23 January 2023

Standing Committee on Plants, Animals, Food and Feed Section Animal Health and Welfare

AHW.A.09.EFSA.(IDC)





Francesca Baldinelli Scientific Officer Animal Health Team



MONITORING HPAI OUTBREAKS

Quarterly reports undating on the Al situation in and

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SCIENTIFIC REPORT



Joint sc

APPROVED: 8 March 2023

doi: 10.2903/j.efsa.2023.7917

Avian influenza overview December 2022 – March 2023

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European Food Safety Authority,
European Centre for Disease Prevention and Control,
European Union Reference Laboratory for Avian Influenza,
Cornelia Adlhoch, Alice Fusaro, José L Gonzales, Thijs Kuiken, Stefano
Marangon, Grazina Mirinaviciute, Éric Niqueux, Karl Stahl, Christoph
Staubach, Calogero Terregino, Alessandro Broglia and Francesca Baldinelli

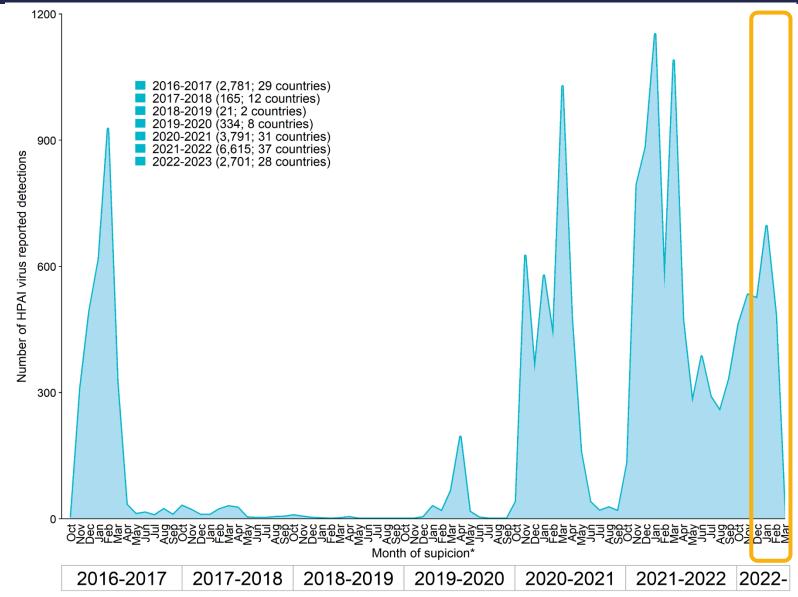
due



HPAI IN EUROPE IN BIRDS

Distribution of HPAI virus detections reported in EU/EEA and the UK by epidemic seasons and month of suspicion

1 Oct 2016 – 2 Dec 2022 (14,629)



*When the date of suspicion is not available then the date of confirmation is used to assign the month of suspicion.

Source: EFSA/ECDC/EURL avian influenza reports https://efsa.onlinelibrary.wiley.com/doi/toc/10.1002/(ISSN)1831-

