DA

● The genotype distribution in birds in Europe, 2023-2024

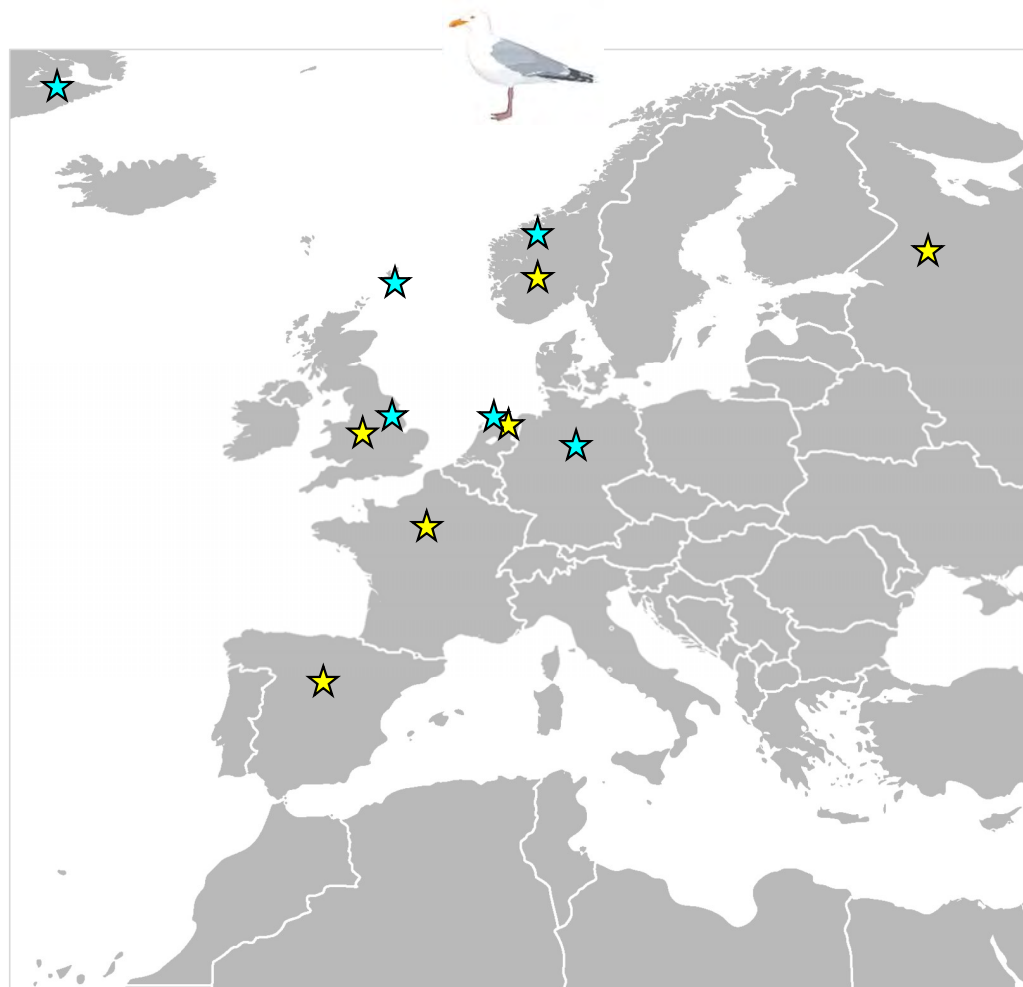


● The genotype distribution in birds in Europe, 2023-2024

- Infections in *Laridae* are mainly associated to two genotypes:

EA-2022-BB (H5N1) ★

EA-2021-I (H5N5) ★



★ = I (H5N5)

★ = BB

● The circulation of EA-2022-BB genotype in birds in Europe, 2023-2024

EA-2022-BB (H5N1)

- Genotype EA-2022-BB, which circulated extensively among Laridae in Europe from February to September 2023, has only been detected at low level in the current epidemiological year. Since December 2023, this genotype has only been reported in France and Spain.

