Virological analyses for influenza virus infections in 2023/2024

Ruth Harvey, The Francis Crick Institute
EU/EEA respiratory virus network meeting, 12 June 2024

Global Circulation of influenza viruses

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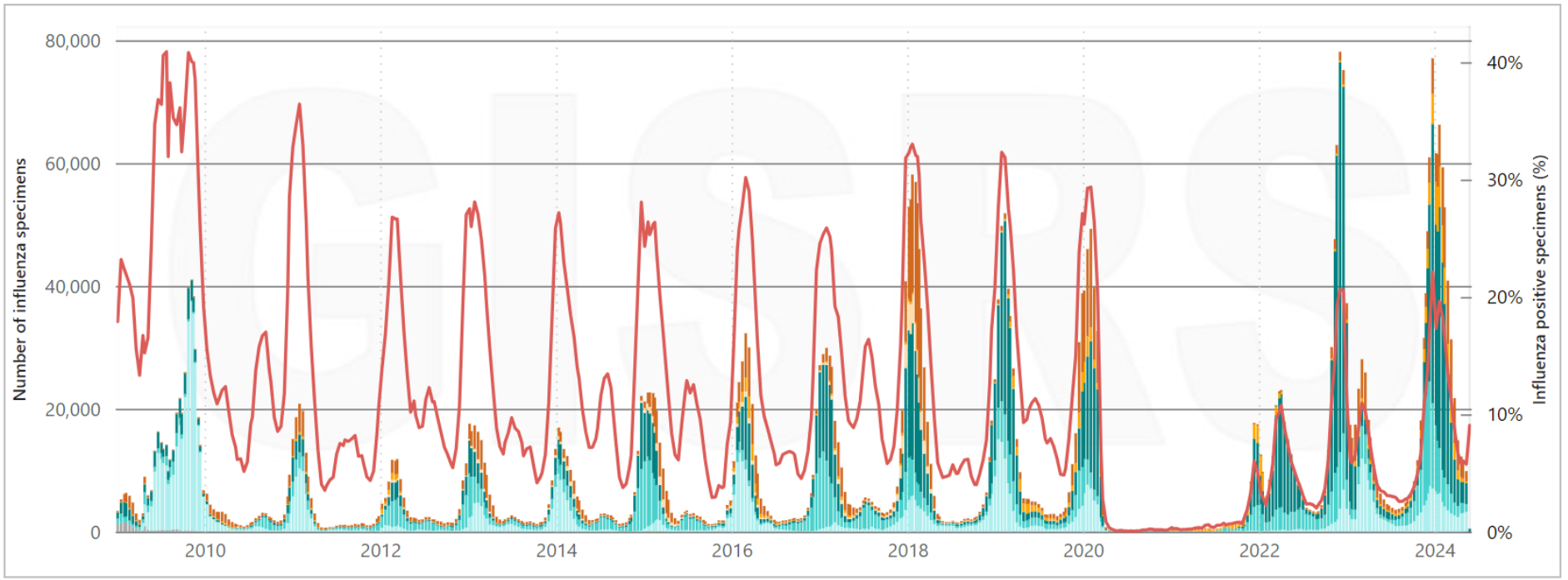