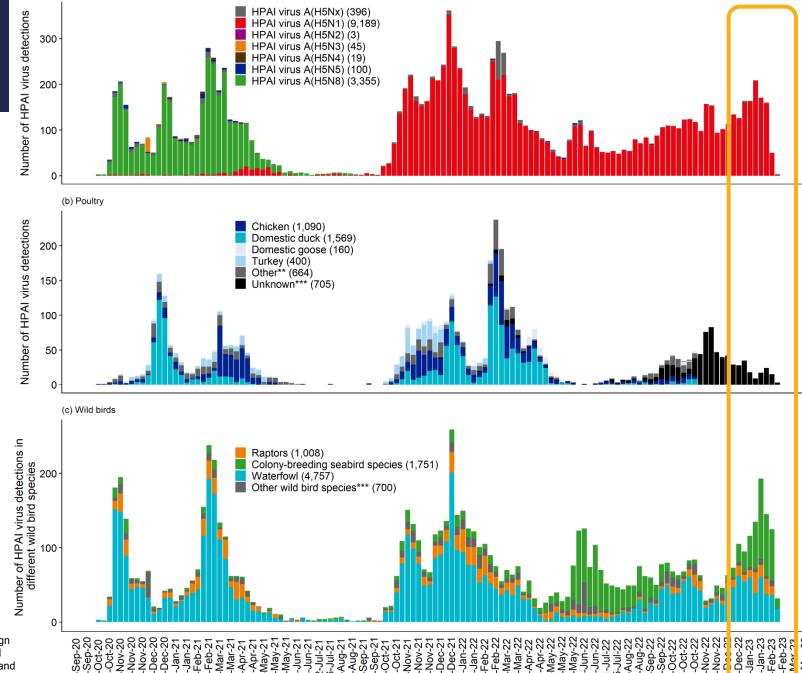
4732.avianinfluenza

HPAI IN EUROPE IN BIRDS

(a) All birds

Distribution of total number of HPAI virus detections reported in Europe by week of suspicion and

- a. virus subtype
- b. affected poultry categories
- c. affected wild bird categories
- 5 Oct 2020 1 Mar 2023

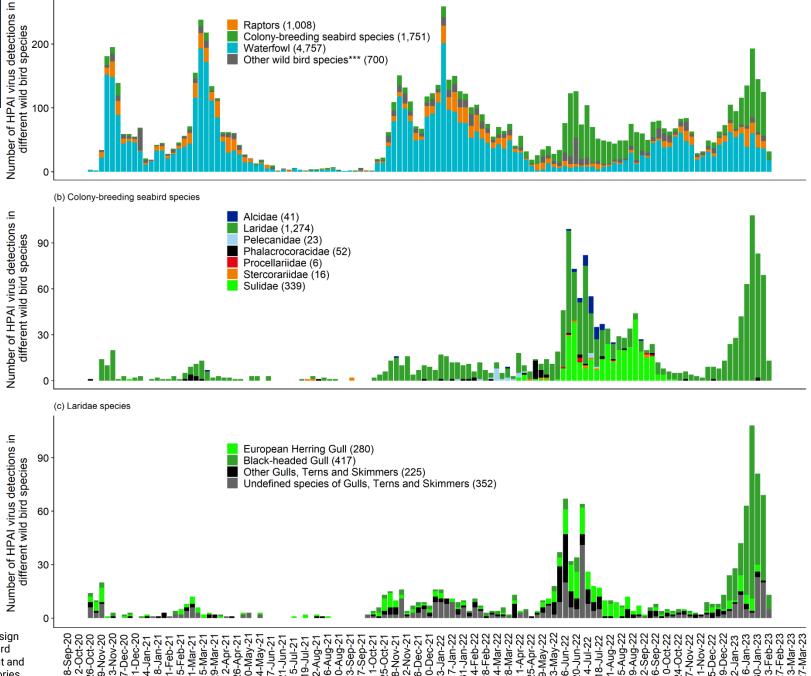


^{*} When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion. ** 'Other domestic species' category contains mixed, unknown bird species, or categories different from those displayed (i.e guinea fowl, peacock, pheasant and quail). *** 'Other wild species' category contains mixed, unknown bird species, or categories different from those displayed

HPAI IN EUROPE IN BIRDS

(a) Wild birds

Distribution of total number of HPAI virus detections reported in Europe by week of suspicion in wild birds 5 Oct 2020 - 1 Mar 2023



Raptors (1,008)