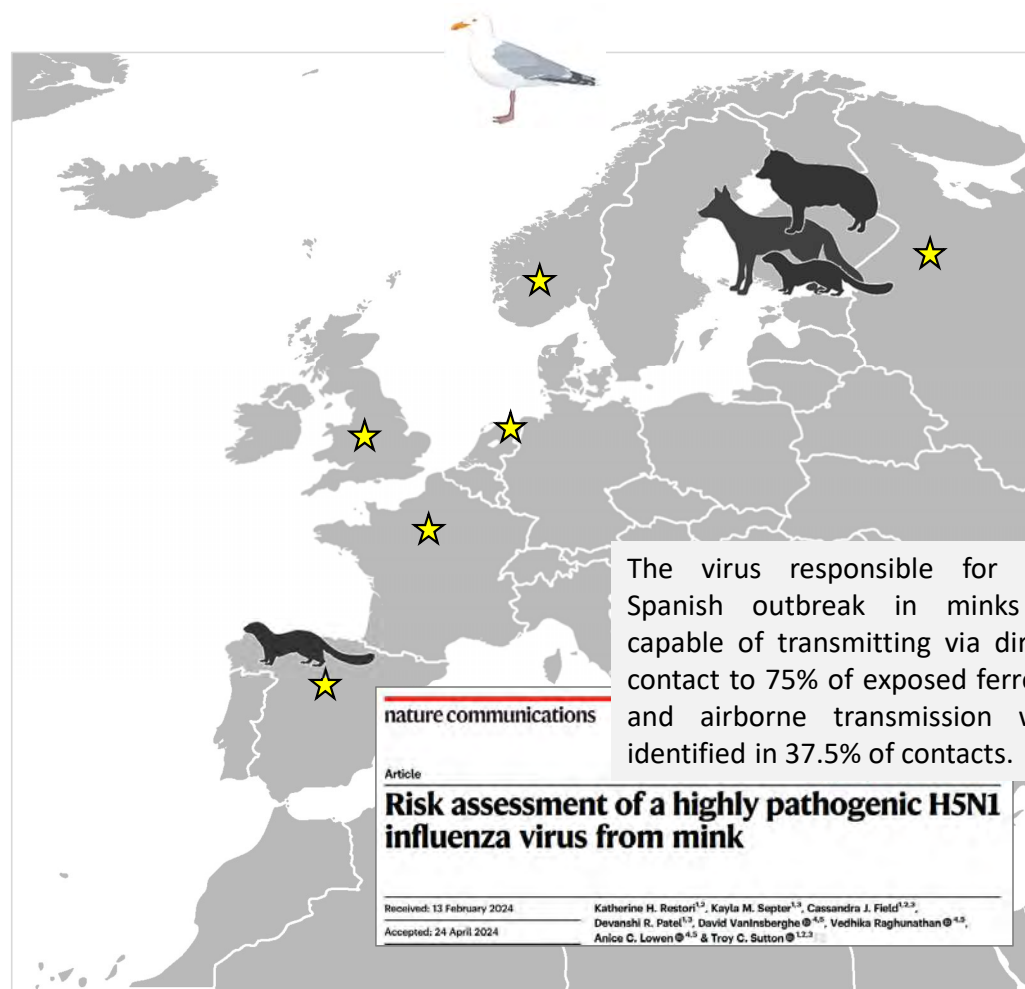


★ = BB

● The circulation of EA-2022-BB genotype in birds in Europe, 2023-2024

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- Genotype EA-2022-BB was responsible for all the outbreaks reported in fur farms in Europe in 2022–2023 (Spain and Finland)



● The circulation of EA-2022-BB genotype in birds in Europe, 2023-2024

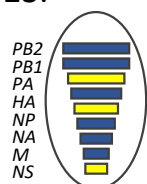
EA-2022-BB (H5N1)

- Genotype EA-2022-BB, which circulated extensively among Laridae in Europe from February to September 2023, has only been detected at low level in the current epidemiological year. Since December 2023, this genotype has only been reported in France and Spain.
- Genotype EA-2022-BB was responsible of all the outbreaks reported in fur farms in Europe in 2022–2023 (Spain and Finland)
- A novel genotype (**EA-2023-DT**) originating from a reassortment event of the PB1 gene between the EA-2022-BB and a gull-adapted H13 subtype has been circulating among *Laridae* and *Sulidae* in Spain since November 2023.



★ = BB

EA-2023-DT



EA-2022-BB



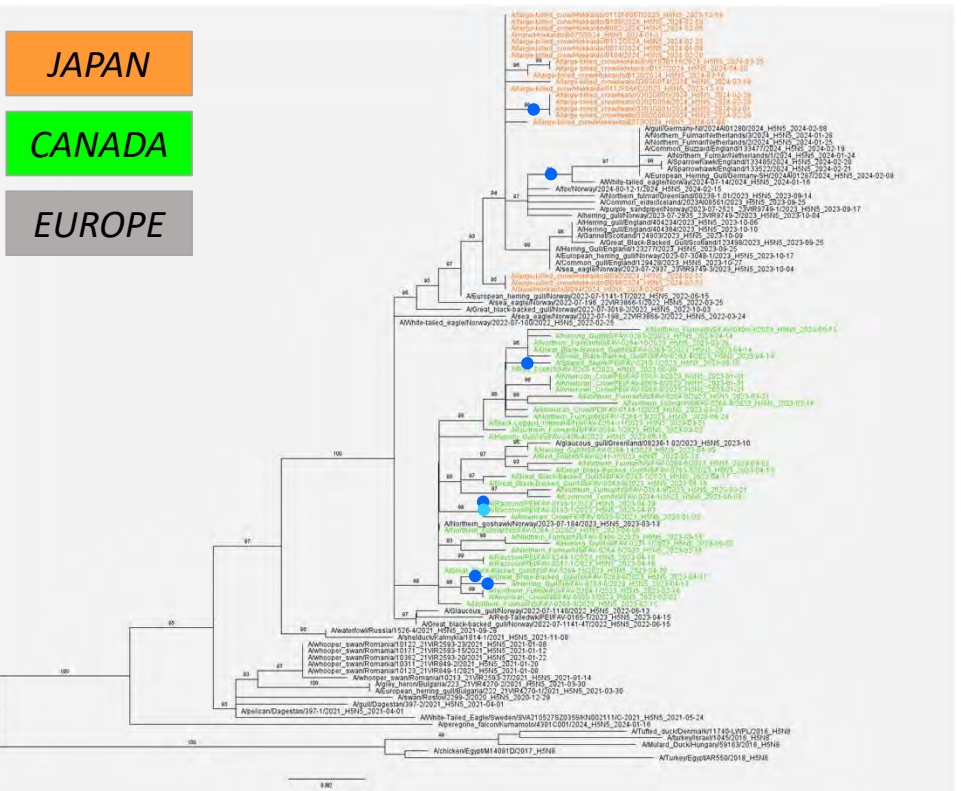
EA-2023-DT

■ European H5N1
■ H13

Evolution and spread of genotype EA-2021-I A(H5N5)

HA phylogeny

- JAPAN
- CANADA
- EUROPE



- = I (H5N5)
- ☆ = I (H5N5) – NA stalk deletion
- = PB2-E627K
- = PB2-T271A
- (light yellow) = 2020-21
- (yellow) = 2021-22
- (orange) = 2022-23
- (red) = 2023-24

