Influenza virus characteristics and update from the September 2022 Vaccine Composition Meeting

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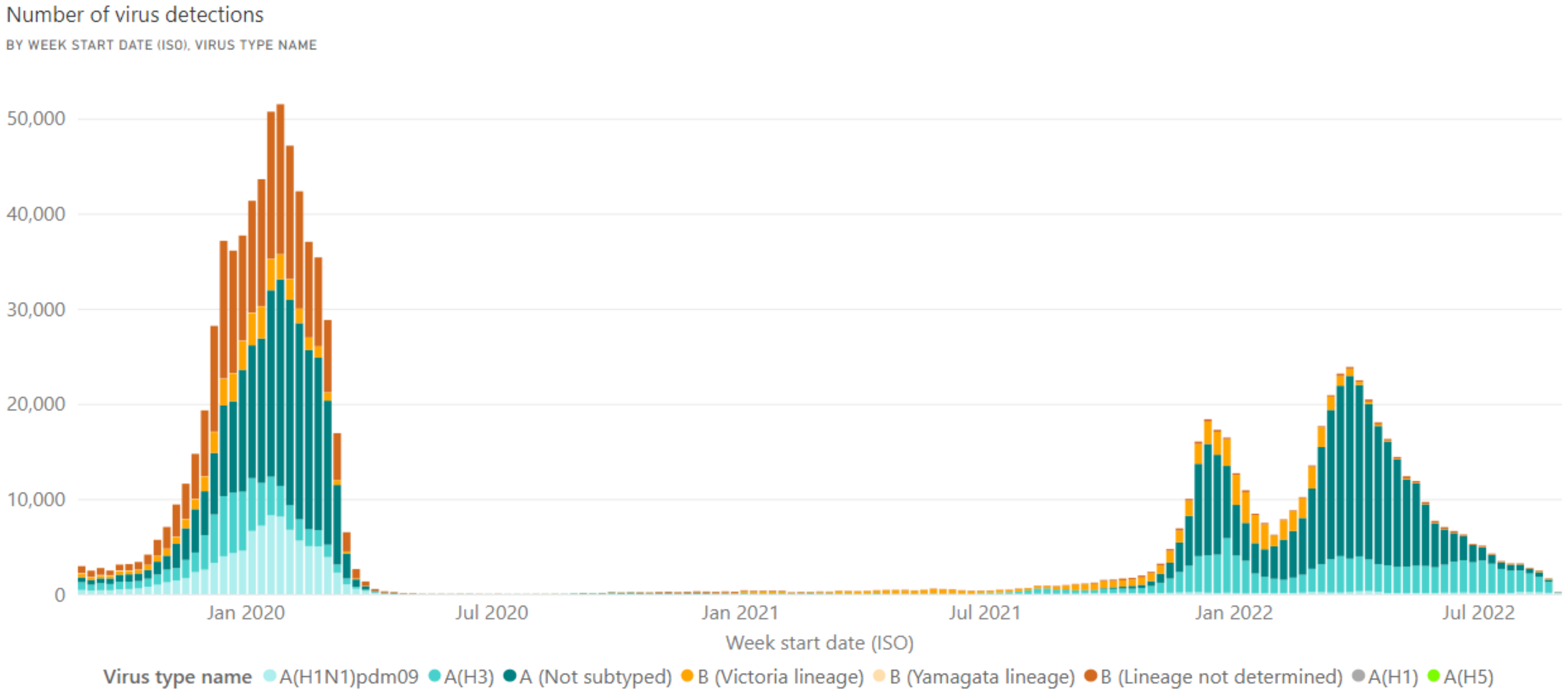
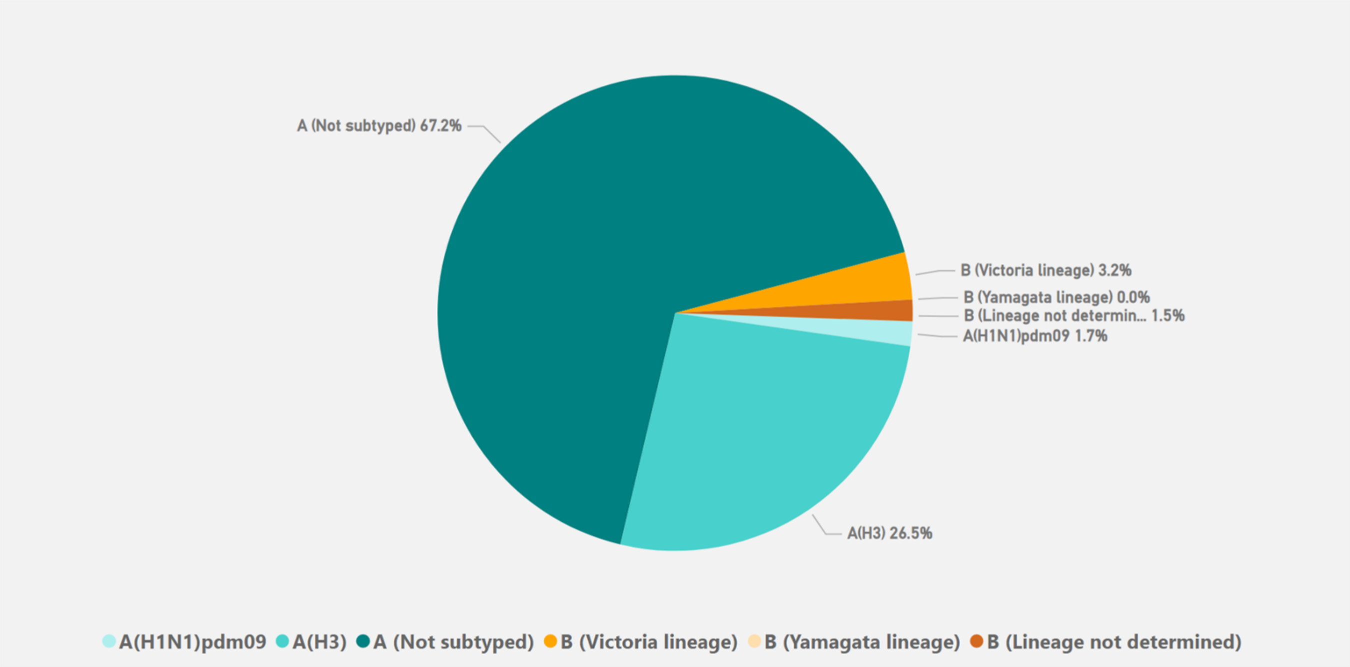
ECDC and WHO Europe Joint Annual Influenza and COVID-19 Surveillance Meeting, 5-7 October 2022

Number of specimens positive for influenza by type/subtype/lineage


Number of virus detections

BY WEEK START DATE (ISO), VIRUS TYPE NAME

Percentage of influenza A viruses by type/subtype/lineage (Feb-Aug 22)

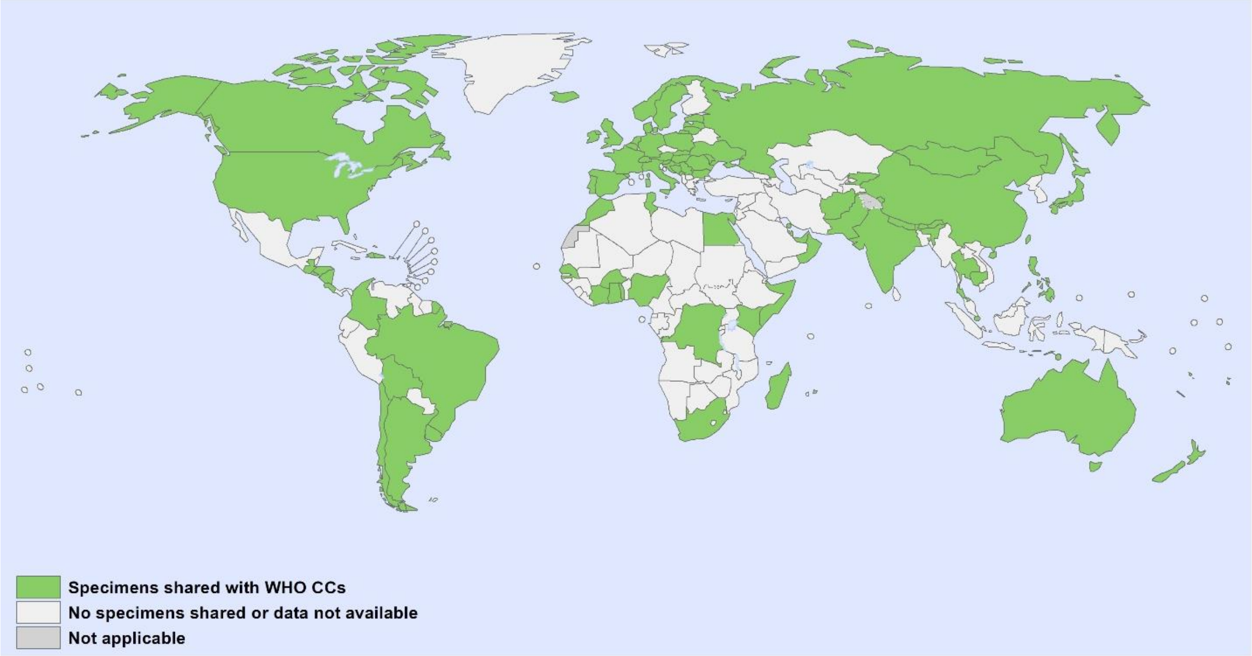


Data source: FluNet, (www.who.int/flunet), Global Influenza Surveillance and Response System (GISRS)

Countries, areas and territories that shared viruses with WHO CCs (Feb – Aug 2022)

Countries, areas and territories sharing specimens with WHO Collaborating Centres (WHO CCs) from February to August 2022

16 September 2022



🟩 **Specimens shared with WHO CCs**

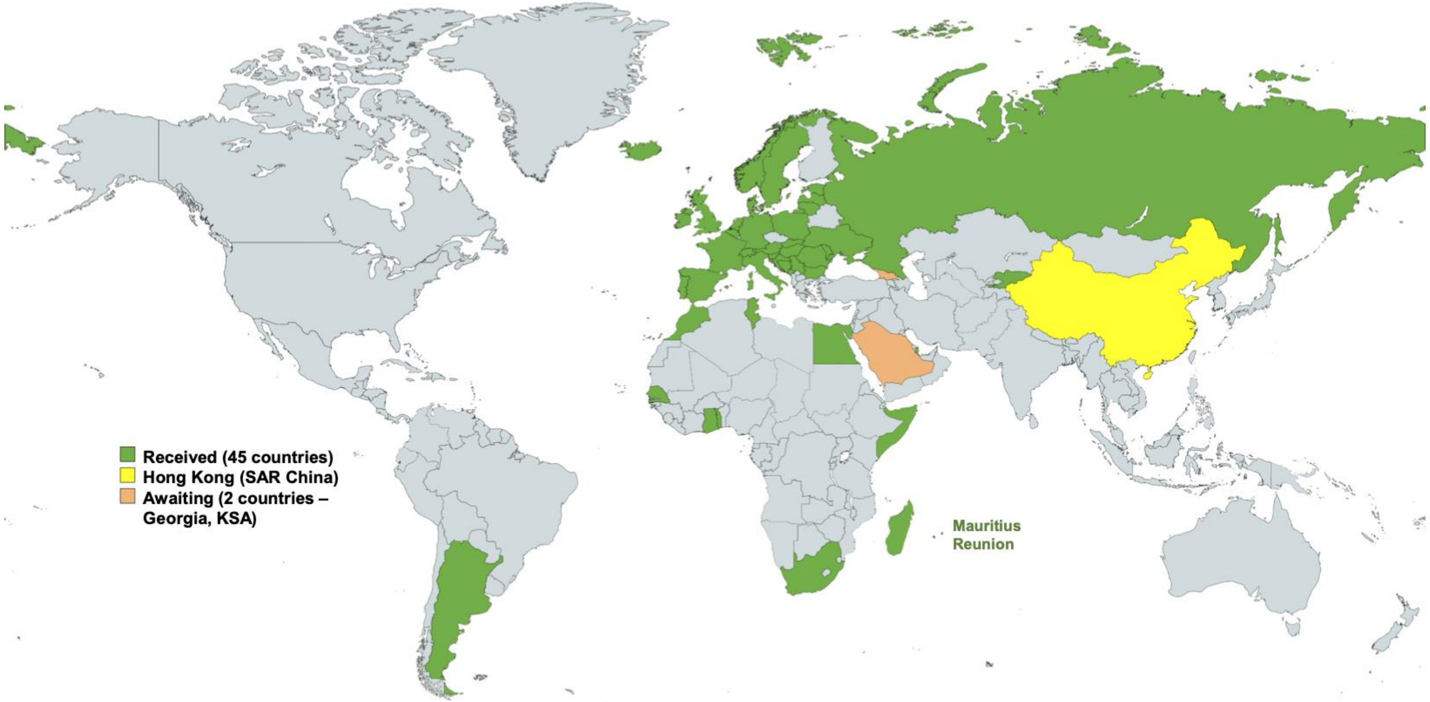
☐ **No specimens shared or data not available**

▨ **Not applicable**

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: WHO CC reports for the WHO influenza vaccine composition consultation in September 2022
Map Production: WHO Global Influenza Programme
World Health Organization

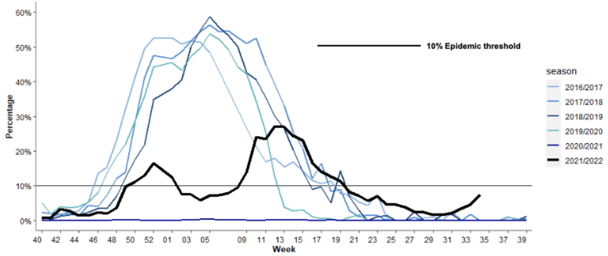
Figure 1. Countries Sharing Influenza-positive Samples Collected after 2022-01-31 with FCI-WIC.