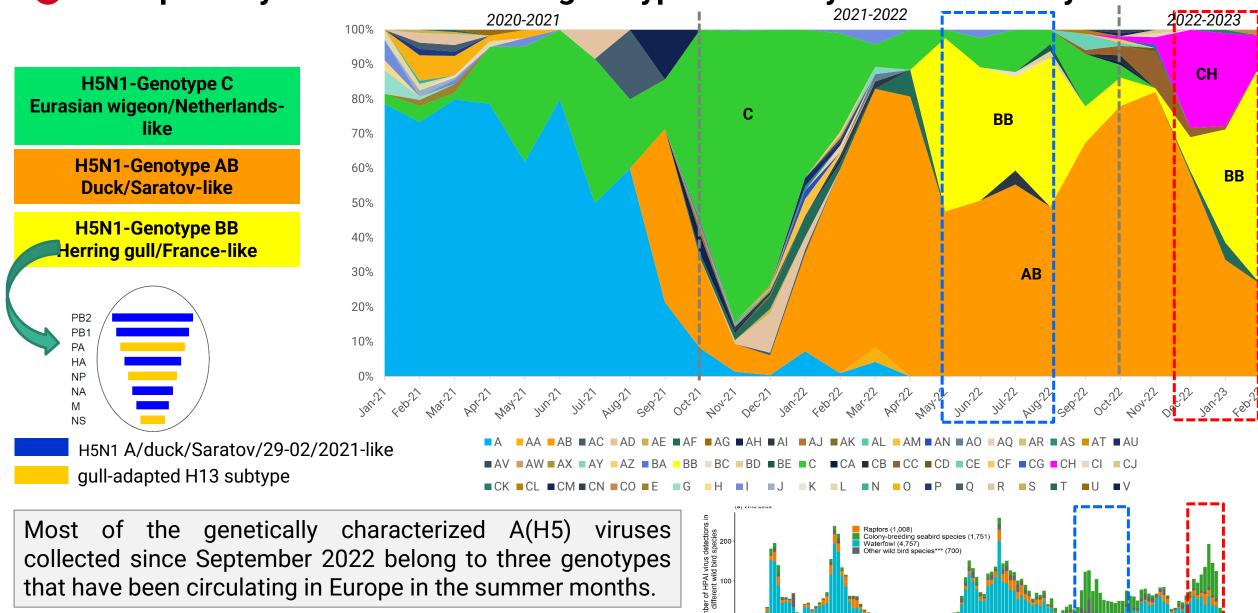
Waterfowl (4,757)

Colony-breeding seabird species (1,751)

^{*} When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion. ** 'Other domestic species' category contains mixed, unknown bird species, or categories different from those displayed (i.e quinea fowl, peacock, pheasant and quail). *** 'Other wild species' category contains mixed, unknown bird species, or categories different from those displayed



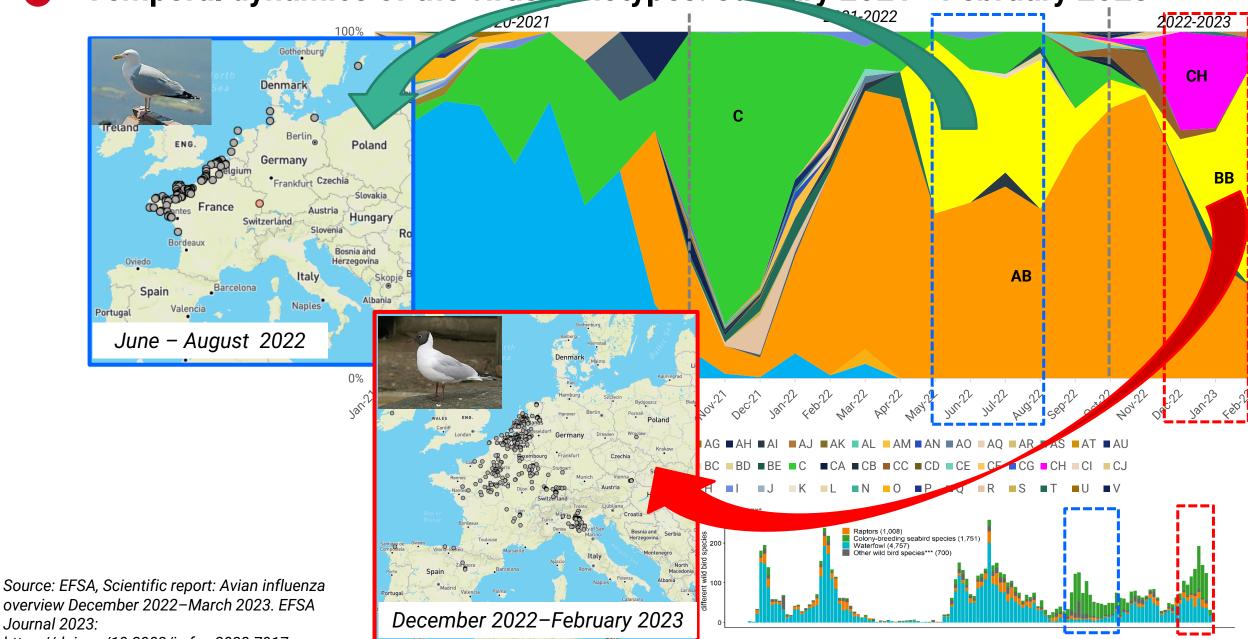
Temporal dynamics of the virus genotypes: January 2021 - February 2023