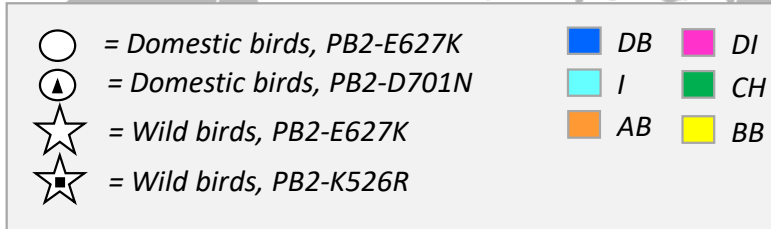
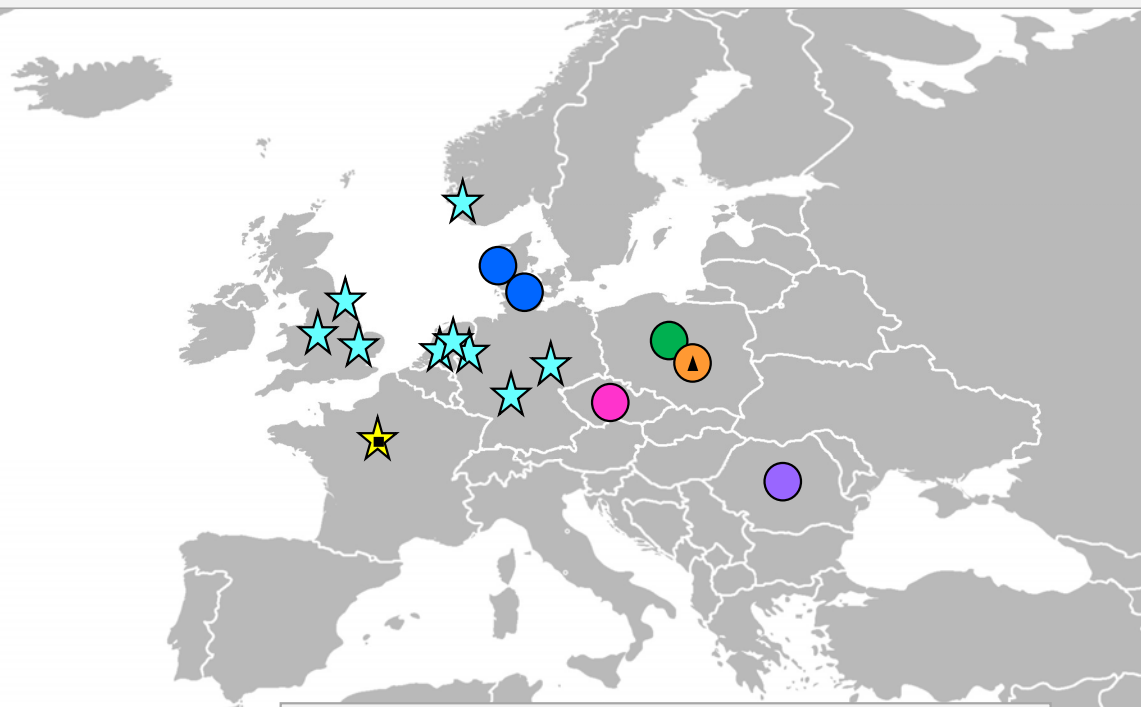
Mutations of interest, October 2023-May 2024

➤ 16 HPAI H5 viruses collected from birds contain mutations in the PB2 protein associated with **adaptation to mammals** (E627K, D701R or K526R):

- Nine A(H5N5), genotype EA-2021-I collected from wild birds in four countries (E627K)
- One A(H5N1), genotype EA-2022-BB collected from a wild bird in France (K526R)
- Six A(H5N1) collected from domestic birds in four countries and belonging to four distinct genotypes (E627K or D701N)

➤ To date, no key mutations associated to the switch in the virus binding preference from avian to human-type receptors have been identified in the H5 collected in Europe.

Geographic distribution in Europe of H5Nx viruses with molecular markers of mammalian adaptation PB2 E627K, K526R and D701N, 2023-2024




H10N3 from China: a strain to keep monitored

Received: 24 November 2022 | Accepted: 4 January 2023
DOI: 10.1002/jmv.28476

RESEARCH ARTICLE

JOURNAL OF
MEDICAL VIROLOGY WILEY

Genetic analysis and biological characterization of H10N3 influenza A viruses isolated in China from 2014 to 2021

Yuancheng Zhang | Jianzhong Shi | Pengfei Cui | Yaping Zhang | Yuan Chen |
Yujie Hou | Liling Liu | Yongping Jiang | Yuntao Guan | Hualan Chen |
Huihui Kong  | Guohua Deng

Journal Pre-proof

Continued Evolution of H10N3 Influenza Virus with Adaptive Mutations Poses an Increased Threat to Mammals

Shiping Ding, Jiangtao Zhou, Junlong Xiong, Xiaowen Du, Wenzhuo Yang, Jinyu Huang, Yi Liu, Lihong Huang, Ming Liao, Jiahao Zhang, Wenbao Qi

PII: S1995-820X(24)00084-1
DOI: <https://doi.org/10.1016/j.virs.2024.06.005>



Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

First human case of avian influenza A (H10N3) in Southwest China

Guiming Liu

Home > Science China Life Sciences > Article

Emergence of a novel reassortant avian influenza virus (H10N3) in Eastern China with high pathogenicity and respiratory droplet transmissibility to mammals

Research Paper | Published: 17 September 2021
Volume 65, pages 1024–1035, (2022) [Cite this article](#)

[Kaituo Liu](#), [Pingyun Ding](#), [Yuru Pei](#), [Ruyi Gao](#), [Wenwen Han](#), [Huafen Zheng](#), [Zhuxing Ji](#), [Miao Cai](#), [Jinyuan Gu](#), [Xiuli Li](#), [Min Gu](#), [Jiao Hu](#), [Xiaowen Liu](#), [Shunlin Hu](#), [Pinghu Zhang](#), [Xiaobo Wang](#), [Xiaoquan Wang](#)  & [Xiufan Liu](#) 