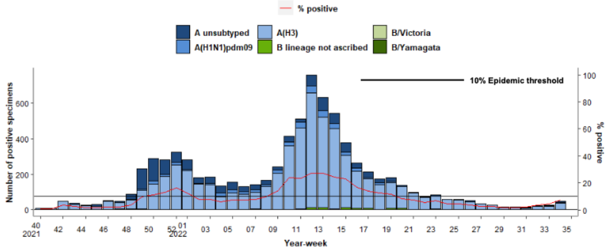
Created with mapchart.net

Figure E2. Seasonal influenza activity in the WHO European Region: weeks 40/2021-34/2022

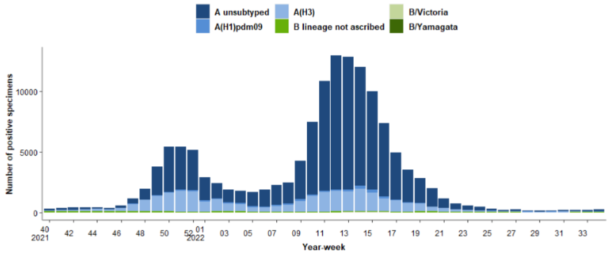
A. Percentage of sentinel ILI/ARI specimens testing positive for influenza by season



B. Sentinel specimens testing positive for influenza by week, (sub)type and percentage positive, 2021/22 season



C. Non-sentinel specimens testing positive for influenza by week, (sub)type and percentage positive, 2021/22 season



Distribution of viruses

- 146,890 detections
- Context of increased numbers of samples from ILI and/or ARI criteria
- A:B 98%:2% across region except Central Asia (283 detections)

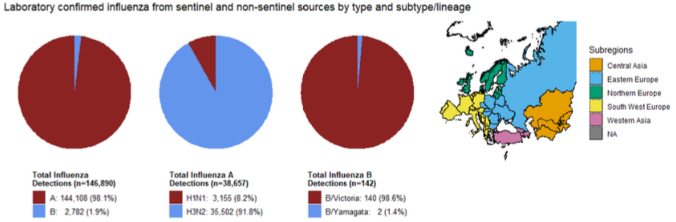
- H3:H1 92%:8% across region except Western Europe (66%:34%)

- B: 99% Bvic; 1% Byam reported but unconfirmed.

(? LAIV-associated based on timing, patient age and limited HA sequence data)

Table B: Restriction to sentinel sources:
Similar regional distribution, Type A (99%), of this 94% H3N2, of the Type B all BVic.

Table E2. Distribution of Influenza Detections in the WHO European Region[a], weeks 40/2021-34/2022



a WHO European Region Member States grouped into sub-regions according to United Nations geographic composition. Available from: (http://unstats.un.org/UNSD/METHODS/M49/M49REGIN.HTM)

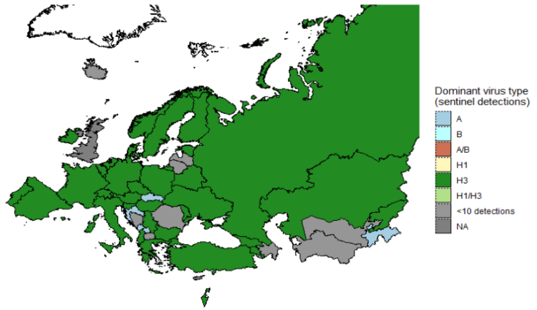
A. Laboratory confirmed influenza from sentinel and non-sentinel sources by geographic sub-region and influenza type and subtype/lineage

Influenza type	South West Europe	Western Europe	Eastern Europe	Northern Europe	West Asia	Central Asia	WHO European Region
Influenza A	**26,314 (99%)**	**47,327 (99%)**	**12,029 (96%)**	**56,711 (97%)**	**1,473 (100%)**	**254 (90%)**	**144,108 (98%)**
Influenza A subtyped	10,263	7,410	9,226	10,053	1,472	233	38,657
A(H1N1)pdm09	186 (2%)	2,545 (34%)	42 (0%)	381 (4%)	1 (0%)	0 (0%)	3,155 (8%)
A(H3N2)	10,077 (98%)	4,865 (66%)	9,184 (100%)	9,672 (96%)	1,471 (100%)	233 (100%)	35,502 (92%)
Influenza B	**219 (1%)**	**454 (1%)**	**452 (4%)**	**1,622 (3%)**	**6 (0%)**	**29 (10%)**	**2,782 (2%)**
Influenza B lineage determined	10	82	0	48	1	1	142
B/Yamagata-lineage	0 (0%)	2 (2%)	0	0 (0%)	0	0	2 (1%)
B/Victoria-lineage	10 (100%)	80 (98%)	0	48 (100%)	1	1	140 (99%)
Total	**26,533**	**47,781**	**12,481**	**58,333**	**1,479**	**283**	**146,890**

B. Laboratory confirmed influenza from sentinel sources by geographic sub-region and influenza type and subtype/lineage

Influenza type	South-West Europe	Western Europe	Eastern Europe	Northern Europe	West Asia	Central Asia	WHO European Region
Influenza A	**2,516 (99%)**	**2,051 (98%)**	**824 (98%)**	**1,314 (98%)**	**878 (100%)**	**201 (98%)**	**7,784 (99%)**
Influenza A subtyped	1,795	1,852	627	1,261	878	180	6,593
A(H1N1)pdm09	44 (2%)	337 (18%)	11 (2%)	24 (2%)	1 (0%)	0 (0%)	417 (6%)
A(H3N2)	1,751 (98%)	1,515 (82%)	616 (98%)	1,237 (98%)	877 (100%)	180 (100%)	6,176 (94%)
Influenza B	**21 (1%)**	**35 (2%)**	**21 (2%)**	**31 (2%)**	**4 (0%)**	**4 (2%)**	**116 (1%)**
Influenza B lineage determined	3	10	0	8	1	1	23
B/Yamagata-lineage	0	0 (0%)	0	0	0	0	0 (0%)
B/Victoria-lineage	3	10 (100%)	0	8	1	1	23 (100%)
Total	**2,537**	**2,086**	**845**	**1,345**	**882**	**205**	**7,900**

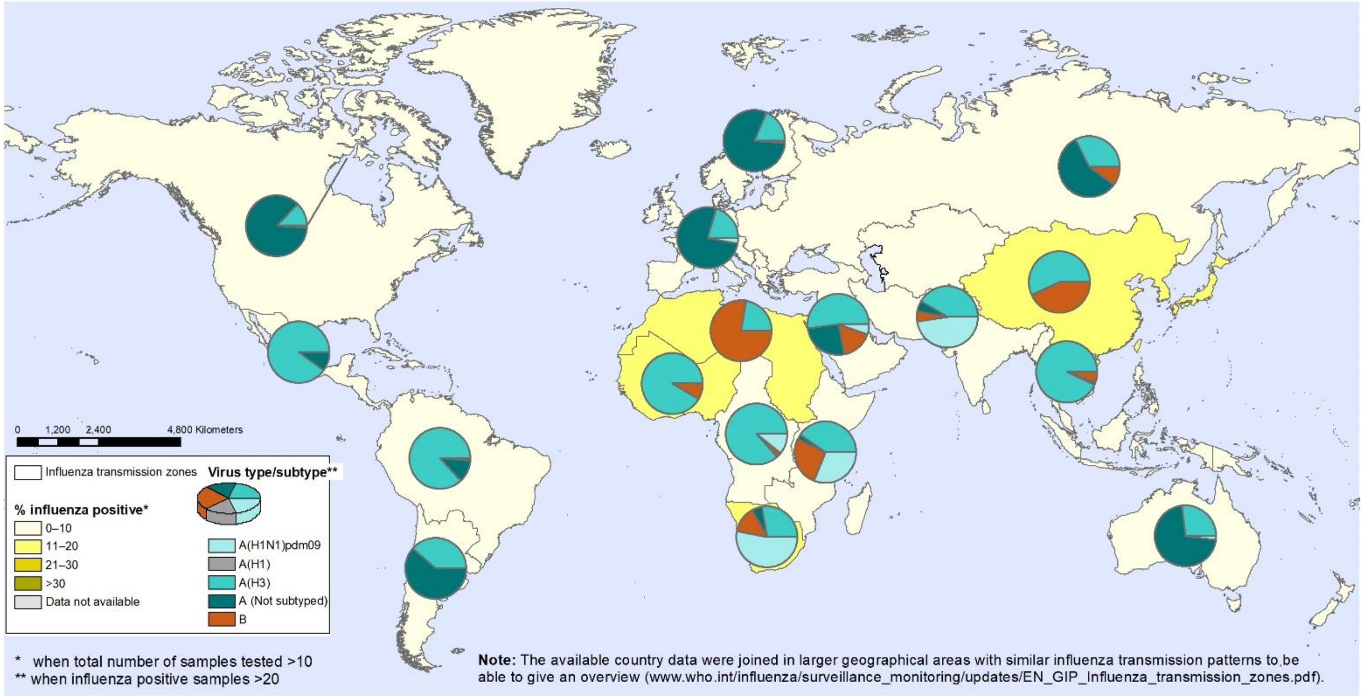
Figure E1. Influenza circulation[b] in the WHO European Region by (sub)type and Country, territory or area, 2021-2022 season



[b] Dominance of (sub)type is based on at least 60% of detections and co-dominance is based on between 40% and 60% of detections. Calculations are only considered valid if at least 10 viruses were detected

Influenza activity – (Feb – Aug 22)

Distribution of influenza virus type/subtype by influenza transmission zone, between February and August 2022