Source: EFSA, Scientific report: Avian influenza overview December 2022–March 2023. EFSA Journal 2023: https://doi.org/10.2903/j.efsa.2023.7917



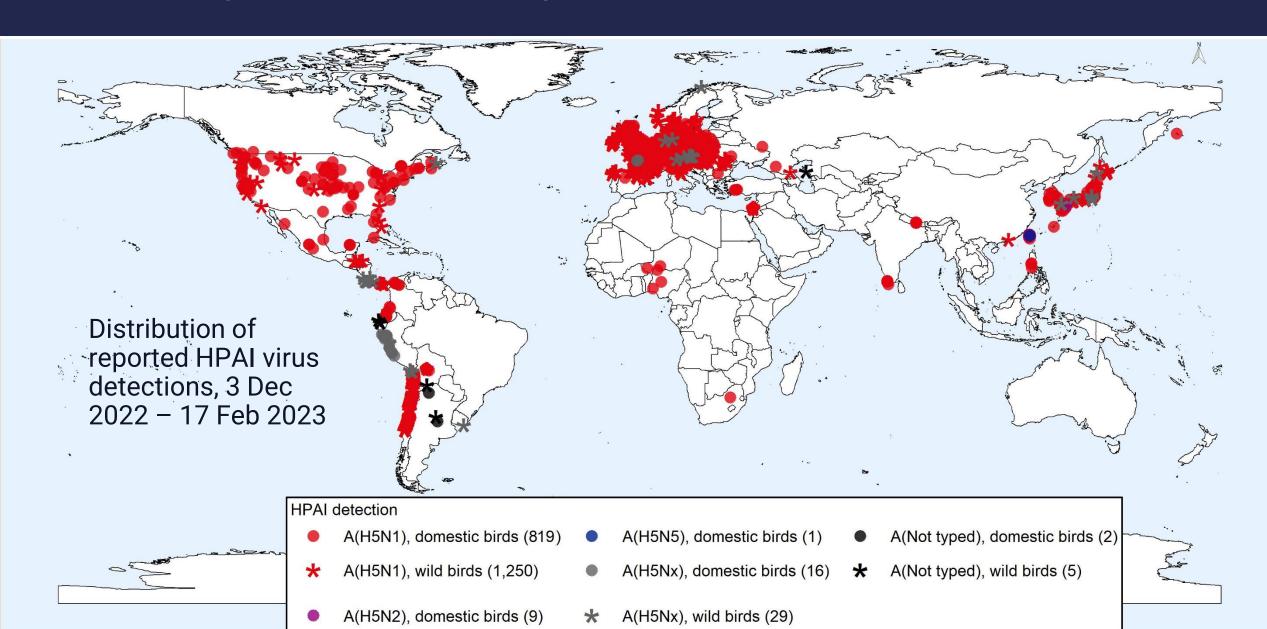
Temporal dynamics of the virus genetypes: January 2021 - February 2023