Novel H10N3 avian influenza viruses: a potential threat to public health

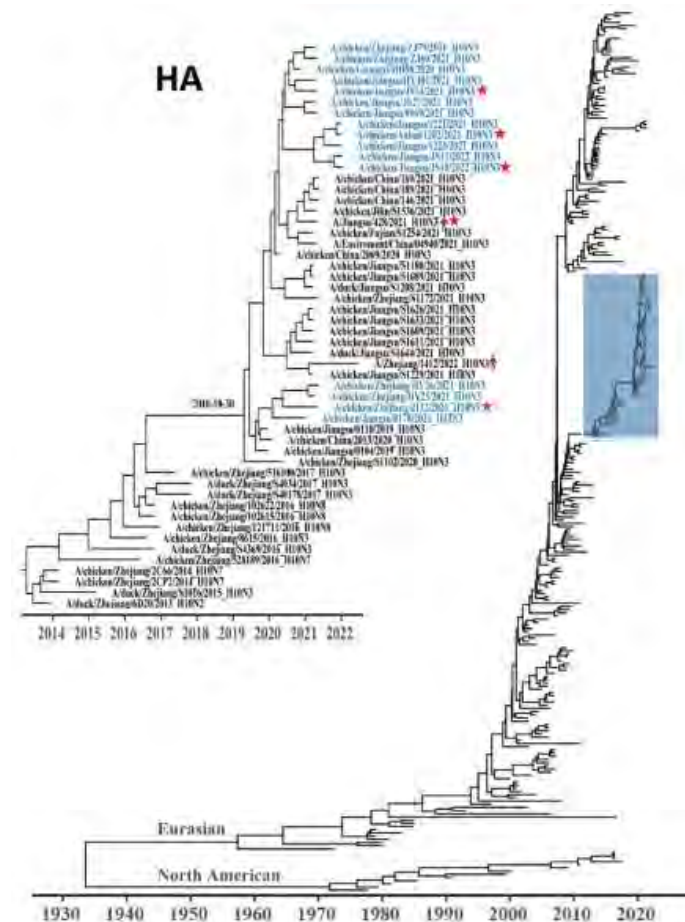
Lancet Microbe 2024; 5: e417

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[https://doi.org/10.1016/S2666-5247\(23\)00409-3](https://doi.org/10.1016/S2666-5247(23)00409-3)

H10N3 from China: a strain to keep monitored

- The HA and NA genes of all the A(H10N3) viruses collected in China since 2019 formed a monophyletic group with the Eurasian lineage. In contrast, the internal genes originated from multiple reassortment events with A(H9N2) viruses.



Liu et al., 2024 [https://doi.org/10.1016/S2666-5247\(23\)00409-3](https://doi.org/10.1016/S2666-5247(23)00409-3)

H10N3 from China: a strain to keep monitored

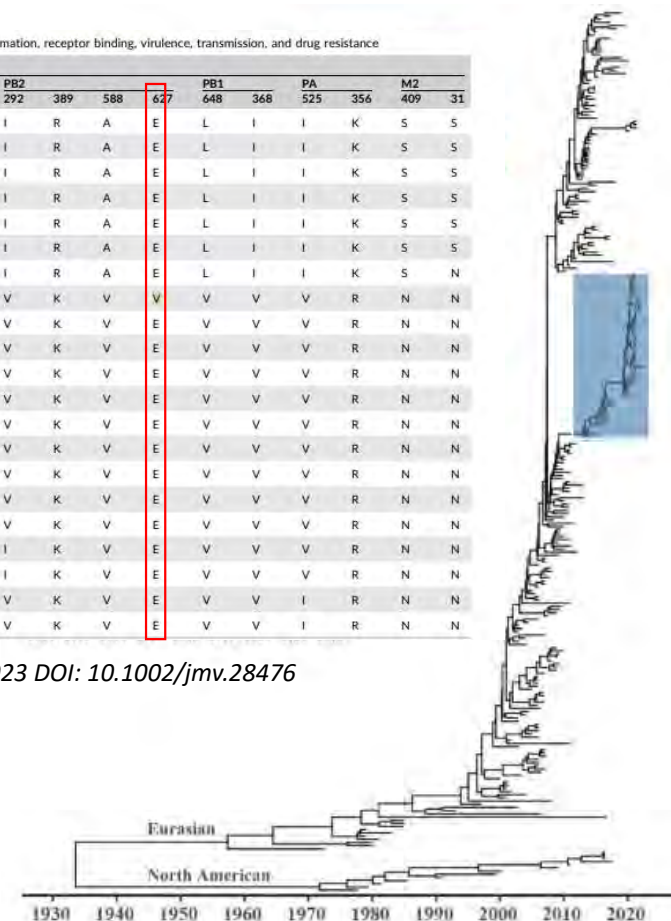
- The HA and NA genes of all the A(H10N3) viruses collected in China since 2019 formed a monophyletic group with the Eurasian lineage. In contrast, the internal genes originated from multiple reassortment events with A(H9N2) viruses.
- Most of these viruses contain several amino acid **mutations associated with mammalian adaptation** in the polymerases proteins and surface glycoproteins, including S221P, Q222R and **G228S** (H3 numbering) in the receptor binding site of the HA, which could enhance the binding capacity for both avian and human receptors.

Virus	PB2															
	L89V ¹	D147T ²	220S ³	G199P ⁴	T198C ⁵	K186T ⁶	K186R ⁷	S170P ⁸	E199V ⁹	K208P ¹⁰	K209V ¹¹	Q219E ¹²	S218E ¹³	D276V ¹⁴	A176T ¹⁵	D176G ¹⁶
A/Chicken/Shanghai/027/2021		T				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/HY24/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/Z279/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/HY461/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Shanxi/S156/2021		I				R	K			K		Q	V	E	L	D
A/Eurasian/China/04040/2021		I				R	K			K		Q	V	E	L	D
A/Shanghai/120/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/China/180/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/China/189/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/China/191/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/0108/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/0574/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/Z160/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/S1172/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/S1220/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Zhejiang/HY29/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/India/1202/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Guangxi/1221/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/1222/2021		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/05103022		I				R	K			K		Q	V	E	L	D
A/Chicken/Tangshan/S111/2021		I				R	K			K		Q	V	E	L	D
A/Shanghai/110/2021		V				R	K			K		Q	V	E	L	D