Influenza viruses genetically characterized by WHO CCs

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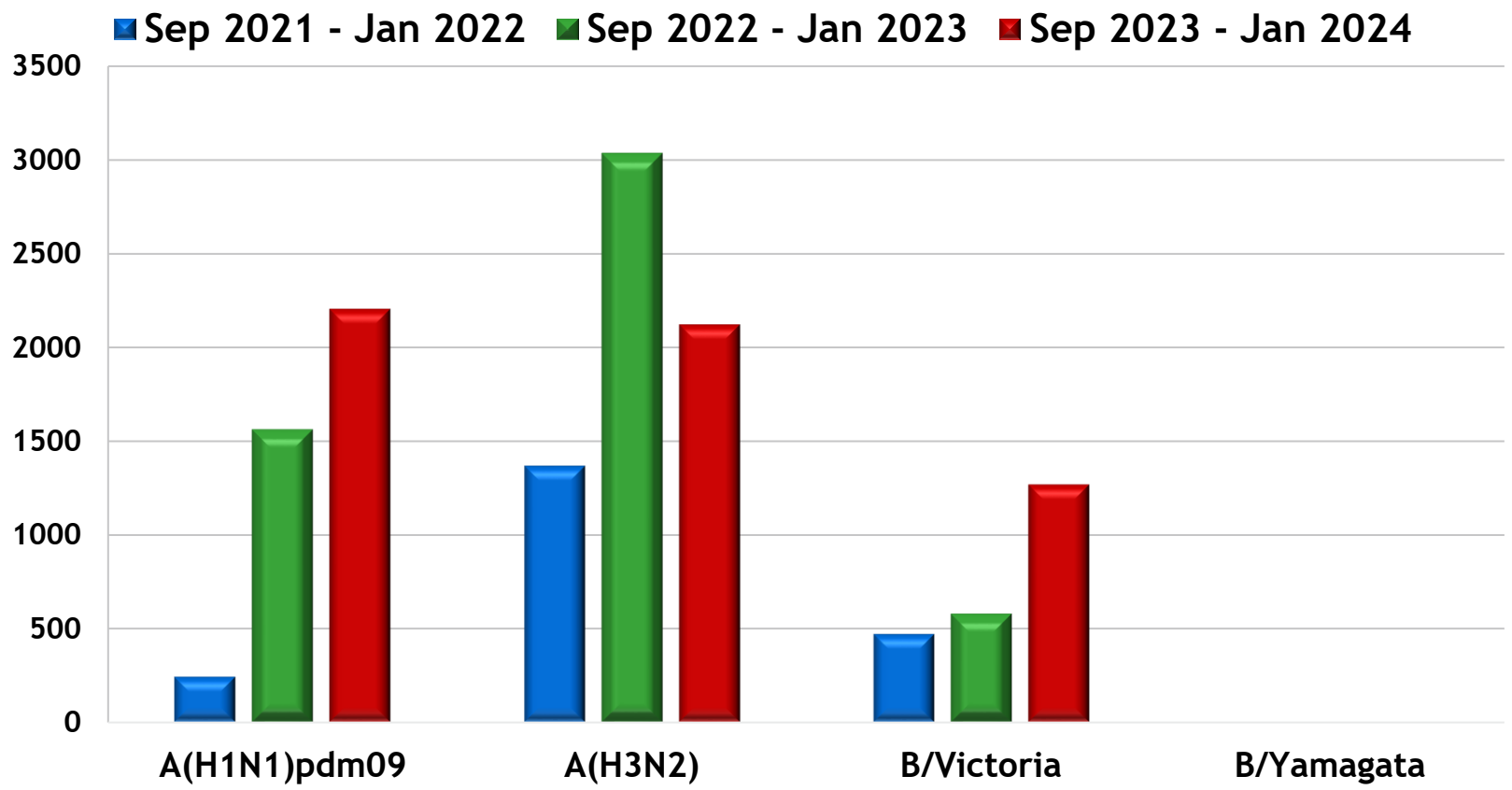

Total viruses antigenically characterized past 3 NH seasons

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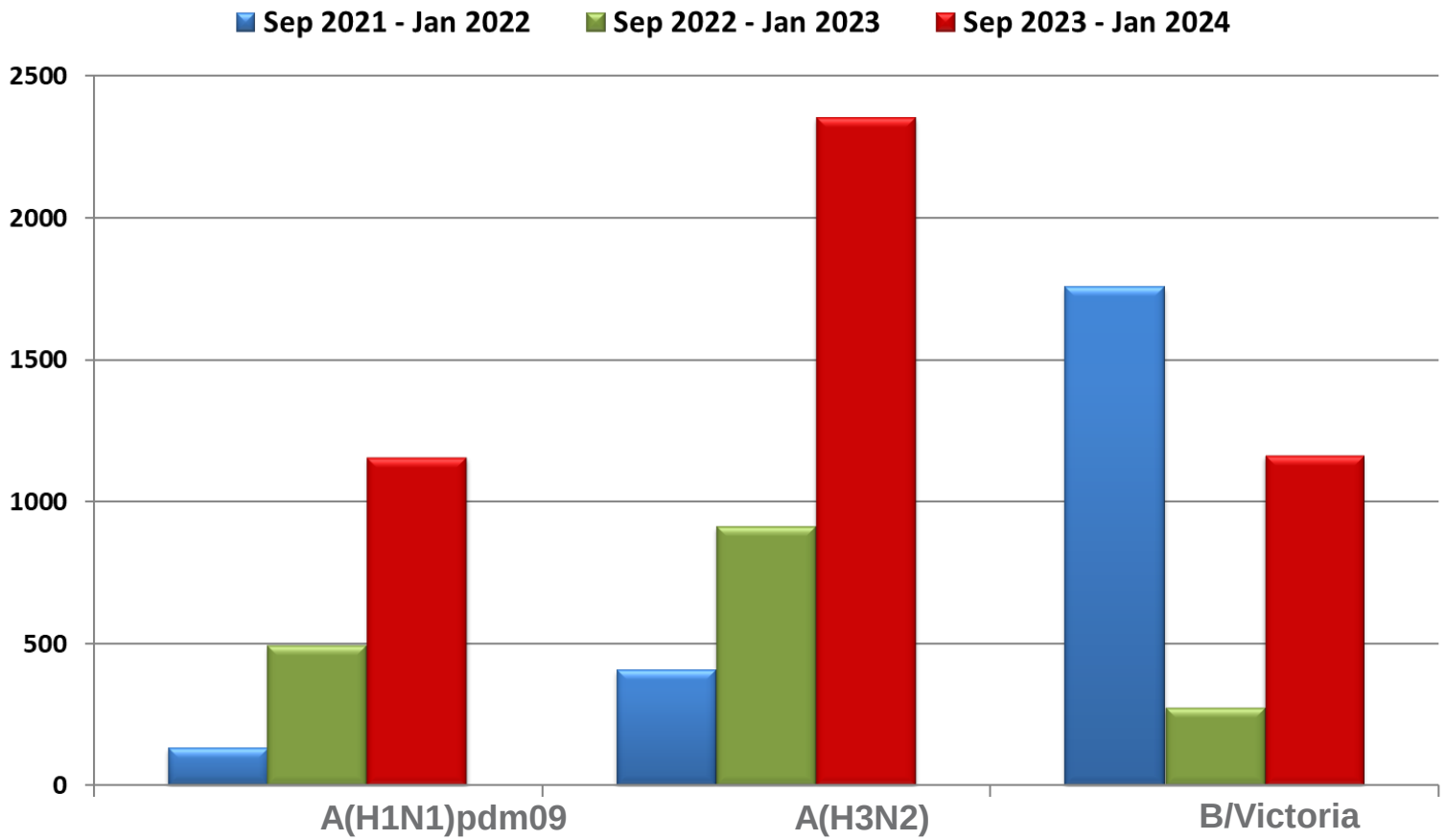