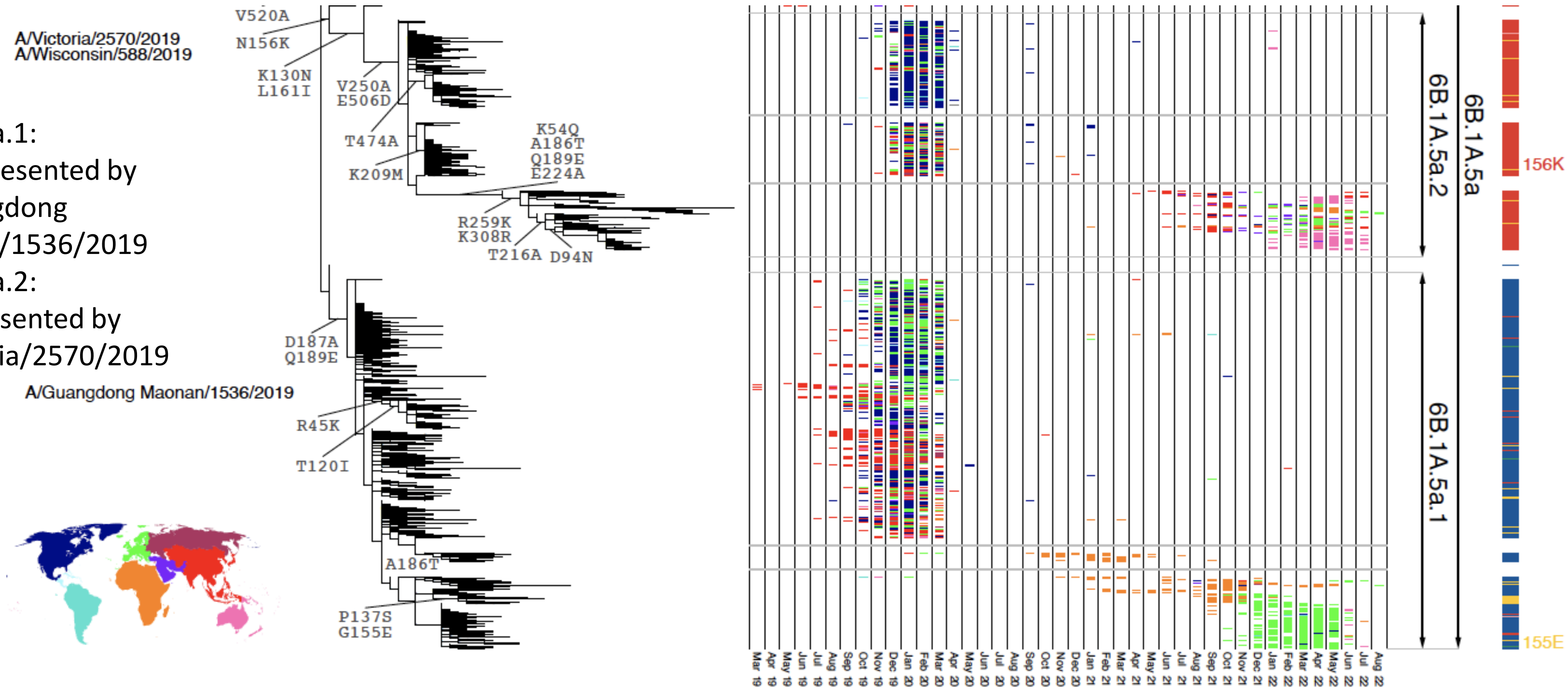
* when total number of samples tested >10
** when influenza positive samples >20

Note: The available country data were joined in larger geographical areas with similar influenza transmission patterns to be able to give an overview (www.who.int/influenza/surveillance_monitoring/updates/EN_GIP_Influenza_transmission_zones.pdf).

Data Source:
Global Influenza Surveillance and Response System (GISRS),
FluNet (www.who.int/tools/flunet)

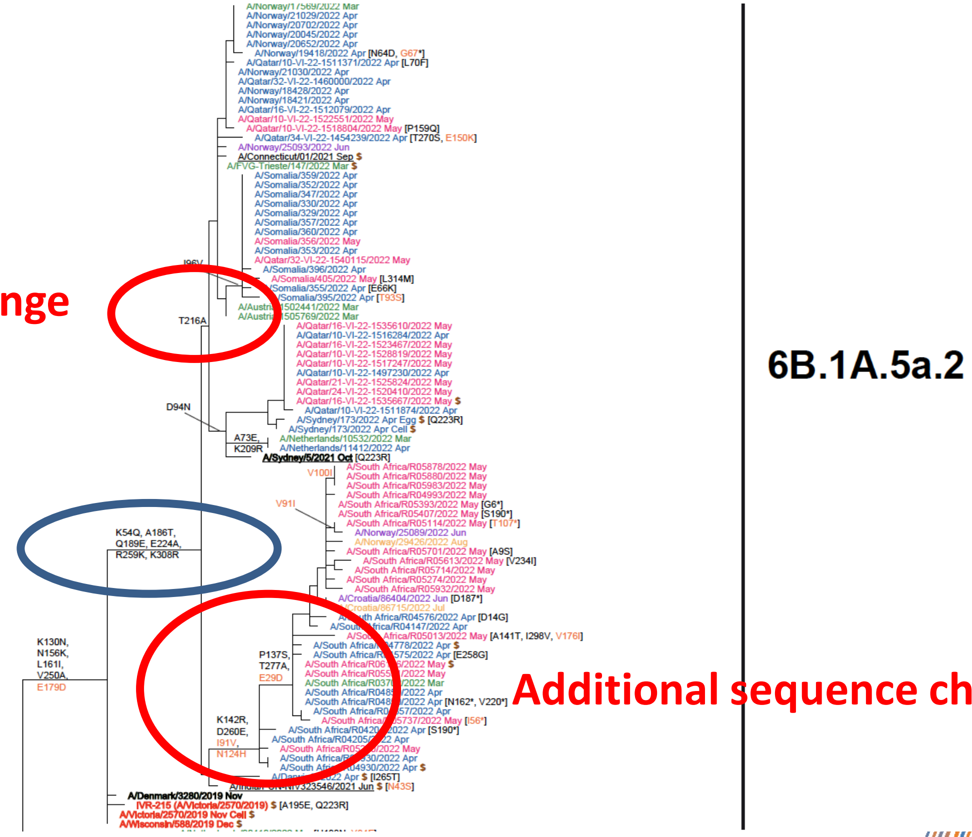
HA gene sequencing of recent H1N1pdm09 viruses

6B.1A.5a.1:
364 represented by A/Guangdong Maonan/1536/2019
6B.1A.5a.2:
32 represented by A/Victoria/2570/2019



Phylogenetic tree of HA genes from Prof. Derek Smith and Dr Sarah James, University of Cambridge

HA gene sequences of recent H1N1pdm09 viruses – zoom in on subclade 6B.1A.5a.2



Additional sequence change

Shared sequence changes

Additional sequence changes

GISRS
GLOBAL INFLUENZA SURVEILLANCE & RESPONSE SYSTEM
YEARS

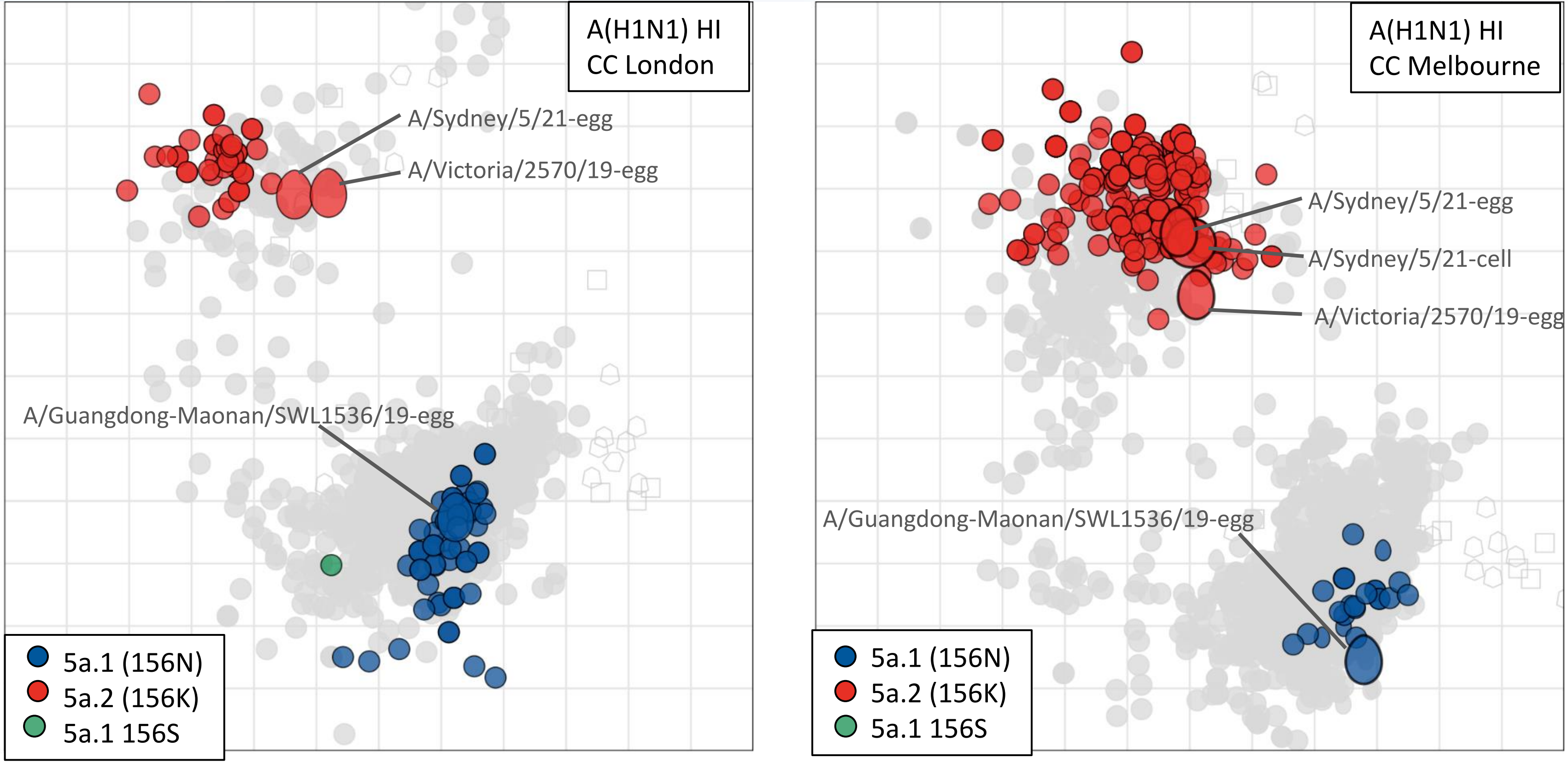
HI analysis of recent H1N1pdm09 viruses

HI analysis with post-infection ferret antisera

Results from VIDRL show the distinct recognition by antisera raised against 6B.1A.5a.1 and 6B.1A.5a.2 viruses

			Haemagglutination inhibition titres						
			Post-infection ferret antisera						
	Virus passage details	Ferret Antiserum Clade	E4 Guang/SWL1536 A.5a.1	SIAT1 Vic2455 A.5a.1	S3, MDCK1 Togo881 A.5a.1	MDCK1 Vic2570 A.5a.2	E4 Vic2570 A.5a.2	E3 Syd5 A.5a.2	**human sera pool**
Reference viruses									
A/Guangdong-Maonan/SWL1536/2019	E4	6B.1A.5a.1	**1280**	2560	2560	<80	<80	80	320
A/Victoria/2455/2019	MDCK3	6B.1A.5a.1	1280	**1280**	1280	<80	<80	80	640
A/Togo/881/2020	S3, MDCK2	6B.1A.5a.1	2560	2560	**2560**	<80	80	160	640
A/Victoria/2570/2019	MDCK1	6B.1A.5a.2	80	80	<80	**320**	320	320	160
A/Victoria/2570/2019	E6	6B.1A.5a.2	80	80	<80	1280	**1280**	1280	640
A/Sydney/5/2021	E3	6B.1A.5a.2	<80	80	<80	2560	1280	**2560**	640
Test viruses									
A/Sydney/894/2022	MDCK1	6B.1A.5a.2	<80	<80	<80	1280	1280	1280	320
A/Perth/184/2022	MDCK1, MDCK1	6B.1A.5a.2	<80	<80	<80	640	1280	1280	320
A/Canberra/222/2022	MDCK1	6B.1A.5a.2	<80	<80	<80	1280	1280	2560	320
A/Darwin/488/2022	SIAT2	6B.1A.5a.2	<80	<80	<80	640	1280	1280	320
A/South Africa/R05765/2022	MDCK1, MDCK1	6B.1A.5a.2	<80	<80	<80	640	640	640	80
A/South Africa/R05258/2022	MDCK1, MDCK1	6B.1A.5a.2	<80	<80	<80	1280	1280	1280	160
A/South Africa/R04994/2022	MDCK1, MDCK1	6B.1A.5a.2	<80	<80	<80	1280	1280	2560	160
A/South Africa/R03645/2022	MDCK1, MDCK1	6B.1A.5a.2	<80	<80	<80	1280	1280	2560	160
A/Sydney/877/2022	MDCK1	6B.1A.5a.1	1280	2560	2560	<80	<80	80	640
A/Sydney/866/2022	MDCK1	6B.1A.5a.1	2560	2560	2560	<80	80	80	640
A/Sydney/869/2022	MDCK1	6B.1A.5a.1	2560	2560	2560	<80	<80	80	640
A/South Africa/R05655/2022	MDCK1, MDCK1	6B.1A.5a.1	1280	1280	1280	<80	<80	<80	320
A/South Africa/R05558/2022	MDCK1, MDCK1	6B.1A.5a.1	1280	2560	1280	<80	<80	80	320
A/South Africa/R05539/2022	MDCK1, MDCK1	6B.1A.5a.1	1280	2560	1280	<80	<80	80	640

