

# Influenza Updates

*The newsletter of the WHO Collaborating Centre for Reference and Research on Influenza in Melbourne*

 @WHOCCFluMelb

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## Recommendations for Northern Hemisphere 2026-2027 vaccine

The WHO Consultation on the Composition of Influenza Vaccines for the Northern Hemisphere 2026-2027 was announced in London, United Kingdom on 27 February 2026. The WHO made the following [recommendations](#):

For vaccines for use in the 2026-2027 northern hemisphere influenza season, WHO recommends the following:

### Egg-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1454/2025 (H3N2)-like virus; and
- a B/Tokyo/EIS13-175/2025 (B/Victoria lineage)-like virus.

### Cell culture-, recombinant protein- or nucleic acid-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1415/2025\_(H3N2)-like virus; and
- a B/Pennsylvania/14/2025 (B/Victoria lineage)-like virus.

## Contribution of National Influenza Centres to Influenza vaccines

We thank everyone who has sent us influenza samples prior to the WHO influenza vaccine Consultation in February 2025. Your viruses provided essential data on recently circulating strains and helped to inform the choice of recommended vaccine strains.

In this context, we would like to acknowledge the contribution and critical role played by WHO National Influenza Centres and other submitting laboratories in providing influenza samples and associated data to WHO Collaborating Centres, not only for the purposes of analysis and surveillance, but also for the provision of potential vaccine candidates. Please continue to send us your samples. The need for constant surveillance remains as influenza viruses continue to circulate and evolve.



WHO Collaborating Centre  
for Reference and  
Research on Influenza  
VIDRL



A joint venture between The University of Melbourne and The Royal Melbourne Hospital





## Preparation for the upcoming influenza season

Table: Timing and desired virus specimens in shipments

TYPE OF INFLUENZA SEASONALITY	Hemisphere Vaccine Composition Consultation	WHAT TO SHIP*	When to ship
Defined Single peak	Northern (February)	specimens collected <b>from 1st September</b> onwards	DECEMBER – MID JANUARY <i>specimens must reach WHO CC no later than mid-January</i>
	Southern (September)	specimens collected <b>from 1st February</b> onwards	JULY – MID AUGUST <i>specimens must reach WHO CC no later than mid-August</i>
Not defined – possibly >1 peak or year-round activity	Northern (February) <b>OR</b>	specimens from the <b>PERIODS OF PEAK ACTIVITY</b>	DECEMBER – MID JANUARY
	Southern (September)	specimens from the <b>PERIODS OF PEAK ACTIVITY</b>	JULY – MID AUGUST
<b>OTHER SITUATIONS</b>			
In situations, when more shipments are required using the WHO SFP	contact GIP at <a href="mailto:gisrs@who.int">gisrs@who.int</a> or Christian Fuster at <a href="mailto:fusterc@who.int">fusterc@who.int</a> to discuss shipping support. Requests will be managed <b>on a case-by-case basis</b> .		
<b>un-subtypeable influenza viruses detected,, zoonotic influenza or unusual influenza activity observed</b>	contact GIP immediately at <a href="mailto:gisrs@who.int">gisrs@who.int</a> or Christian Fuster at <a href="mailto:fusterc@who.int">fusterc@who.int</a> (telephone for emergency: + 41 79 4755576)		

\* For maximal utility and to capture current evolution across type/subtype the shipment should be dispatched as soon as a sufficient representative number (10 per subtype) of clinical specimens/isolates are available (ideally no more than 40 samples should be included per shipment, with paired clinical plus isolate counting as one sample). The criteria for selection of specimens to send to a WHO CC are described in the WHO Operational Guidance for Sharing Seasonal Influenza Viruses. Please note that aliquots of the same specimens or viruses should not be sent to multiple WHO CCs. **Shipments that do not comply with these requirements will not be accepted.**



## Shipping instructions

### 1. Shipments supported by the WHO Shipping Fund Project:

A, Eligibility for shipment support is based on [World Bank income classification](#) and applies during the recommended surveillance period (see table at the end of this message), as follows:

- i. **Low- and lower-middle-income countries**, are eligible for **up to four shipments** per calendar year.
- ii. **Upper middle-income countries** are eligible for **up to two shipments** (see *point d for additional information*) per calendar year.
- iii. **High-income countries** are eligible for **one shipment** (see *point d for additional information*) per calendar year.

B. **Shipments may be re-routed** when necessary to optimize costs and support efficient GISRS operations.

C. In exceptional circumstances where additional shipments are required, including but not limited to:

- viruses yielding lower-than-expected titres in haemagglutination inhibition testing with WHO reference reagents or influenza-specific sheep or ferret antisera;
  - influenza A-positive specimens that cannot be subtyped;
  - clinical specimens or virus isolates from severe cases or unusual outbreaks; or
  - antiviral-resistant viruses identified in unexposed individuals
- laboratories should contact GIP without delay to facilitate shipment in such situations.