Influenza A(H1N1)pdm09 activity

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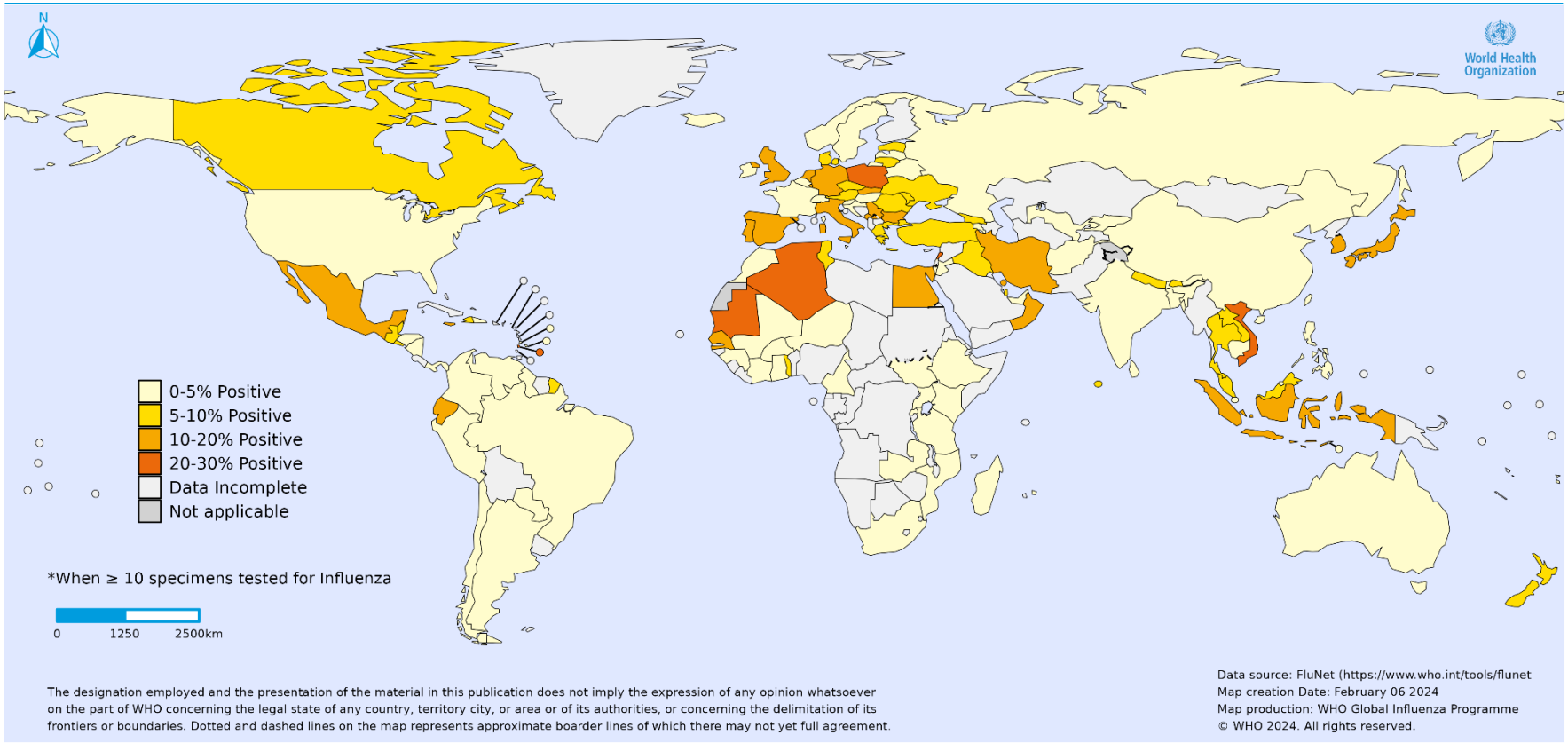