Antigenic cartography of A(H1N1)pdm09 HI results



Antigenic cartography from Prof. Derek Smith and Dr Sarah James, University of Cambridge

Since March 2022 (older viruses in grey)

Post vaccination human serology results

Seven panels of post-vaccination antisera were used for the analysis of recent circulating viruses:

Egg-propagated vaccines (children, adult and elderly): A/Victoria/2570/2019 (6B.1A.5a.2)

Cell culture-based vaccines (children and adults): A/Wisconsin/588/2019 (6B.1A.5a.2)

A(H1N1)pdm09 – Summary (1)

- Globally, relatively few A(H1N1) pdm09 viruses with collection dates after January 2022 have been detected

- All of those A(H1N1)pdm09 viruses characterised genetically have fallen within HA clade **6B.1A.5a** (**5a**)

- Two **5a** subclades have circulated in **2022**

- Subclade **6B.1A.5a.1** (**5a.1** - <u>predominantly circulating in Europe</u>) defined by HA1 amino acid substitutions **D187A, Q189E**

- Subclade **6B.1A.5a.2** (**5a.2** - <u>more general global circulation</u>) defined by HA1 amino acid substitutions **K130N, N156K, L161I, V250A**

- **5a.2** viruses have evolved further with all recently circulating viruses having HA1 amino acid substitutions **K54Q, A186T, Q189E, E224A, R259K, K308R**

A(H1N1)pdm09 – Summary (2)

- Post-infection ferret antisera raised against **5a.1** viruses (A/Guangdong-Maonan/SWL1536/2019-like) showed good recognition of circulating **5a.1** viruses but recognised **5a.2** viruses poorly

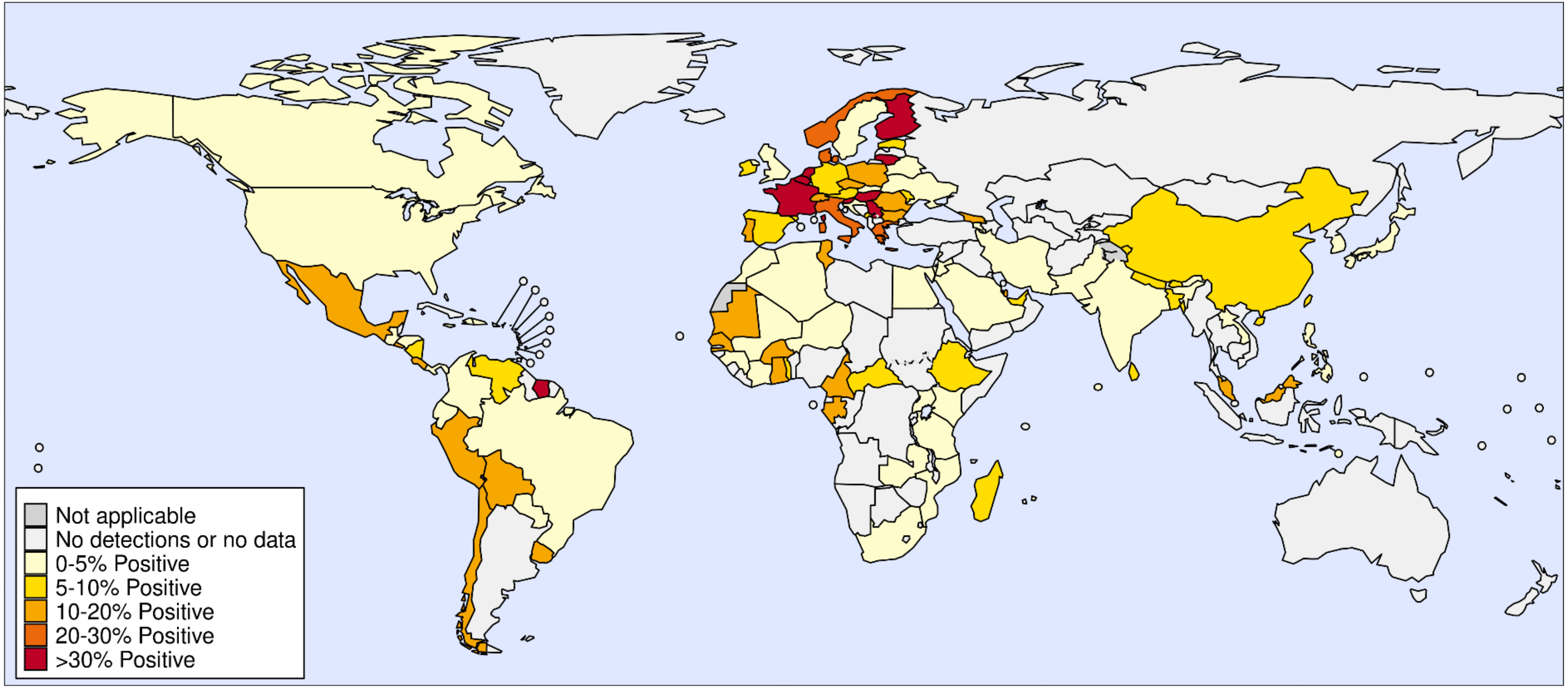
- Post-infection ferret antisera raised against **5a.2** viruses (A/Victoria/2570/2029-like) showed good recognition of circulating **5a.2** viruses but recognised **5a.1** viruses poorly

- A number of genetic groups defined by different HA amino acid substitutions have emerged among **5a.2** viruses

- Viruses in some of these **5a.2** groups are recognised less well by post-vaccination human sera – e.g. a group of viruses recently detected in Africa, the Americas and Europe with **HA1 K142R** amino acid substitution, often with **P137S**

- Those A(H1N1)pdm09 viruses characterised (n = 607) remained susceptible to the PA inhibitor Baloxavir marboxil, while only 5/879 (0.6%) showed reduced susceptibility to at least one Neuraminidase Inhibitor

Influenza A(H3N2) activity



Influenza A(H3N2), February 2022 to August 2022, percent of all samples tested

Colour intensity shows the percent of influenza A(H3N2) positive among all samples tested during this period per country

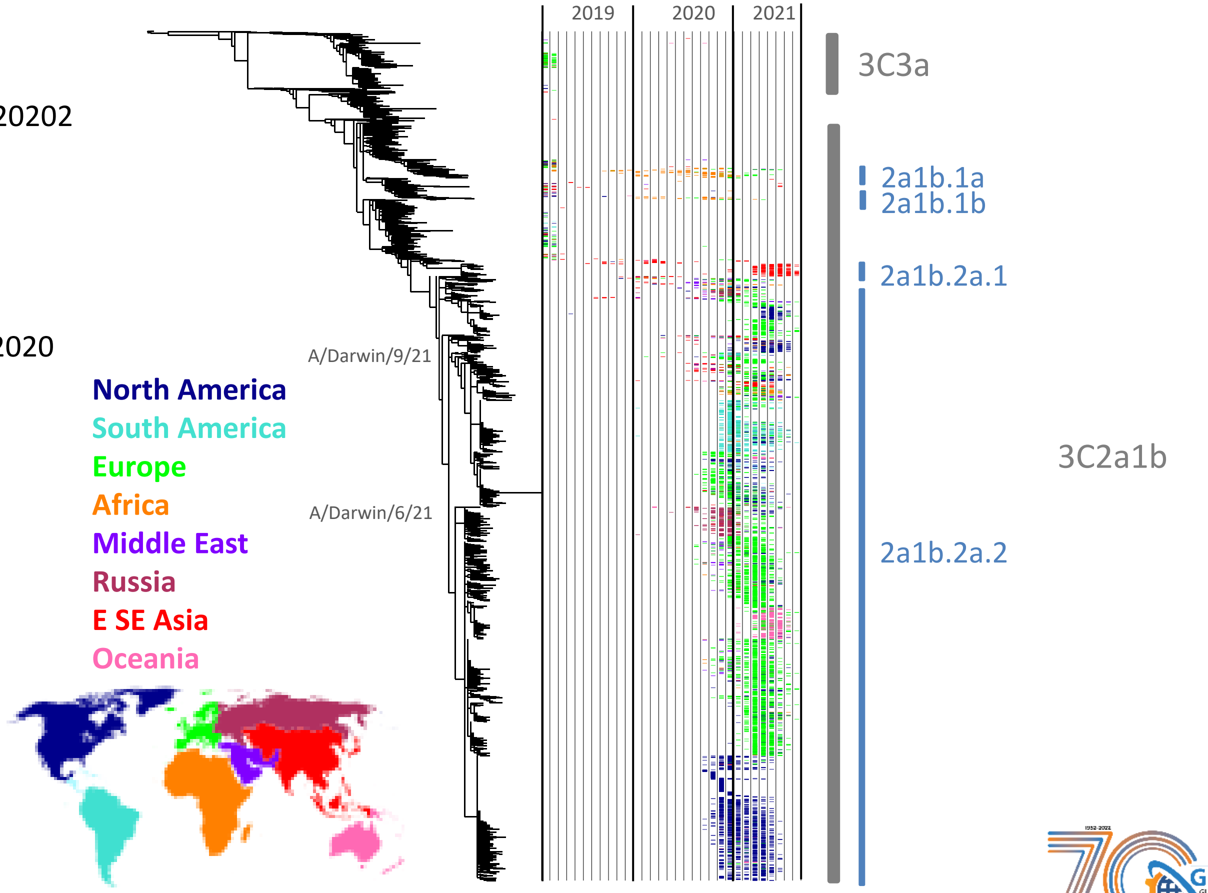
Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (9 Sep 2022)

Phylogenetic analysis of A(H3N2) HA gene

3C.2a1b.2a.2:
4885 represented by A/Bangladesh/4005/20202

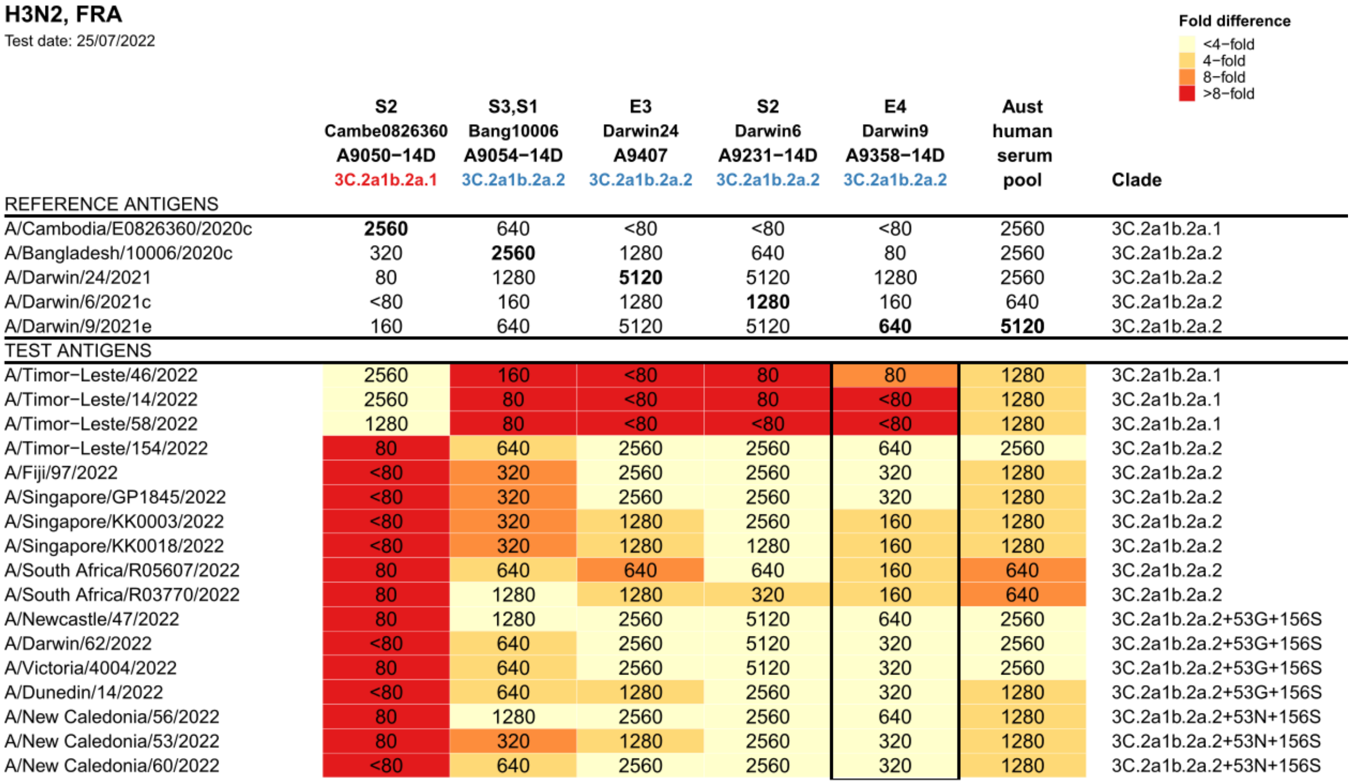
3C.2a1b.1a:
20 represented by A/Denmark/3264/2019