TABLE 2 Residues involved in glycosylation site formation, receptor binding, virulence, transmission, and drug resistance

Virus	Amino acid at position												
	HA ¹ 94 ^a	222	228	PB2 292	389	588	627	PB1 648	368	PA 525	356	M2 409	31
DK/HuN/512411/2014	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/51016/2015	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/54369/2016	T	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/54034/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/540178/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/HuN/541034/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/HuN/510835/2018	I	Q	G	I	R	A	E	L	I	I	K	S	N
CK/ZJ/51102/2020	I	Q	S	V	K	V	V	V	V	V	R	N	N
CK/ZJ/51172/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/FJ/51254/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51089/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51180/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
DK/JS/51208/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51229/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51609/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51611/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51626/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
T	R	S	I	K	V	E	V	V	V	R	N	N	N
T	R	S	I	K	V	E	V	V	V	R	N	N	N
I	R	S	V	K	V	E	V	V	I	R	N	N	N
I	R	S	V	K	V	E	V	V	I	R	N	N	N

Zhang et al., 2023 DOI: 10.1002/jmv.28476

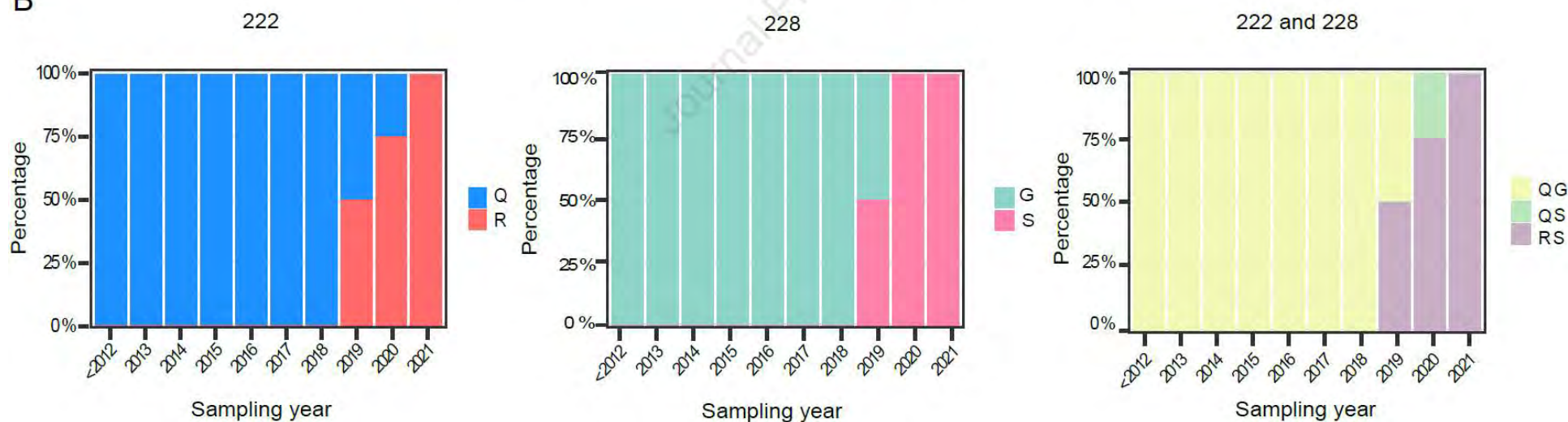


Liu et al., 2024 [https://doi.org/10.1016/S2666-5247\(23\)00409-3](https://doi.org/10.1016/S2666-5247(23)00409-3)

H10N3 from China: a strain to keep monitored



B



Ding, S., Zhou, J., Xiong, J., Du, X., Yang, W., Huang, J., Liu, Y., Huang, L., Liao, M., Zhang, J., Qi, W., Continued Evolution of H10N3 Influenza Virus with Adaptive Mutations Poses an Increased Threat to Mammals, *Virologica Sinica*, <https://doi.org/10.1016/j.virs.2024.06.005>.

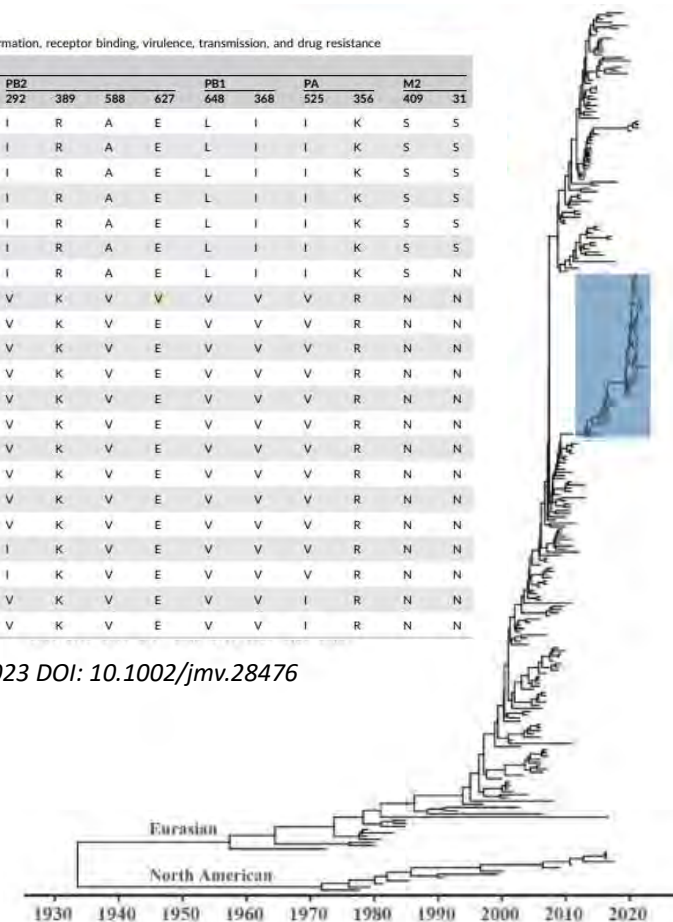
H10N3 from China: a strain to keep monitored