Colour intensity shows the percent of positive influenza A(H1N1) among all samples tested during this period per country

Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (6 February 2024)

Global A(H1N1)pdm09 Clade Subclade Distribution from 1 Sept 2023 to the present based on HA Sequence Availability

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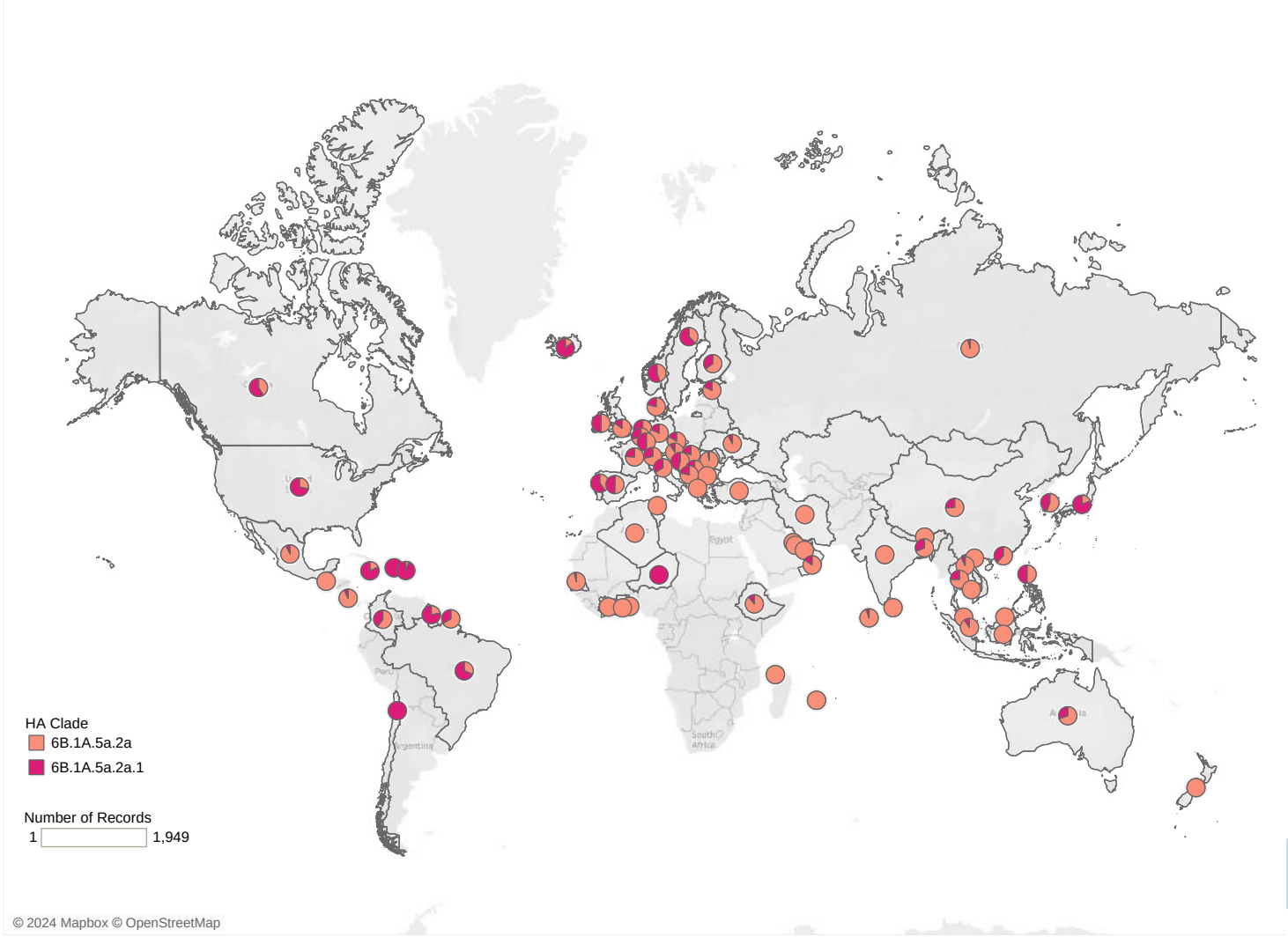