3C.2a1b.2a.1:
3 represented by A/Cambodia/e0826360/2020



Slide courtesy of Dr Sarah James and
Prof Derek Smith, Univ of Cambridge

Antigenic characterization (VN assay)



H3N2, FRA

Test date: 25/07/2022

Fold difference
<4−fold
4−fold
8−fold
>8−fold

	S2 **Cambe0826360** **A9050−14D** 3C.2a1b.2a.1	**S3,S1** **Bang10006** **A9054−14D** 3C.2a1b.2a.2	**E3** **Darwin24** **A9407** 3C.2a1b.2a.2	**S2** **Darwin6** **A9231−14D** 3C.2a1b.2a.2	**E4** **Darwin9** **A9358−14D** 3C.2a1b.2a.2	**Aust human serum pool**	**Clade**
REFERENCE ANTIGENS							
A/Cambodia/E0826360/2020c	**2560**	640	<80	<80	<80	2560	3C.2a1b.2a.1
A/Bangladesh/10006/2020c	320	**2560**	1280	640	80	2560	3C.2a1b.2a.2
A/Darwin/24/2021	80	1280	**5120**	5120	1280	2560	3C.2a1b.2a.2
A/Darwin/6/2021c	<80	160	1280	**1280**	160	640	3C.2a1b.2a.2
A/Darwin/9/2021e	160	640	5120	5120	**640**	**5120**	3C.2a1b.2a.2
TEST ANTIGENS							
A/Timor−Leste/46/2022	2560	160	<80	80	80	1280	3C.2a1b.2a.1
A/Timor−Leste/14/2022	2560	80	<80	80	<80	1280	3C.2a1b.2a.1
A/Timor−Leste/58/2022	1280	80	<80	<80	<80	1280	3C.2a1b.2a.1
A/Timor−Leste/154/2022	80	640	2560	2560	640	2560	3C.2a1b.2a.2
A/Fiji/97/2022	<80	320	2560	2560	320	1280	3C.2a1b.2a.2
A/Singapore/GP1845/2022	<80	320	2560	2560	320	1280	3C.2a1b.2a.2
A/Singapore/KK0003/2022	<80	320	1280	2560	160	1280	3C.2a1b.2a.2
A/Singapore/KK0018/2022	<80	320	1280	1280	160	1280	3C.2a1b.2a.2
A/South Africa/R05607/2022	80	640	640	640	160	640	3C.2a1b.2a.2
A/South Africa/R03770/2022	80	1280	1280	320	160	640	3C.2a1b.2a.2
A/Newcastle/47/2022	80	1280	2560	5120	640	2560	3C.2a1b.2a.2+53G+156S
A/Darwin/62/2022	<80	640	2560	5120	320	2560	3C.2a1b.2a.2+53G+156S
A/Victoria/4004/2022	80	640	2560	5120	320	2560	3C.2a1b.2a.2+53G+156S
A/Dunedin/14/2022	<80	640	1280	2560	320	1280	3C.2a1b.2a.2+53G+156S
A/New Caledonia/56/2022	80	1280	2560	2560	640	1280	3C.2a1b.2a.2+53N+156S
A/New Caledonia/53/2022	80	320	1280	2560	320	1280	3C.2a1b.2a.2+53N+156S
A/New Caledonia/60/2022	<80	640	2560	2560	320	1280	3C.2a1b.2a.2+53N+156S

Source: WHO CC VIDRL

A(H3N2) Summary (1): Global Circulation

- ☐ Influenza A(H3N2) viruses predominated globally
- ☐ HA phylogenetics:
  - A majority of circulating A(H3N2) viruses in this period belonged to the 3C.2a1b.2a.2 (**2a.2**) subclade, with shared HA1 substitutions Y159N, T160I (resulting in the loss of a glycosylation site), L164Q, G186D, D190N, F193S and Y195F.
  - 2a.2 viruses have diversified into genetic groups that typically encode:
    - H156Q
    - H156S and D53G
    - H156S and D53N
    - D53G
  - Viruses belonging to 3C.2a1b.2a.1 (**2a.1**) with shared HA1 substitutions G186S, F193S, Y195F and S198P, predominated in China. Some viruses had additional substitutions K171N and I48T in HA1.

A(H3N2) Summary (2): Antigenic Characteristics

- **2a.2** viruses are antigenically distinct from **2a.1** viruses
- Ferret antisera to:
  - A/Darwin/6/2021 (SH 22 Cell) and A/Darwin/9/2021 (SH Egg) **2a.2**
    - Recognized 2a.2 viruses with the HA1 substitution H156S well
    - Reacted less well with 2a.2 viruses without the H156S substitution
    - Reacted poorly with 2a.1 viruses
  - A/Cambodia/e0826360/2020 (NH 21-22 Cell) **2a.1**
    - Reacted well with 2a.1 viruses but poorly with 2a.2 viruses

A(H3N2) Summary (3)

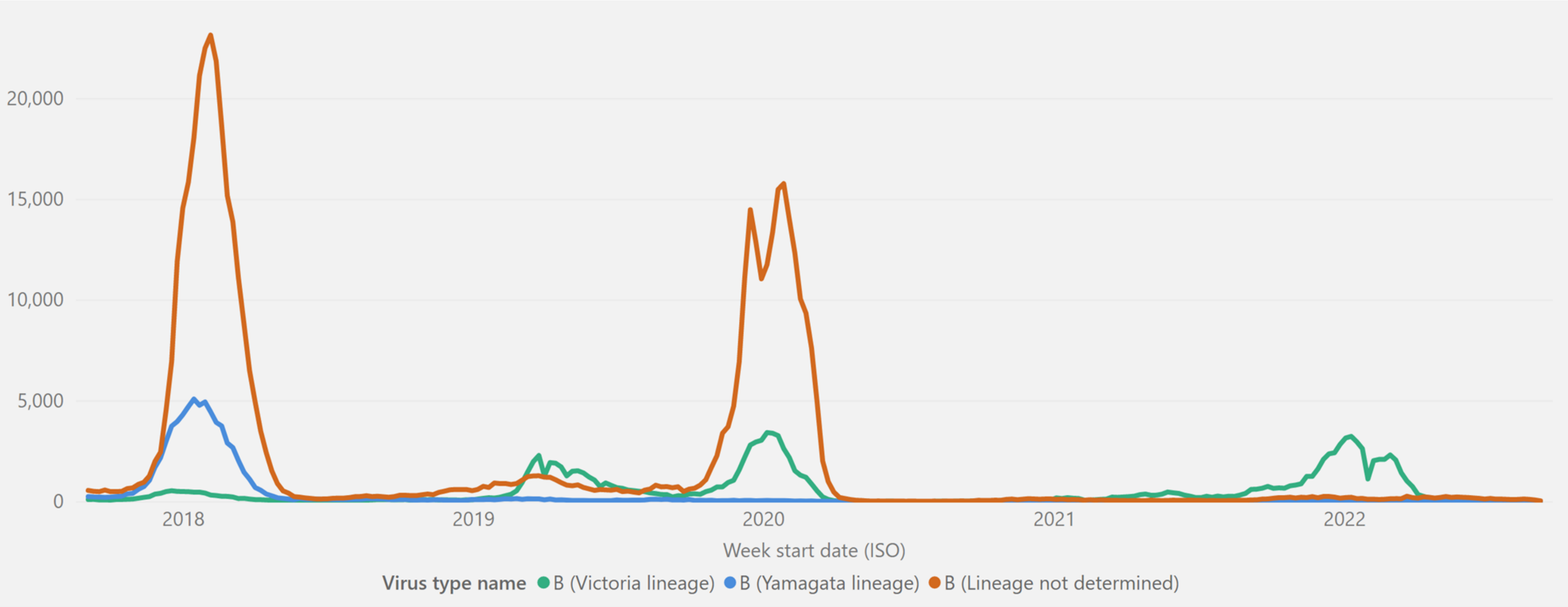
Human serology studies with serum panels from individuals vaccinated with A/Darwin/9/2021-like (**2a.2**) viruses:

- Geometric mean HI and VN titers against recent representative A(H3N2) **2a.2** and **2a.1** viruses were not significantly reduced compared to titers against cell culture-propagated A/Darwin/6/2021
- Reductions of VN GMTs were more pronounced when compared to egg-propagated A/Darwin/9/2021-like reference viruses

Antiviral Susceptibility

- Genetic and/or phenotypic testing showed that none of the 4,577 A(H3N2) viruses collected since 1 February 2022 showed reduced inhibition to neuraminidase inhibitors.
- Of 3,250 A(H3N2) viruses collected and analyzed since 1 February 2022, one showed genetic evidence of reduced susceptibility to baloxavir.

Global circulation of influenza B viruses

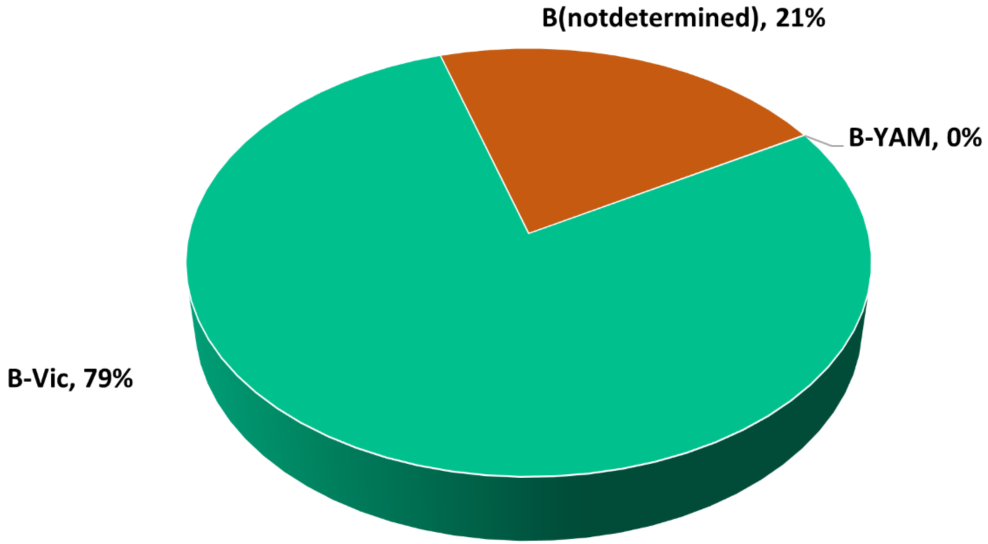


Select week start date (ISO)