- These studies demonstrated that some of the poultry A(H10N3) viruses:
 - showed the **capability to bind with both SA α -2,3-Gal and SA α -2,6-Gal receptors** (Liu et al., 2024; Liu et al., 2022)
 - are **highly virulent or lethal to mice** (Liu et al., 2024; Zhang et al., 2022; Liu et al., 2022)
 - **could be transmitted between guinea pigs via direct contact or respiratory droplets** (Liu et al., 2024; Zhang et al., 2022; Liu et al., 2022)
- The A(H10N3) virus responsible for the recent **human case** is highly related to the viruses circulating in poultry. However, compared to these strains the virus from the human case contains the additional mutations **HA-Q226L** (H3 numbering) and **PB2-D701N** associated with increased virus adaptation to mammals (Liu et al., 2024).

TABLE 2 Residues involved in glycosylation site formation, receptor binding, virulence, transmission, and drug resistance

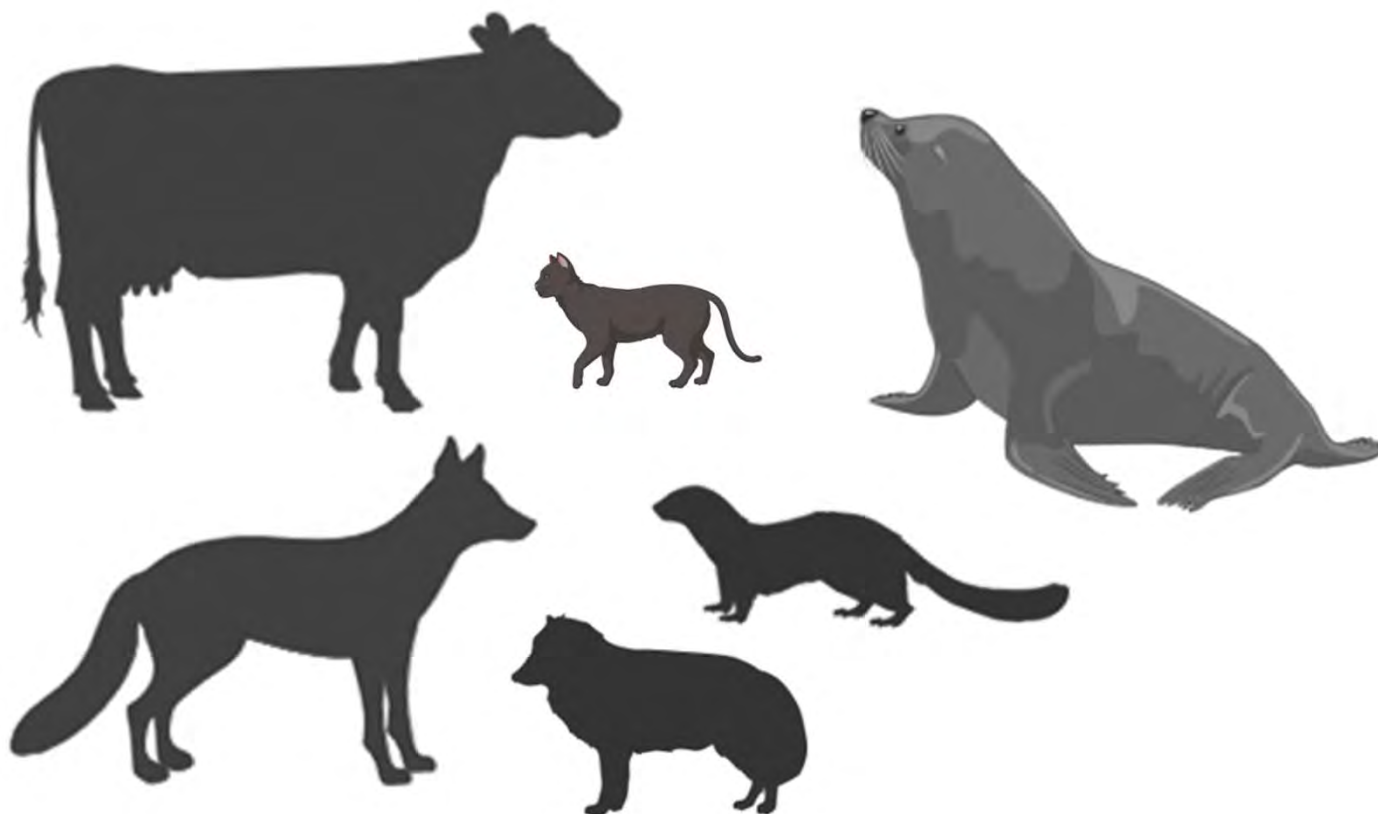
Virus	Amino acid at position												
	HA* 94*	222	228	PB2 292	389	588	627	PB1 648	368	PA 525	356	M2 409	31
DK/HuN/512411/2014	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/51016/2015	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/54369/2016	T	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/54034/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/ZJ/540178/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/HuN/541034/2017	I	Q	G	I	R	A	E	L	I	I	K	S	S
DK/HuN/510835/2018	I	Q	G	I	R	A	E	L	I	I	K	S	N
CK/ZJ/51102/2020	I	Q	S	V	K	V	V	V	V	V	R	N	N
CK/ZJ/51172/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/FJ/51254/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51089/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51180/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
DK/JS/51208/2021	I	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51229/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51609/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51611/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51626/2021	T	R	S	V	K	V	E	V	V	V	R	N	N
CK/JS/51633/2021	T	R	S	I	K	V	E	V	V	V	R	N	N
DK/JS/51644/2021	T	R	S	I	K	V	E	V	V	V	R	N	N
CK/JL/51536/2021	I	R	S	V	K	V	E	V	V	I	R	N	N
JS/428/2021	I	R	S	V	K	V	E	V	V	I	R	N	N