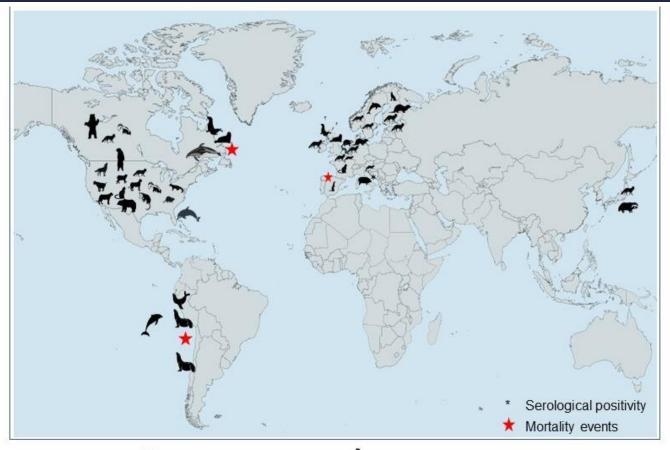
overview December 2022-March 2023. EFSA Journal 2023:

https://doi.org/10.2903/j.efsa.2023.7917

HPAI WORLDWIDE IN BIRDS



HPAI IN MAMMAL SPECIES OTHER THAN HUMANS





Cat (Felis catus)

Coyote (Canis latrans)

Domestic pigs (Sus scrofa)

Eurasian otter (Lutra lutra)

European badger (Meles meles)

European polecat (Mustela putorius)

Ferret (Mustela furo)

Fisher cat (Pekania pennanti)

Common dolphin (Delphinus delphis)

Grey seals (Halichoerus grypus)
Grizzly bear (Ursus arctos horribilis)
Harbour seals (Phoca vitulina)
Lynx (Lynx lynx)
Mountain lion (Puma concolor)
Porpoise (Phocoena phocoena)
Raccoon (Procyon lotor)
Raccoon dog (Nyctereutes procyonoides)

Red foxes (Vulpes vulpes)

South American fur seal (Arctocephalus australis)
South American sea lion (Otaria flavescens)

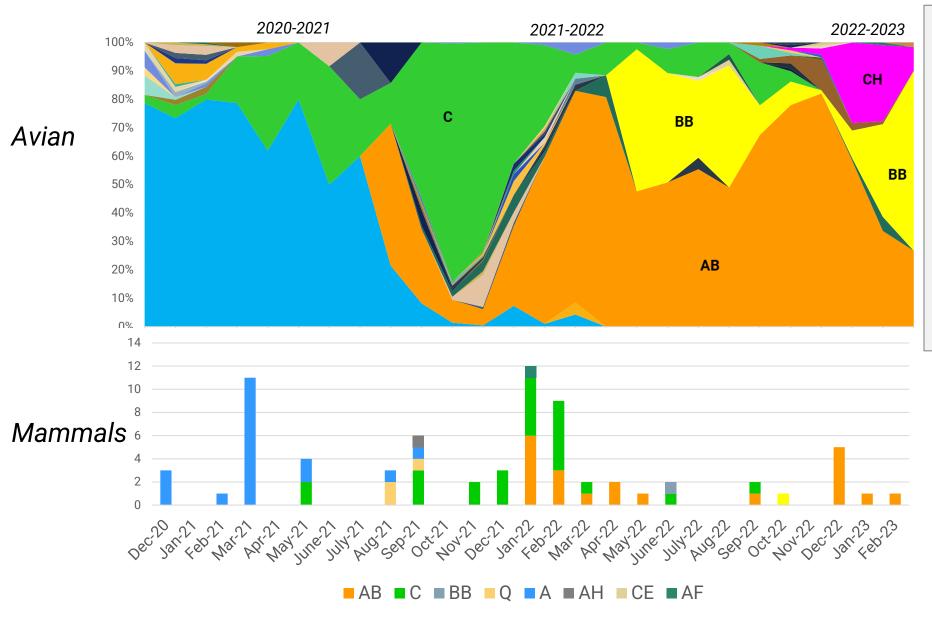
Striped skunks (Mephitis mephitis)
Virginia opossum (Didelphis virginiana)