9/4/2017 9/5/2022

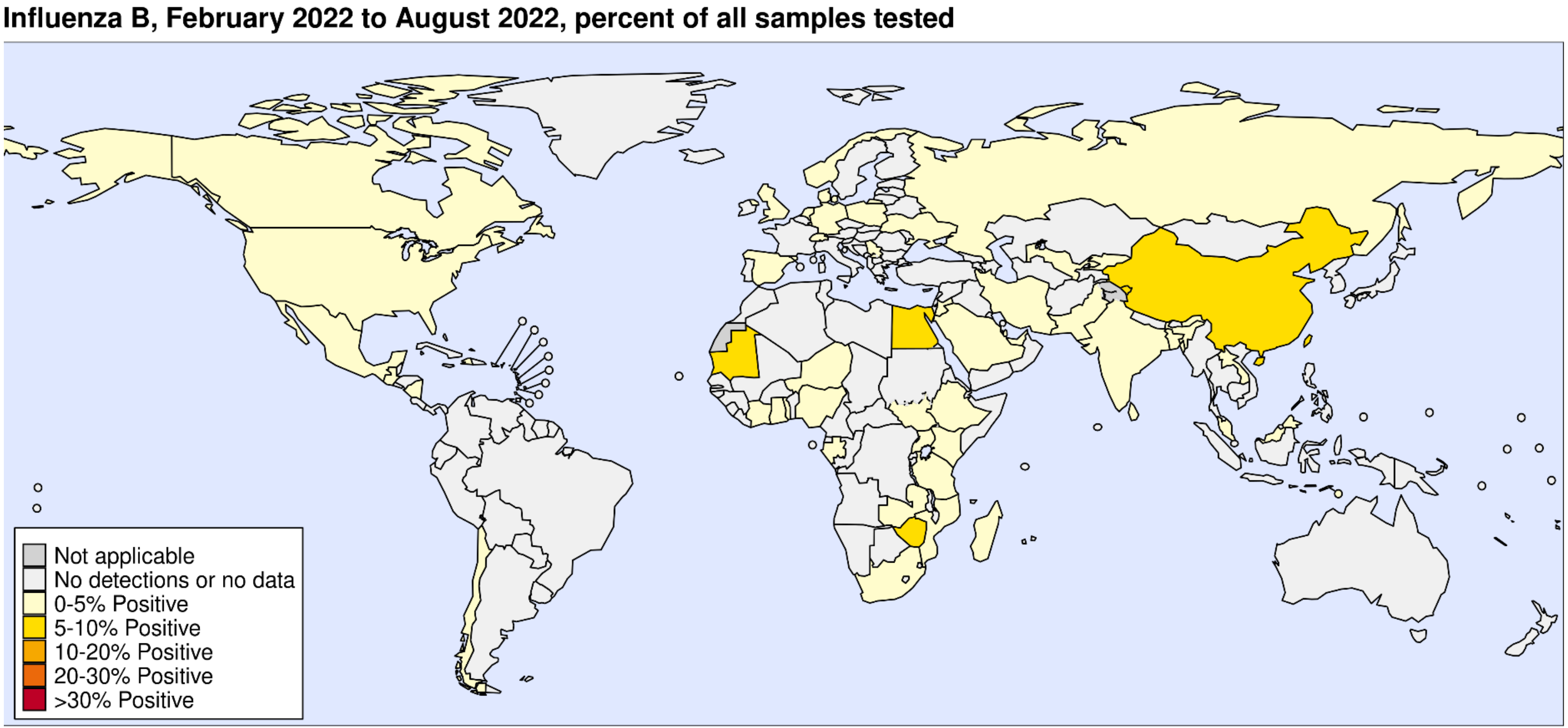
Data source: FluNet, (www.who.int/flunet), Global Influenza Surveillance and Response System (GISRS)

Influenza B virus lineages % (Feb – Aug 2022)



Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (17 Sep 2022)

Influenza B viruses activity

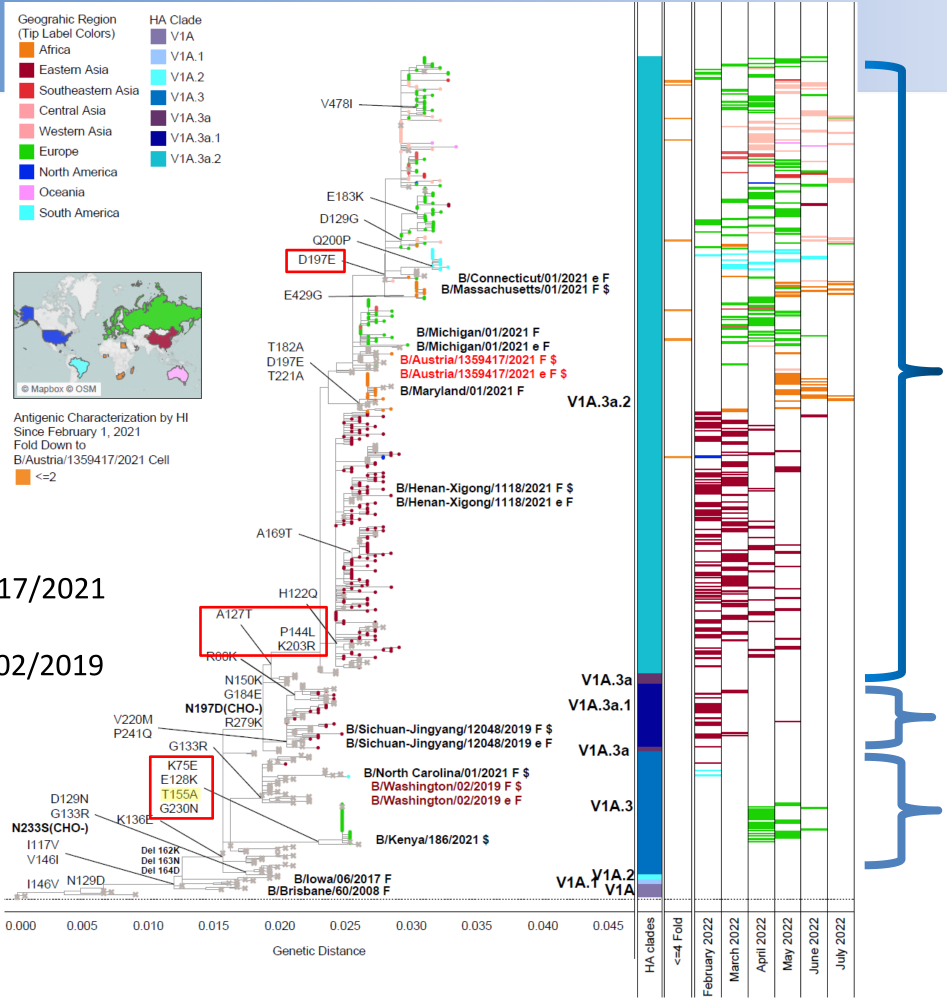


Influenza B, February 2022 to August 2022, percent of all samples tested

Colour intensity shows the percent of influenza B positive among all samples tested during this period per country

Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (9 Sep 2022)

B/Victoria lineage HA phylogenetics



1A.3a.2

(A127T, P144L, K203R)

1A.3a.1

(V220M, P241Q)

1A.3

V1A.3.2:

55 viruses represented by B/Austria/139417/2021

V1A.3:

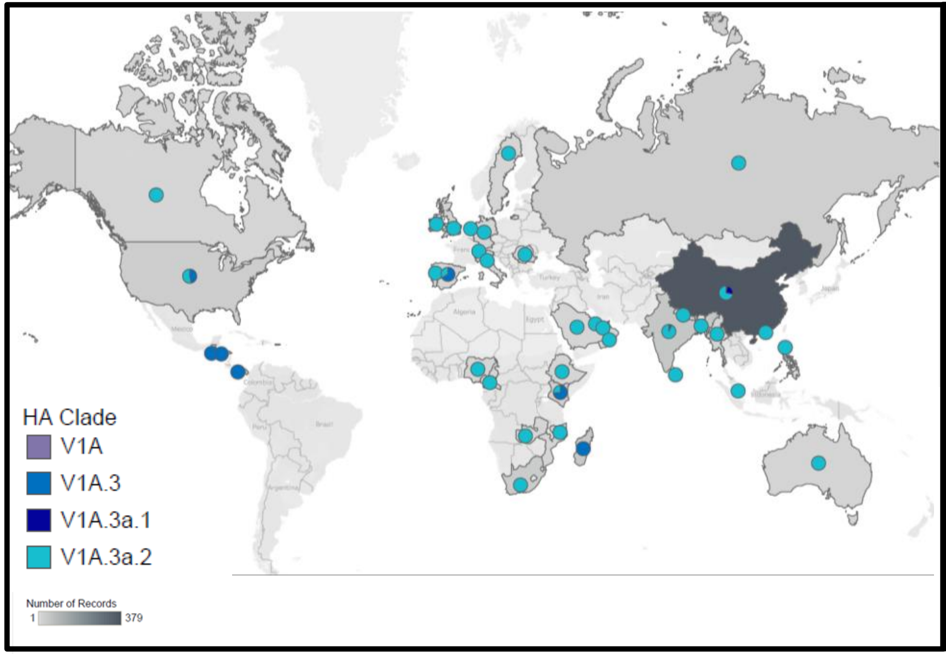
29 viruses represented by B/Washington/02/2019

WHO CC
CDC, USA

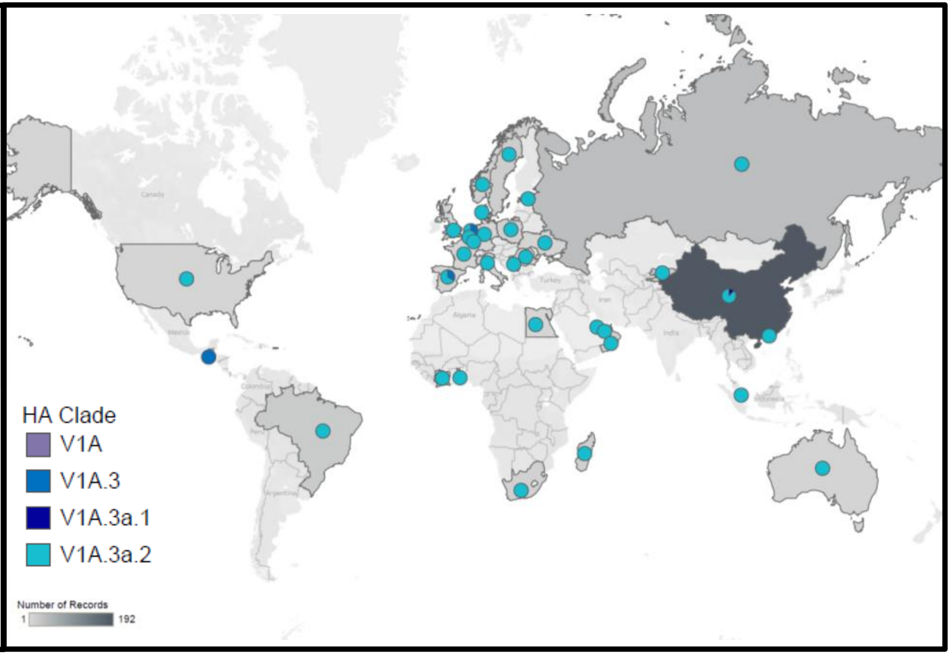
World Health Organization

Global B/Victoria HA clade diversity

Collection Dates
September 1, 2021- January 31, 2022



Collection Dates
February 1, 2022- August 31, 2022



Based on HA sequence availability

WHO CC
CDC, USA

B/Yamagata lineage virus

- There have been no confirmed detections of circulating B/Yamagata/16/88 lineage viruses after March 2020.