Zhang et al., 2023 DOI: 10.1002/jmv.28476

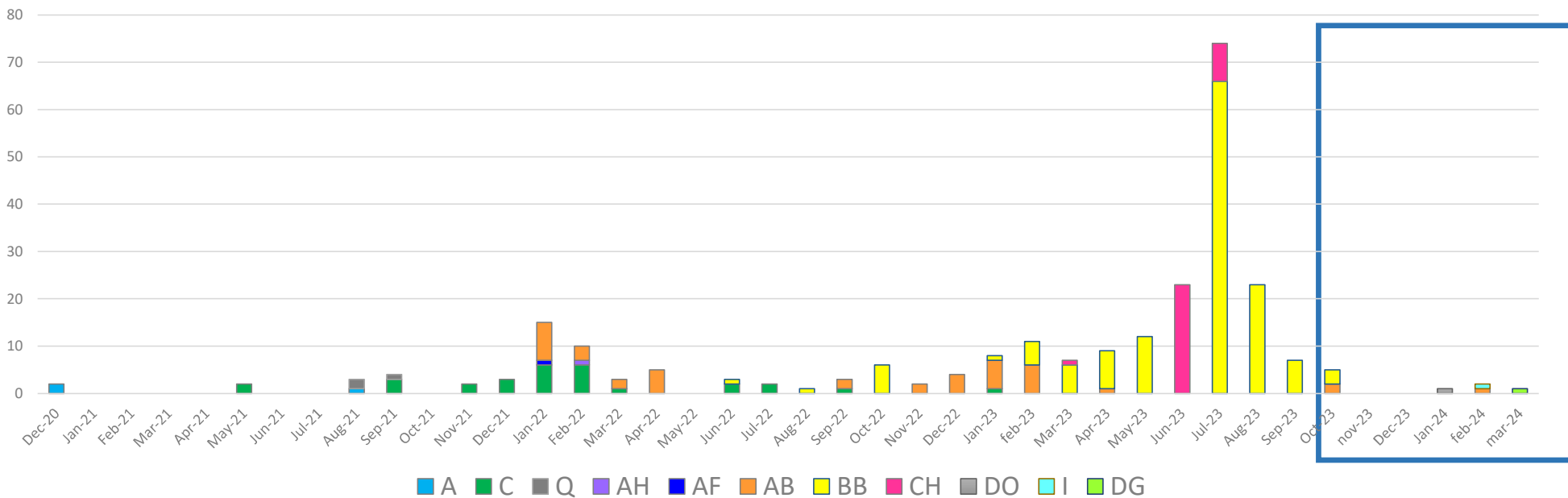


Liu et al., 2024 [https://doi.org/10.1016/S2666-5247\(23\)00409-3](https://doi.org/10.1016/S2666-5247(23)00409-3)


● HPAI H5 outbreaks in mammals




Which genotypes infected mammalian species in Europe?