Based on HA sequence availability from GISAID EpiFlu™

Source: WHO CC CDC, USA

Influenza A(H3N2) activity

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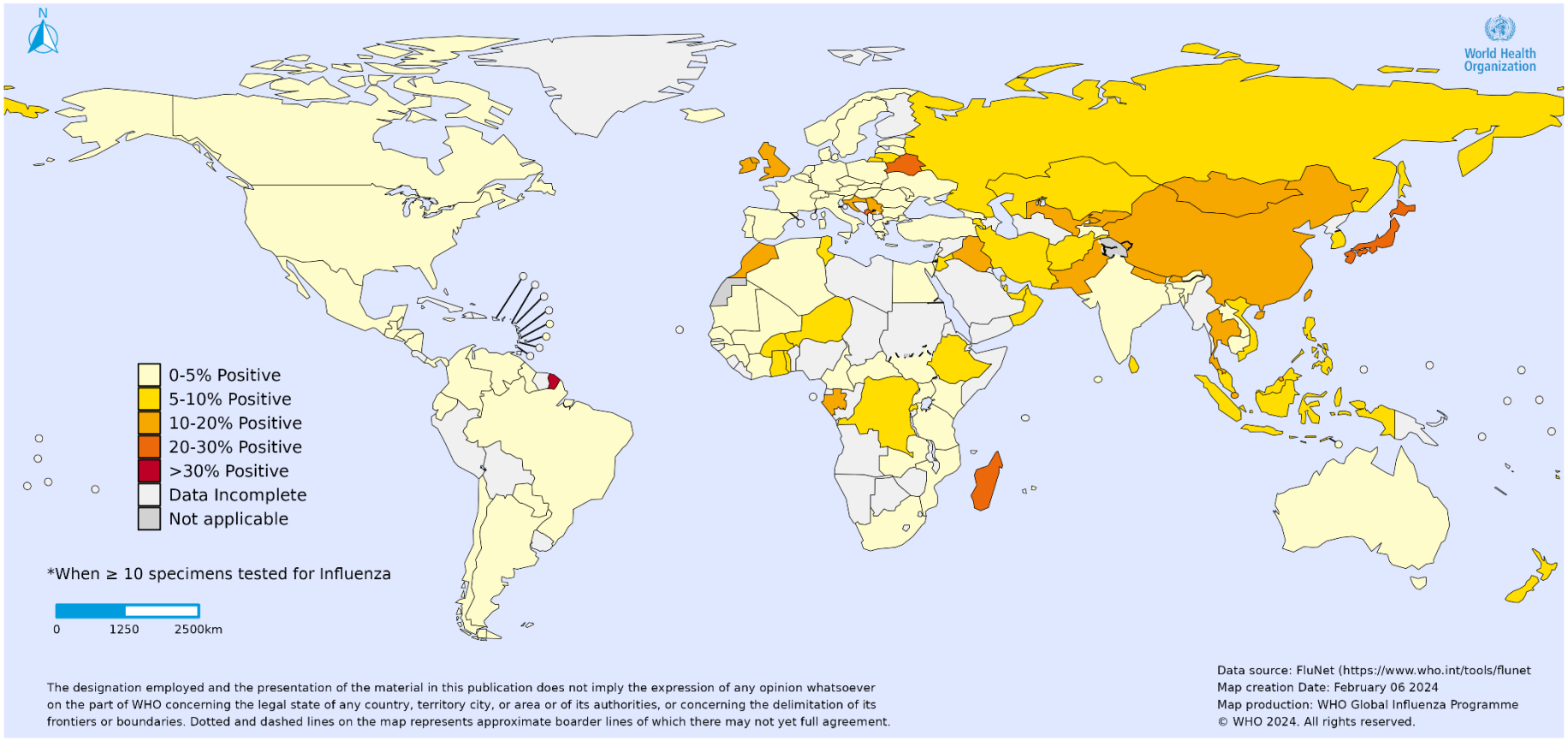

Colour intensity shows the percent of influenza A(H3N2) positive among all samples tested during this period per country

Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (6 February 2024)

Global circulation of A(H3N2) 3C HA Clade_subclade (since 1 Sep 2023) based on HA sequence availability