- No B/Yamagata/16/88 lineage viruses have been available for analysis during this period

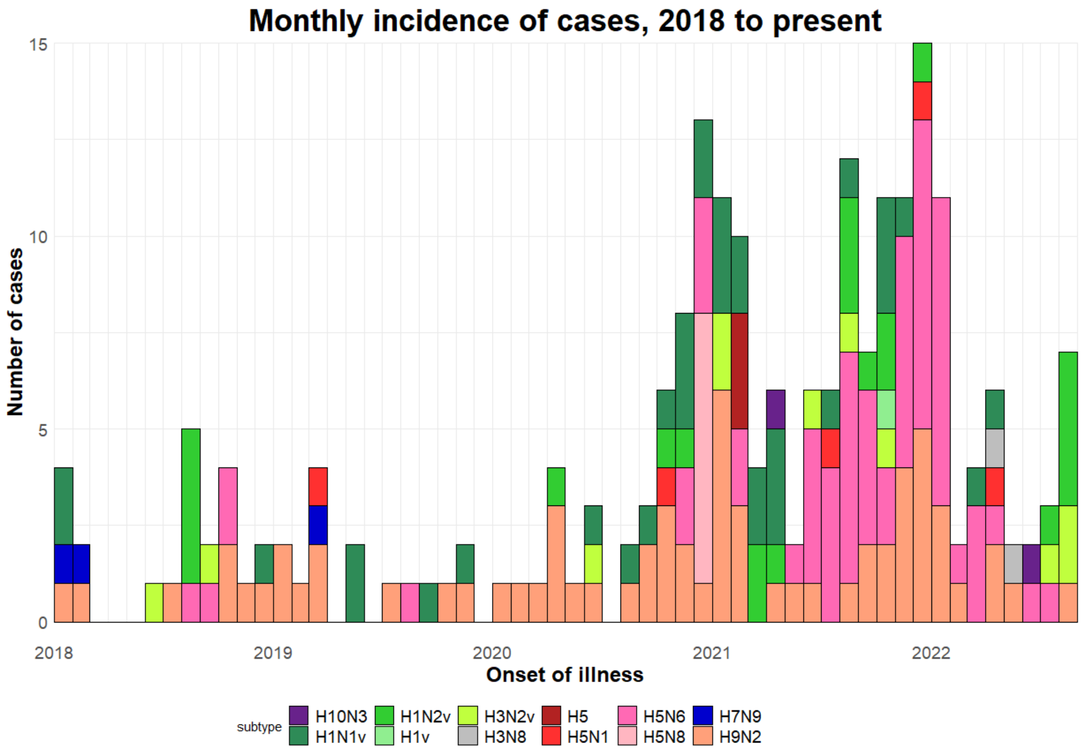
Summary of Influenza B Viruses (1)

- Only influenza B/Victoria lineage viruses were available for analysis
- HA phylogenetics of B/Victoria lineage viruses
  - All HA genes belonged to clade **1A.3**, with a deletion of residues 162-164 and a K136E substitution in HA1
    - A small number of viruses derived from 1A.3 continue to circulate and recent viruses from Kenya and Netherlands have evolved substitutions K75E, E128K, T155A and G230N in HA1
  - Subclade **1A.3a** viruses with HA genes encoding further substitutions of N150K, G184E, N197D (resulting in the loss of a glycosylation site) and R279K in HA1 have predominated
  - Two subgroups have emerged:
    - 1A.**3a.1** has additional HA1 substitutions **V220M and P241Q**, seen exclusively in China and are decreasing in number
    - 1A.**3a.2** with A127T, P144L and K203R seen in Asia, Africa, Oceania, Europe, North America and South America
      - The majority of 1A.**3a.2** viruses have one additional substitution D197E in HA1

Summary of Influenza B Viruses (2)

- **Antigenic characteristics of B/Victoria lineage viruses**
  - Post-infection ferret antisera raised against **B/Austria/1359417/2021-like** viruses (1A.**3a.2**) inhibited the majority of recently circulating viruses well but recognized 1A.**3a.1** poorly
  - Subgroup 1A.**3a.1** and 1A.**3a.2** viruses are **antigenically different**
  - A small number of 1A.**3** viruses, detected in Kenya and the Netherlands, were not recognized well by ferret antisera raised against **B/Washington/02/2019-like** viruses (1A.3) and were poorly recognized by ferret antisera raised against **B/Austria/1359417/2021-like** viruses (3a.2)

27 zoonotic influenza A infections

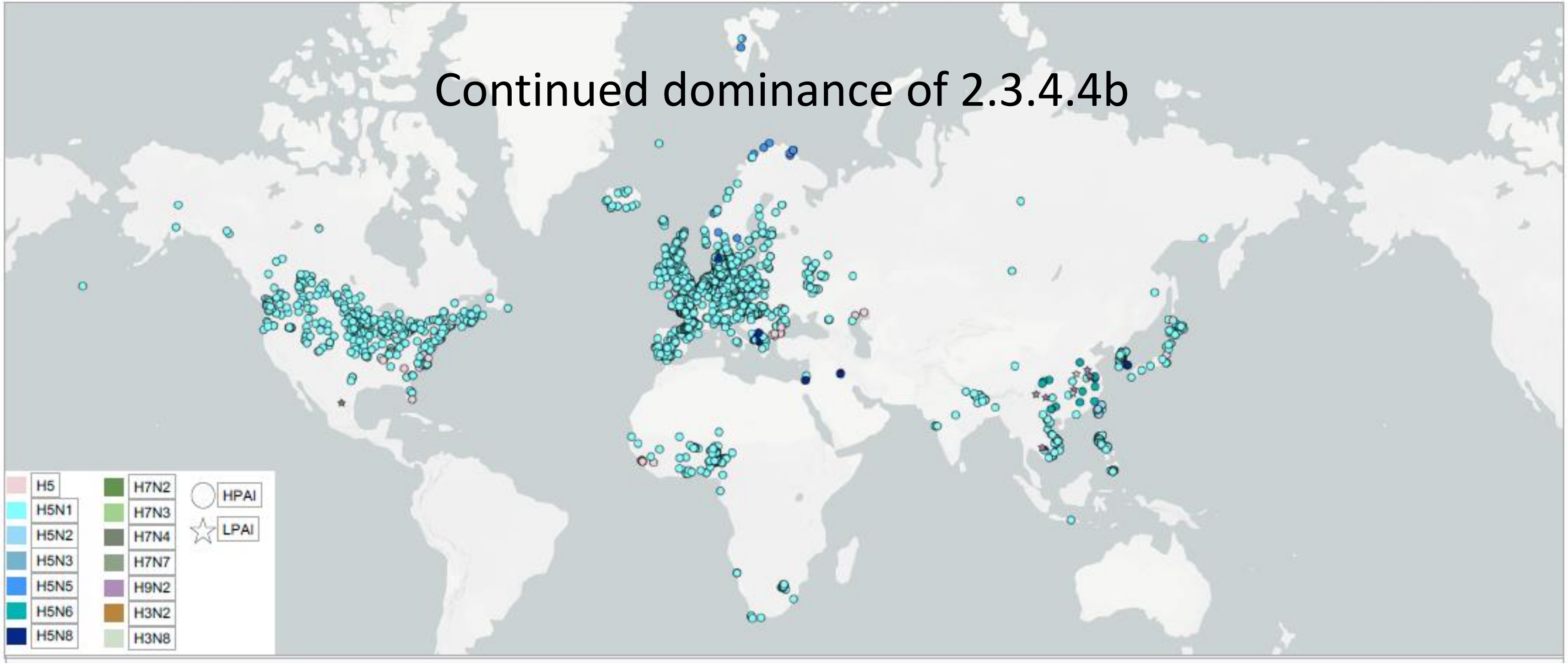


2 (H1N1)v
5 A(H1N2)v
3 A(H3N2)v
2 A(H3N8)
1 A(H5N1)
7 A(H5N6)
6 A(H9N2)

1 A(H10N3)
0 A(H7N9)

Influenza A(H5)

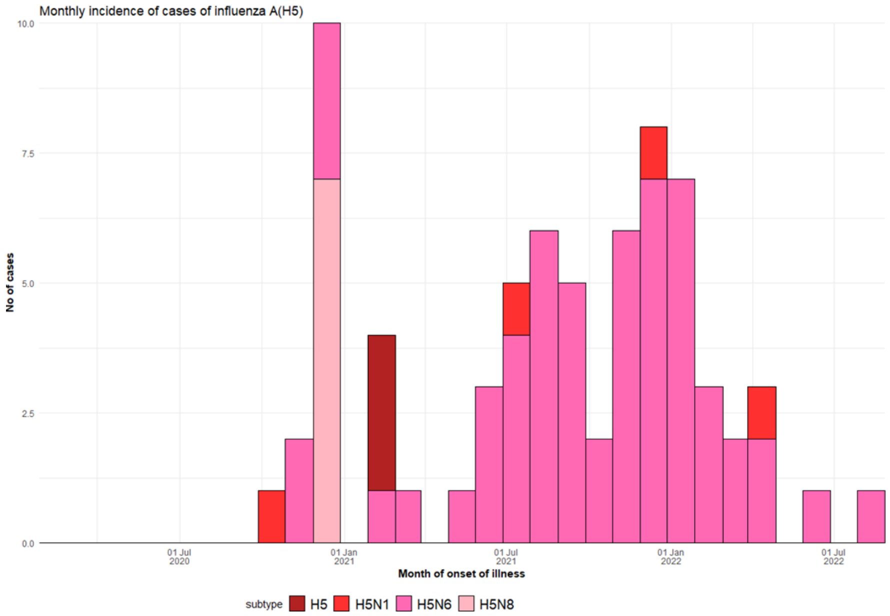
A(H5) activity in birds



Continued dominance of 2.3.4.4b

A(H5) activity in humans

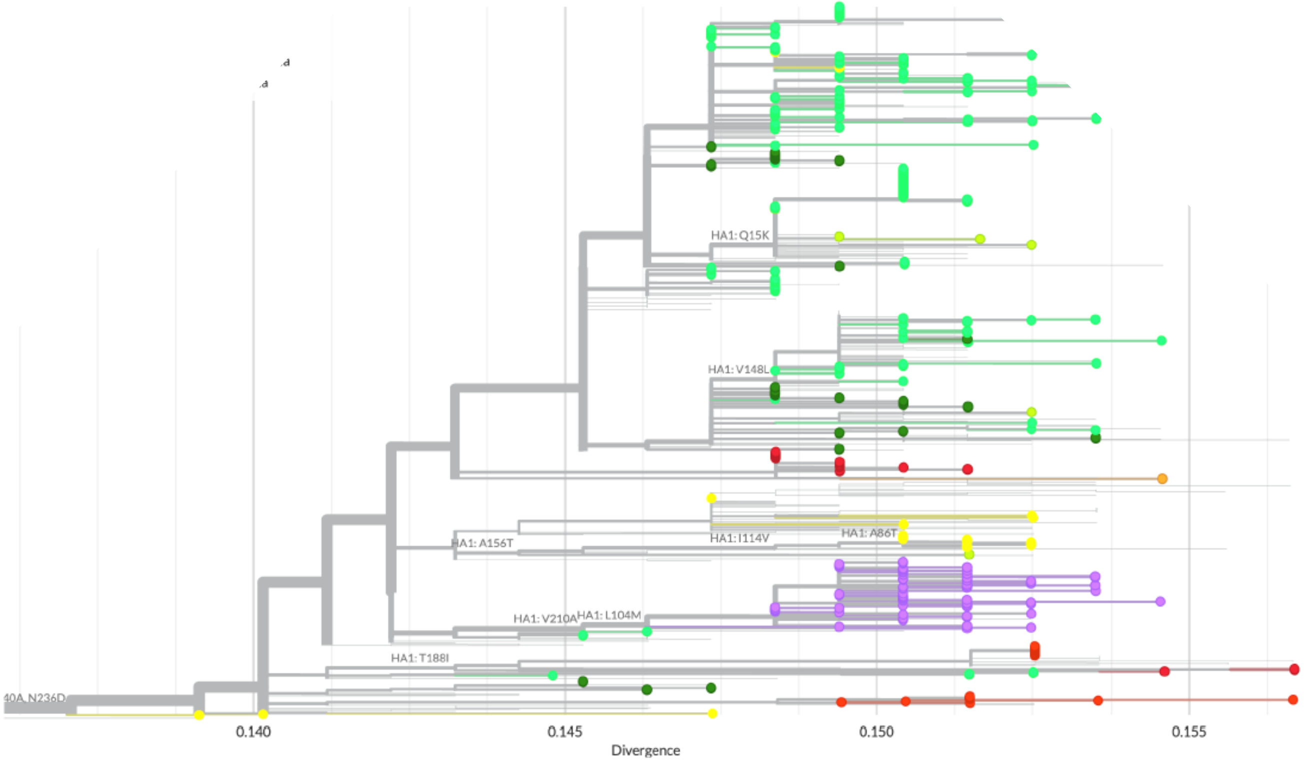
- 7 A(H5N6) in China (clade 2.3.4.4b)
- 1 A(H5N1) in US (clade 2.3.4.4b)