White-sided dolphin (Lagenorhynchus acutus)



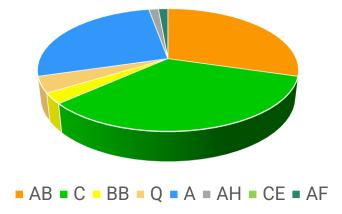


Genetic diversity of A(H5N1) in mammals



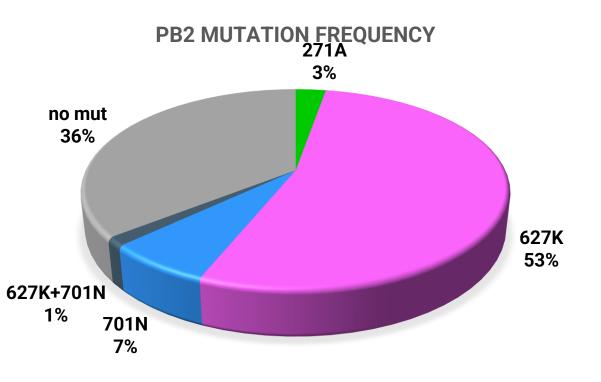
All the characterized viruses belong to 8 different A(H5N1) and A(H5N8) genotypes previously identified in birds, with most of the viruses (75%) belonging to the two most widespread genotypes in birds in Europe:

- C: H5N1 A/Eurasian Wigeon/Netherlands/1/2020like
- AB: H5N1 A/duck/Saratov/29-02/2021-like





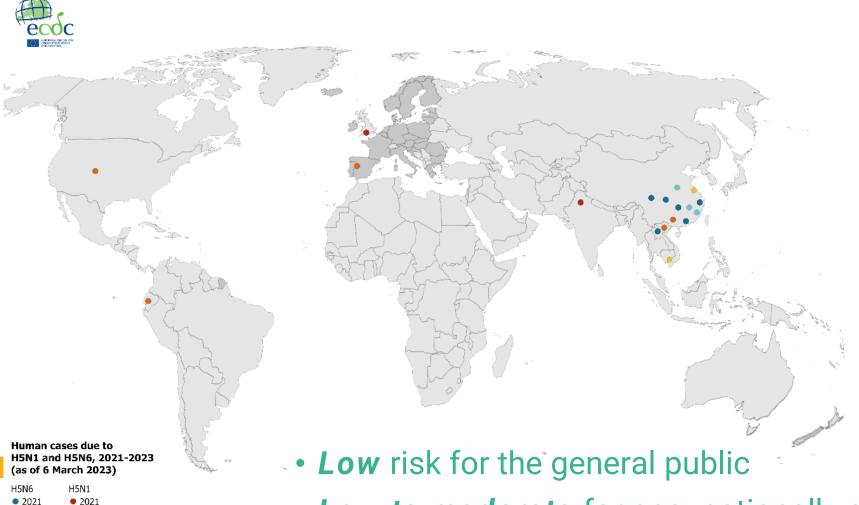
Mutations identified in A(H5N1) from mammals



>60% of the characterized viruses contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K, D701N or T271A) (Suttie et al., 2019).

These mutations have never (T271A) or rarely (E627K, D701N) been identified in the HPAI A(H5) viruses of clade 2.3.4.4b collected in birds in Europe since October 2020 (<0.5% of viral sequences from birds).