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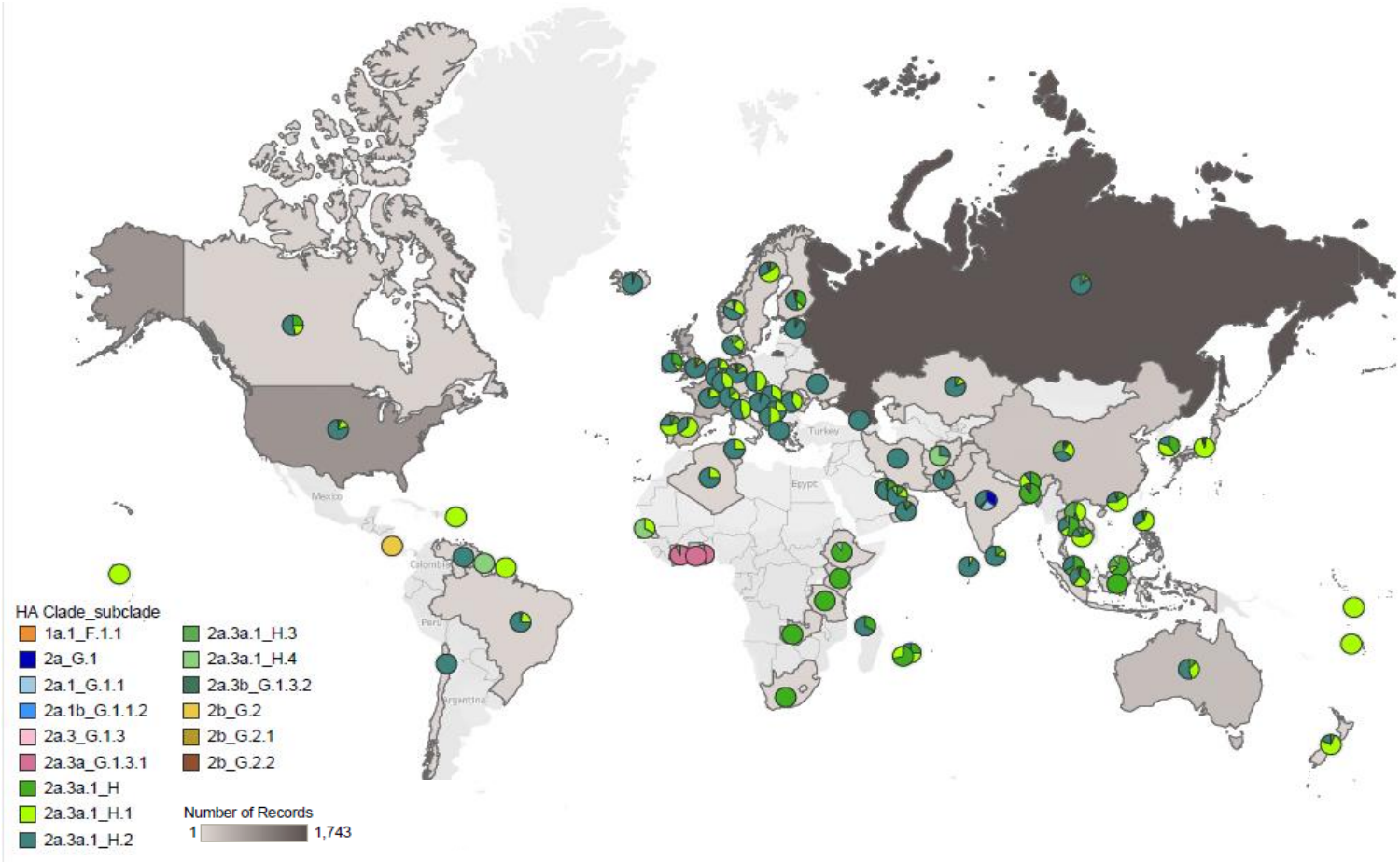