Monthly incidence of cases of influenza A(H5)

Cumulative numbers

- 3 A(H5), 7 A(H5N8), 81 A(H5N6) and 865 A(H5N1)

Geographic clustering of 2.3.4.4b viruses



Europe

Asia

Africa

North America

Antigenic properties of African 2.3.4.4b viruses

Reference Antigen	Clade	Subtype	A/Fujian-Sanyan	A/Astrakhan	A/chicken/Ghana	A/hen/Bulgaria
A/Fujian-Sanyan/21099/2017 xA/PR/8/1934	2.3.4.4b	H5N6	**40**	160	1280	640
A/Astrakhan/3212/2020	2.3.4.4b	H5N8	80	**160**	640	640
A/poultry/Niger/ET3/HALAL/21VIR2131-33/2021	2.3.4.4b	H5N1	10	40	320	160
A/chicken/Ghana/AVL-763/21VIR7050-39/2021	2.3.4.4b	H5N1	10	20	**320**	80
A/hen/Bulgaria/722-1/22VIR778-1/2021	2.3.4.4b	H5N1	10	40	640	**640**
Test antigen						
A/laying-hen/Moldova/68-1 22VIR638-1/2022	2.3.4.4b	H5N1	10	40	320	320
A/ferret/Slovenia/308/22VIR777-9/2022	b		10	10	640	640
	2.3.4.4					

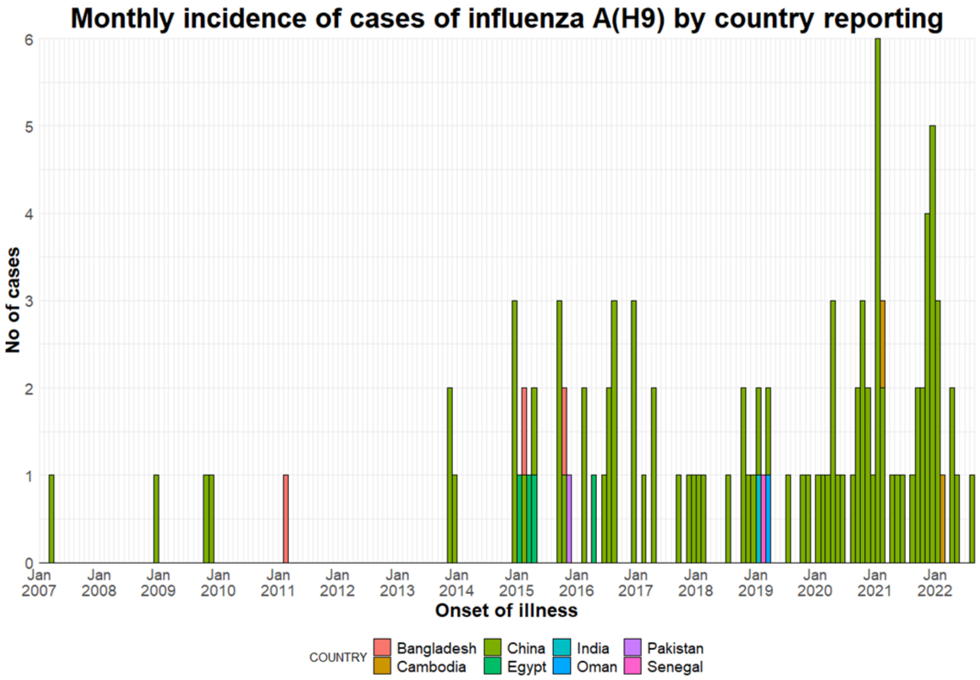
A new CVV antigenically-like A/chicken/Ghana/AVL-76321VIR7050-39/2021 is proposed

Influenza A(H9N2)

Recent A(H9N2) activity

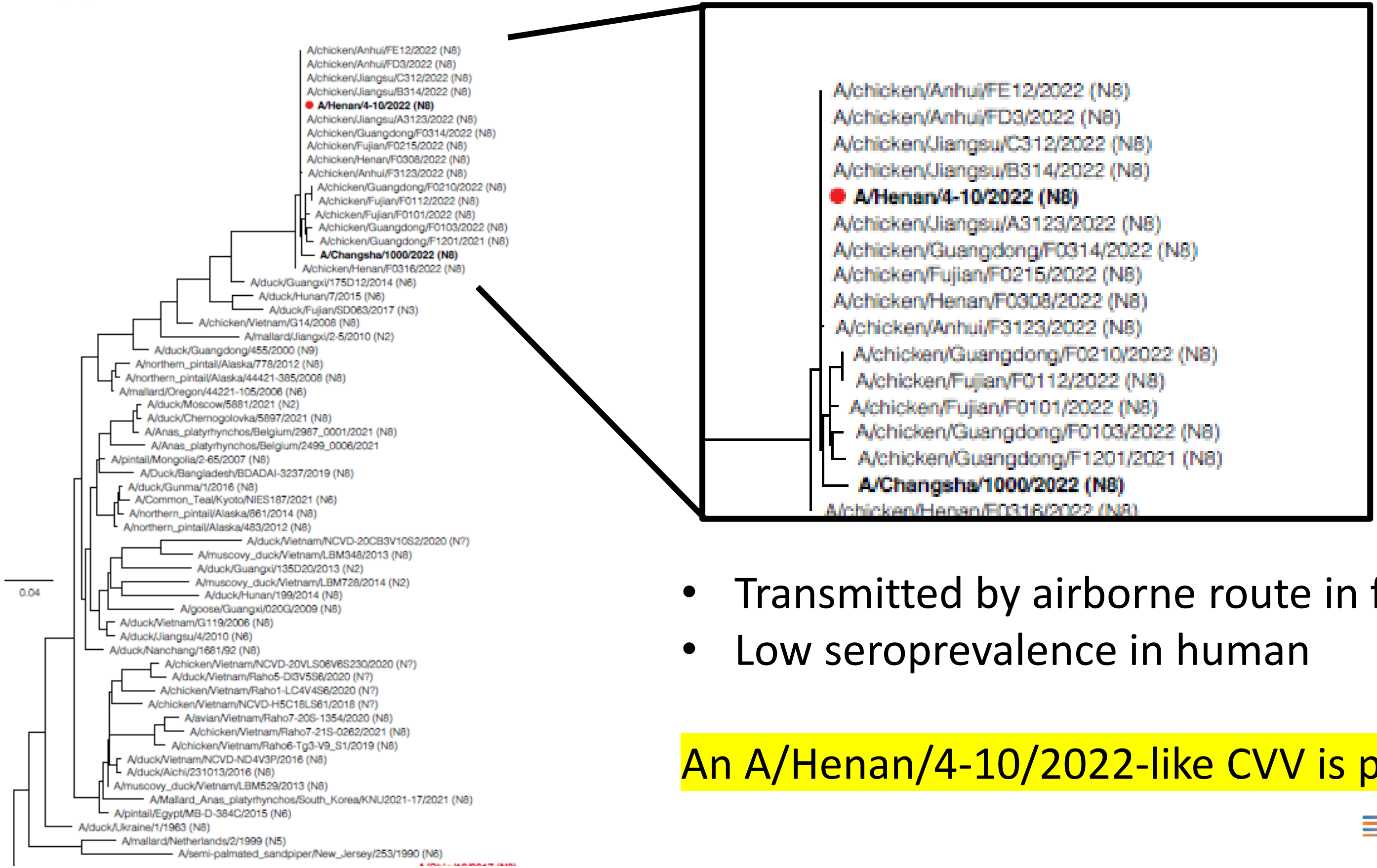
- **Human infections**
  - 5 in China (Y280/G9)
  - 1 in Cambodia (Y280/G9)

- **Avian activity**
  - Y280/G9 lineage viruses detected in China, Cambodia and Viet Nam
  - G1 lineage viruses were detected in Bangladesh and Egypt



Influenza A(H3N8)

Properties of A(H3N8) viruses

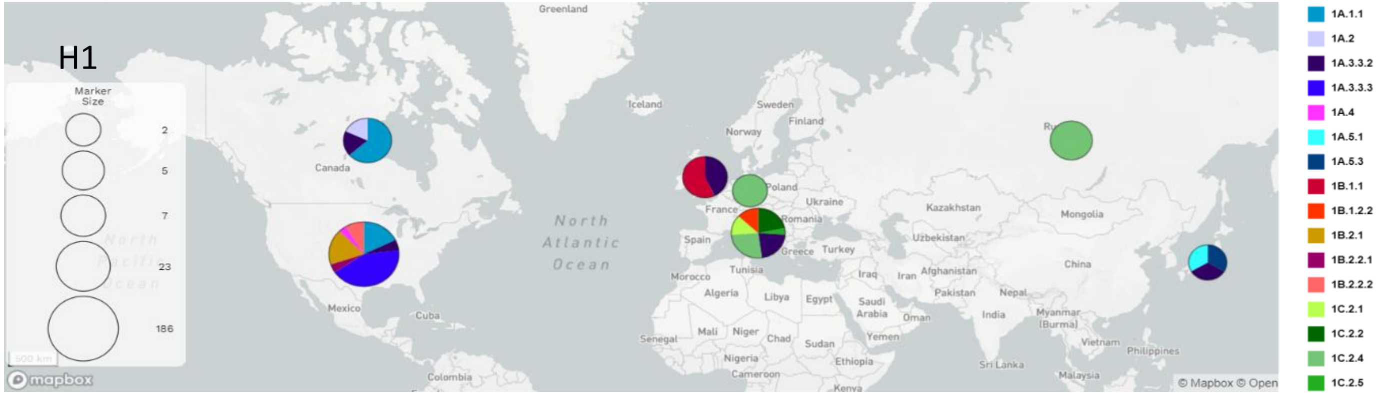


- Transmitted by airborne route in ferrets
- Low seroprevalence in human

An A/Henan/4-10/2022-like CVV is proposed

Influenza A(H1)v and A(H3)v

Influenza virus activity in swine

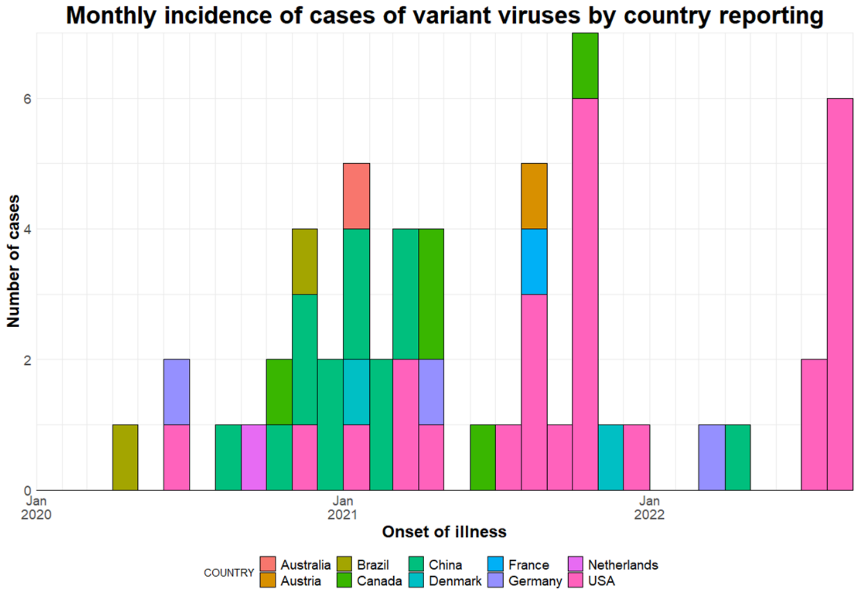


Recent A(H1)v and A(H3)v activity in humans

A(H1N1)v
China (clade 1C.2.3)
Germany (clade 1C.2.2)

A(H1N2)v
5 United States [clades 1B.2.1 (3), 1A.1.1 (1) and 1A.3.3.2 (1)]

A(H3N2)v
3 United States (clade 2010.1.)



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