VIRUS DETECTIONS IN HUMANS



Human infections with avian influenza A(H5Nx) virus clade 2.3.4.4b related to viruses circulating in Europe, 2021–2022

• Low to moderate for occupationally exposed people



20222023

OPTIONS FOR RESPONSE

- Accurate reporting of infected wild bird species and the associated mortality and removal of wild bird carcasses from affected sites to limit virus spread (the benefits—reduction of virus load—need to be weighed up against the possible disturbance of wildlife)
- Better, more accurate and timely reporting of HPAI virus detections in mammals in a way that reliable numbers of infected animals could be used as quantitative information for risk assessment
- Extended and enhanced surveillance of both wild mammals (particularly carnivores) and farmed mammals (particularly American mink and domestic pigs) in risk areas where HPAI is present in wild birds and poultry is recommended



MAIN CONCLUSIONS AND OPTIONS FOR RESPONSE

- Improve virological and serological surveillance in scavenger mammals to prompt identify viruses with zoonotic potential and evaluate the real magnitude of the spread of HPAI viruses in these species
- In domestic mammals, to prevent exposure to possible infected wild birds by increasing biosecurity at farm
- Thoroughly investigate the dynamic of the infection in case of mass mortality events associated with HPAI virus detected in mammalian species



testing a high number of animals and assuring a prompt **generation and sharing of viral sequences** data to shed light on the virus origin, evolution and possible transmission between individuals

EXPERT INVOLVED

Member State representative for avian influenza

Working group experts

- ADLHOCH Cornelia (ECDC)
- FUSARO Alice (EURL)
- GONZALES Josè (WUR)
- KUIKEN Thijs (Erasmus MC)
- MARANGON Stefano (EURL)
- MIRINAVICIUTE Grazina (ECDC)
- NIQUEUX Eric (ANSES)
- STAHL Karl (SVA)
- STAUBACH Christoph (FLI)
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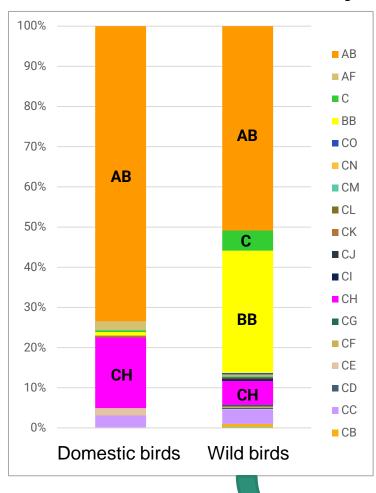