Source: WHO CC, Atlanta, USA, GISAID EpiFlu

Global A(H3N2) HA Clade subclade Diversity

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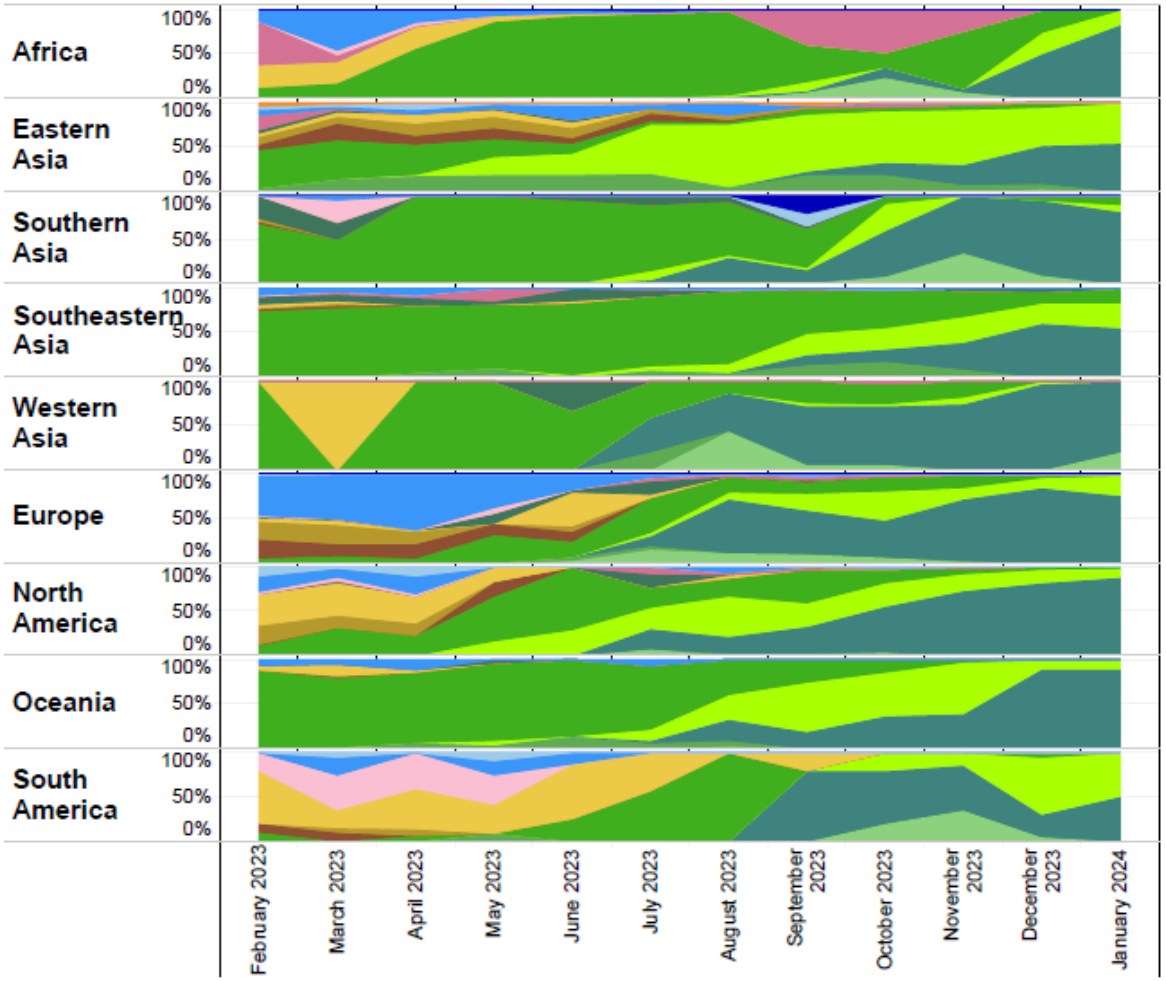