Finland





PB2-E627K



PB2-E627K




Germany


PB2-E627K

Sweden

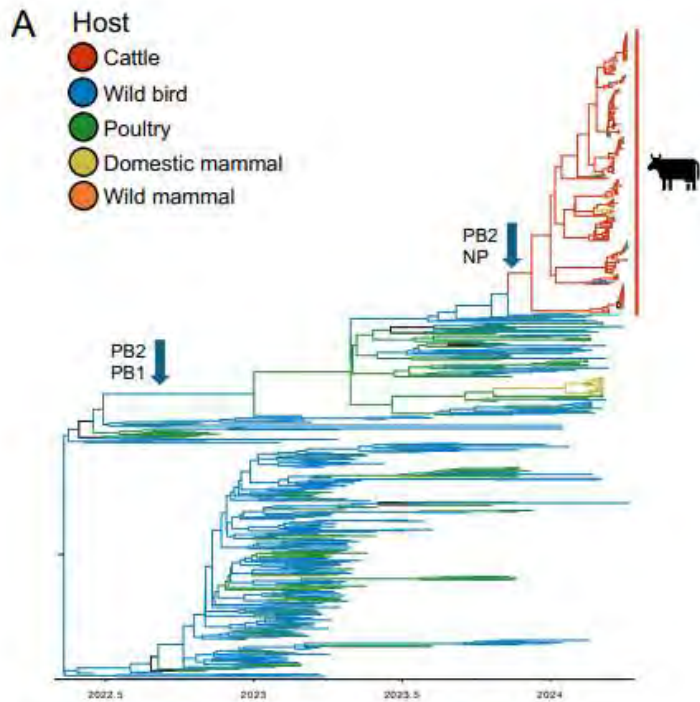


PB2-E627K

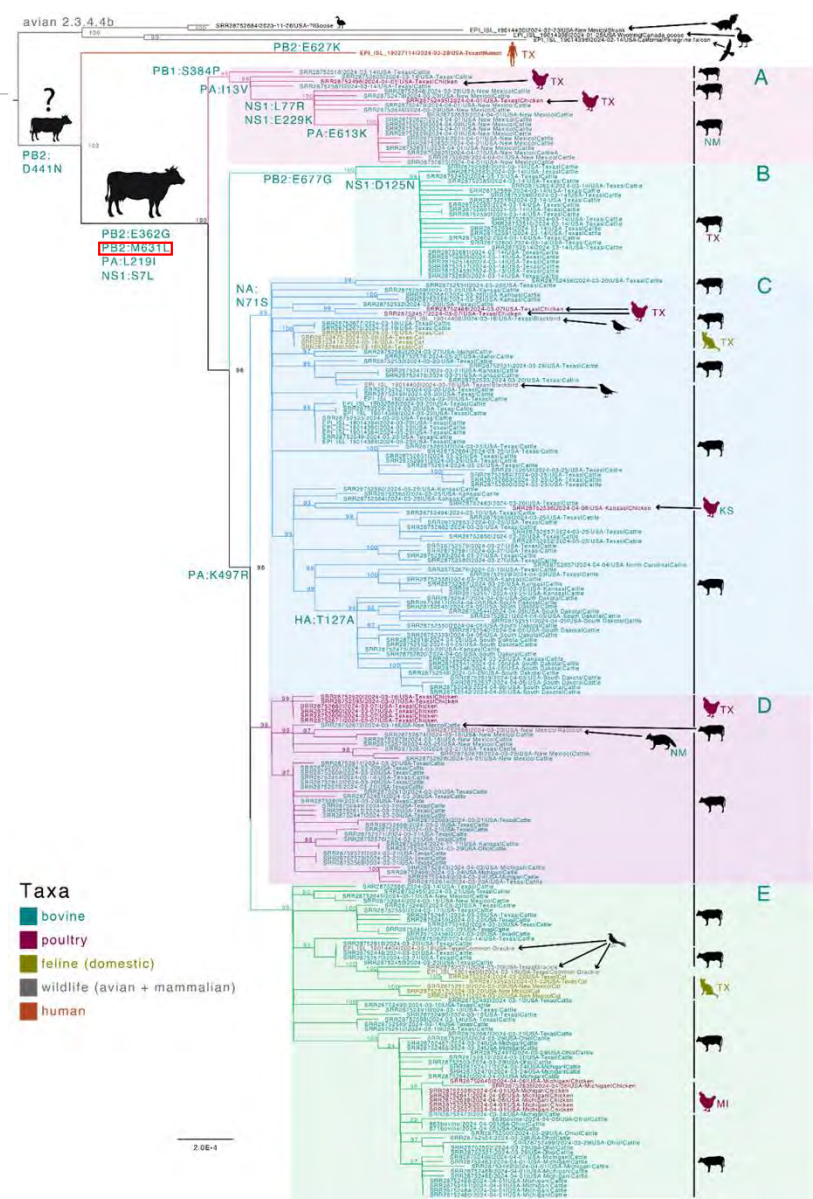
Norway



HPAI H5 outbreaks in cows and peridomestic animals in USA



- The A(H5N1) viruses from cattle belong to clade 2.3.4.4b genotype B3.13, a genotype detected to date only in North America. This genotype is relatively rare in the USA but has been detected in wild birds and mammals.
- B3.13 contains PA, HA, NA and M gene segments from Eurasian A(H5N1) and PB2, PB1, NP and NS gene segments from LPAI wild bird viruses of the American lineage.
- Genotype B3.13 differs from the virus seen in a outbreak (March 2024) where H5N1 2.3.4.4b influenza A virus spilled over from poultry to goats. The outbreak in goats was unrelated to the current cattle outbreak (<https://virological.org/t/preliminary-report-on-genomic-epidemiology-of-the-2024-h5n1-influenza-a-virus-outbreak-in-u-s-cattle-part-1-of-2/970>).
- Results from phylodynamics analyses indicate a single spillover event into cattle, likely from wild birds, which might have occurred approximately four months prior to the first confirmation of HPAI virus infection in cattle by USDA in March 2024.
- The tree topologies clearly indicate sustained virus transmission from cattle-to-cattle, from cattle into poultry and domestic animal species (i.e. domestic cats) as well as back to wild birds (Nguyen et al., 2024).
- In May 2024, the same virus circulating in cows was identified as the causative agent of infection in alpacas kept in a A(H5N1) infected poultry farm, suggesting a mammal-to-bird-to-mammal transmission.



- Multiple mutations associated with increased virulence or mammalian adaptation have been identified across the genome. In particular, the mammalian adaptive marker PB2-M631L (Zhang, 2017) has been detected in 99% of dairy cow sequences, but only sporadically in birds. Moreover, the NP gene that distinguishes B3.13 from all the other North American genotypes may have resulted in a phenotype change that has likely favoured its spread in this new species

<https://virological.org/t/preliminary-report-on-genomic-epidemiology-of-the-2024-h5n1-influenza-a-virus-outbreak-in-u-s-cattle-part-1-of-2/970>

Take home messages

- Surveillance and real-time genetic characterization are highly recommended to promptly identify viruses with mutations that can increase their zoonotic potential. Genetic data are also instrumental to track the virus spread and identify novel incursions of viruses which may represent a threat for human or animal health.
- Reinforcement of the genetic characterization of viruses collected from birds in areas where a high number of infections in mammalian species has been identified is recommended to promptly detect possible mammal-to-avian transmission of viruses containing markers of virus adaptation to mammalian species, which may have a higher zoonotic potential.

Guidance for genomic monitoring of AIV can be found here: <https://www.izsvenezie.com/documents/reference-laboratories/avian-influenza/useful-resources/guidance-representative-genomic-avian-influenza-virus.pdf>

FluMut

A tool to search for molecular markers with potential impact on the biological characteristics of Influenza A viruses of the A(H5N1) subtype

Flumut is available here:

Command line version: <https://github.com/izsvenezie-virology/FluMut>

Graphical user interface: <https://github.com/izsvenezie-virology/FluMutGUI/releases/tag/v.3.0.1>

The complete documentation and tutorial: <https://izsvenezie-virology.github.io/FluMut/>

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Isabella Monne



Lillo Terregino



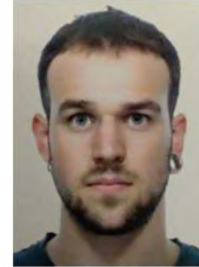
Bianca Zecchin



Ambra Pastori



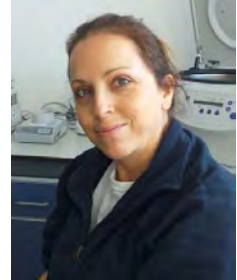
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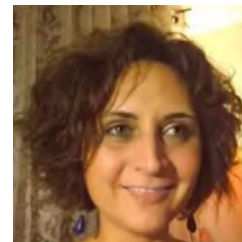
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*Thank you
for your attention*