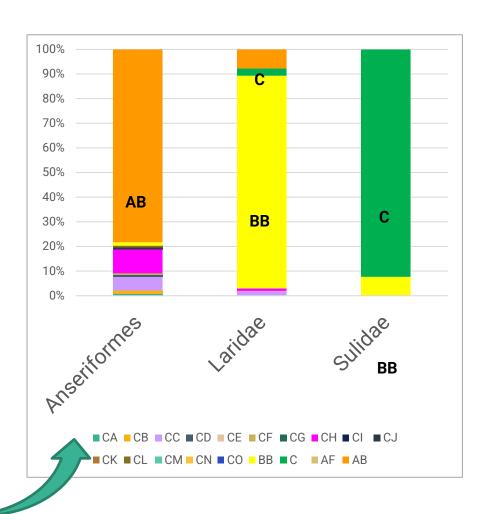


Genotype host distribution



October 2022 - February 2023

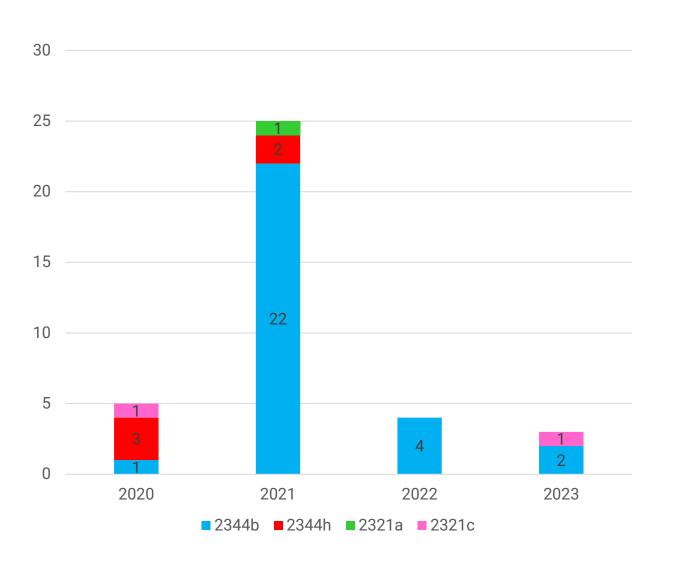






Genetic characteristics of HPAI viruses of the A(H5NX) subtype from human





Based on the data available from GISAID EpiFlu database, since 2020 human infections were caused by four different A(H5) clades of the Gs/GD-lineage:

- 2.3.2.1c (Laos, 2020 and Cambodia, 2023),
- 2.3.2.1a (India, 2021),
- 2.3.4.4h (China, 2020-2021),
- 2.3.4.4b (China, Europe, North and South America).

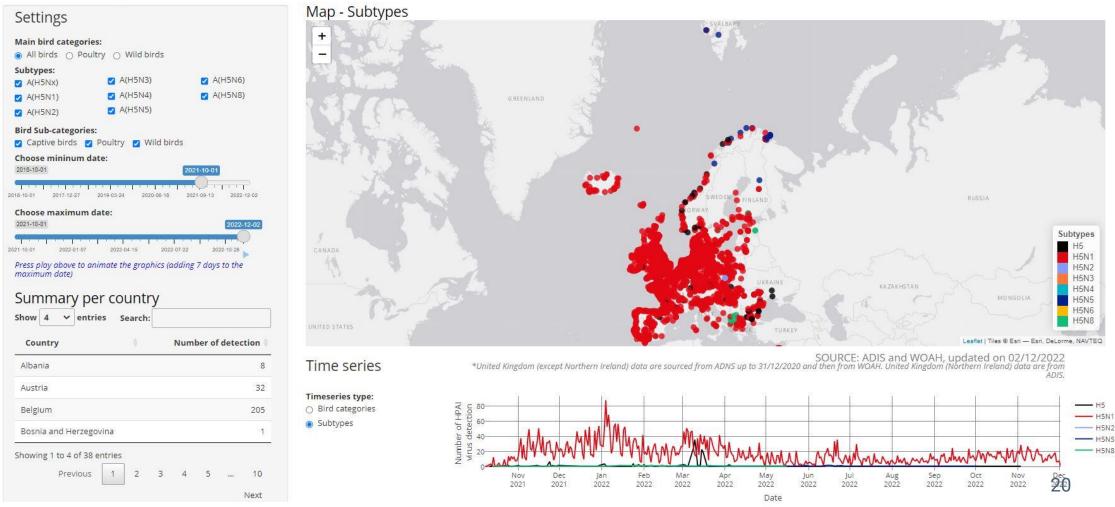
Mutation **Q226L** was identified in two A(H5N6) viruses of clade 2.3.4.4b collected in China in 2021 (Zhu W Fau - Li et al.), associate to the switch in the receptor specificity from avian-type to human-type receptor (Stevens et al., 2006; Chutinimitkul et al.; Russell et al., 2012).

Six clade 2.3.4.4b A(H5N6) viruses collected from human infections in China in 2021 possessed one of the **adaptive markers in the PB2 protein** (Q591K, E627K or D701N) associated with an increased virulence and replication in mammals (Zhu W Fau - Li et al., 2022)

Zhu et al., 2022: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9239879/

DASHBOARD ON HPAI VIRUS DETECTIONS IN EUROPE

Highly pathogenic avian influenza virus detection in Europe



Available at: http://hpai.efsa.aus.vet/