WHO CC CDC, USA

Influenza B virus activity

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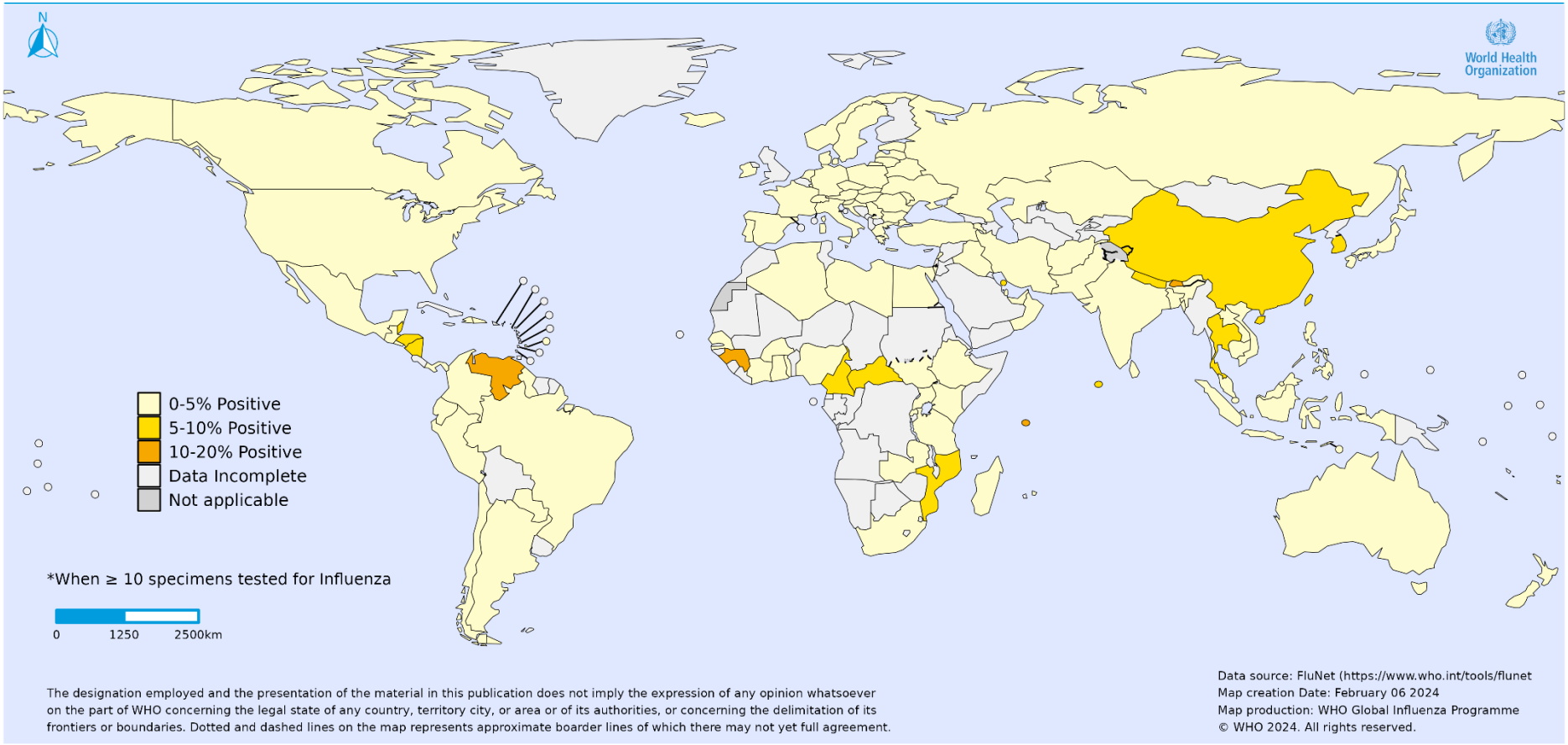

All B Victoria 3a.2

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 (18 Sep 2023)

WHO Vaccine Composition Meeting Recommendation

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Trivalent vaccines for use in the 2024-25 northern hemisphere influenza season contain the following:

- Egg-based vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;

- an A/Thailand/8/2022 (H3N2)-like virus; and

- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

- Cell culture- or recombinant-based vaccines

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;

- an A/Massachusetts/18/2022 (H3N2)-like virus; and

- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

B Yamagata

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- Further to the WHO September 2023 recommendation*, it remains the opinion of the WHO influenza vaccine composition advisory committee that the B/Yamagata lineage antigen should be excluded from influenza vaccines as it is no longer warranted.
- National or regional authorities should make decisions regarding the transition to trivalent influenza vaccines in their jurisdictions.
- Where quadrivalent vaccines are still used, the 4th component: the B/Yamagata lineage component remains unchanged from previous recommendations:
    - a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Lineage testing influenza B positive samples is important – as the B Yamagata lineage component is removed from vaccines, we need to be more vigilant to any potential cases.

* https://cdn.who.int/media/docs/default-source/influenza/who-influenza-recommendations/vcm-southern-hemisphere-recommendation-2024/202309_recommendation.pdf

Lessons learned: Is it an A(H3N2)v???

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- Friday afternoon, late January – we note a long branch length to 6 sequences from Europe in a routine HA tree. Start preliminary analyses
- CDC also notice and email the CC in London -> CC coordination
- Emailed the NICs but by this time late on Friday
- Saturday – continue analyses
- Sunday morning – phone call between WHOCC London and WHO GIP
- Sunday afternoon – TC among three CCs to discuss findings and next steps

Genotype 1

Genotype 2

Genotype 3

Genotype 4

Genotype 5 Seasonal

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•Routine trees showed sequences with long branches and several substitutions. Sequences showed good quality.

•Submitted by two labs (one a NIC, another a hospital lab with limited ex perience in NGS sequencing. Two different countries)

•Blast analysis placed them close to vaccine viruses from around 2004

•Subsequent feedback from sending labs revealed issues with pipeline whi ch used the reference sequence to fill regions of low depth during NGS assembly of some samples.

Lessons learnt: - quality check sequences by

a) running trees;
b) visually inspecting alignments ;
c) tip: check clade classification assigned by GISAID, if it comes up as "unassigned", double-check the sequence and assembly, consult with CC.

A/Wellington/1/2004-like
A/California/7/2004-like
A/Switzerland/8060/2017-like
A/Cambodia/e0826360/2020-like
A/Massachusetts/18/2022-like
A/Hong Kong/45/2018-like
Sequence Not Available