D. Laboratories in **high-income and upper-middle-income countries** are encouraged to explore alternative funding sources, such as support from their own institutions, recipient institutions, national authorities, governments, donor agencies, or other relevant partners, to cover **additional** shipments. ***If, after exploring those options, a laboratory is unable to secure funding for a shipment, it may contact GIP, using the contact details provided below, to explore possible solutions for facilitating up to four shipments a year to a WHO CC.***

In line with previous communications on this matter, this serves as a **reiterated call** for laboratories in these countries to **proactively begin mobilizing** domestic or alternative resources to cover shipment costs from 2028 onwards. Early planning is essential, as SFP support **may be considerably reduced**, and timely preparation will help ensure the smooth function of core GISRS activities.

### 2. Sample selection and timing:

A. Laboratories are encouraged to ensure the timely submission of high-quality, epidemiologically relevant and representative influenza A and B specimens to support timely characterization ahead of each WHO consultation on the composition of influenza virus vaccines (VCM).

B. **A total of no more than 40 samples per shipment** is recommended (clinical specimen and virus isolate pairs count as one sample) across the three subtypes – A(H1N1), A(H3N2), and B. *Laboratories should confirm the maximum number of samples accepted with the receiving WHO CC prior to shipment.*

### 3. Shipments to WHO CC at the United States Centers for Disease Control and Prevention (CDC), Atlanta:

For shipments to WHO CC at CDC Atlanta, laboratories may contact CDC directly for financial and logistical support. CDC may support up to **four shipments per year** from a NIC/NIL. To initiate shipping arrangements, please contact: [InfluenzaVirusSurveillance@cdc.gov](mailto:InfluenzaVirusSurveillance@cdc.gov)

### 4. Countries with more than one NIC:

Under the WHO Shipping Fund Project, shipments from one laboratory per country are supported. In countries with multiple NICs or NIC-affiliated (authorized) laboratories, laboratories are expected to coordinate and agree on which institution will receive WHO Shipping Fund Project support. The remaining laboratories are encouraged to either secure alternative funding or consolidate specimens into a single eligible shipment.

If you have questions or need additional information or assistance, or have an urgent situation and require help, please contact GIP at [fuster@who.int](mailto:fuster@who.int) (Christian Fuster; telephone for emergency: + 41 79 4755576) or [gisrs@who.int](mailto:gisrs@who.int)



## Featured Publications

**Dong, X., Edwards, S., Deng, Y. M., Dapat, C., Hirankitti, A., & Barr, I. G.** (2026). Sequencing RSV Whole Genome Using a Long Amplicon-Based Method with Oxford Nanopore Technologies. *Methods in molecular biology* (Clifton, N.J.), 3003, 149–163. [https://doi.org/10.1007/978-1-0716-5060-8\\_11](https://doi.org/10.1007/978-1-0716-5060-8_11)

**Fox, A., Alafaci, A., Carolan, L., Burrell, R., Sánchez-Ovando, S., Hadiprodjo, A. J., McMinn, A., Macartney, K., León, A. N., Ward, A. B., Wheatley, A., Sullivan, S. G., Crawford, N. W., Britton, P. N., & Subbarao, K.** (2026). Influenza vaccine responses differ between young children previously exposed to influenza antigens via infection versus vaccination. *Communications Medicine*, 10.1038/s43856-026-01610-w. Advance online publication. <https://doi.org/10.1038/s43856-026-01610-w>

## Upcoming conferences



Concessionary LMIC rates are available for a resident of a Low and Middle Income Country

For more information follow: [Options XIII Conference for the Control of Influenza - ISRV](#)

## Recent Grant

A research team from the Centre has been awarded a new collaborative grant of EUR 2,499,882 from The Novo Nordisk Foundation to continue the further preclinical development of a novel long-acting pan-influenza antiviral drug. Read more about it [here](#):





## Recent activities at the Centre (1 January — 30 April 2026)

Below is a summary of surveillance activities at the Centre during this current reporting period. We anticipate that the next few months will be an increasingly busy time for the Centre, as the Southern Hemisphere influenza season commences.

**Samples received:** The Centre received **2234** influenza samples from the laboratories and institutions listed below during the period 1 January—30 April 2026.

**AUSTRALIA:** Canberra Hospital, ICPMR Westmead, The Children's Hospital at Westmead (CHW), Royal Darwin Hospital, Pathology Queensland, Princess Alexandra hospital, (PEHRL) - Pathology Queensland, Queensland Children's Hospital, SA Pathology, Hobart pathology, Australian Clinical Labs (ACL), Alfred Hospital, Austin pathology, Monash Medical centre, Royal Children's Hospital, Royal Melbourne Hospital, Victorian Infectious Diseases Reference Laboratory (VIDRL), Pathwest Laboratory Medicine (QEII)

**CAMBODIA:** Institut Pasteur du Cambodge

**INDIA:** National Institute of Virology

**INDONESIA:** National Health Biology Laboratory

**NEPAL:** National Public Health Laboratory

**NEW CALEDONIA:** Centre Hospitalier De Nouvelle Caledonie

**PAPUA NEW GUINEA:** Institute of Medical Research

**SAMOA:** Tupua Tamases Meaole Hospital

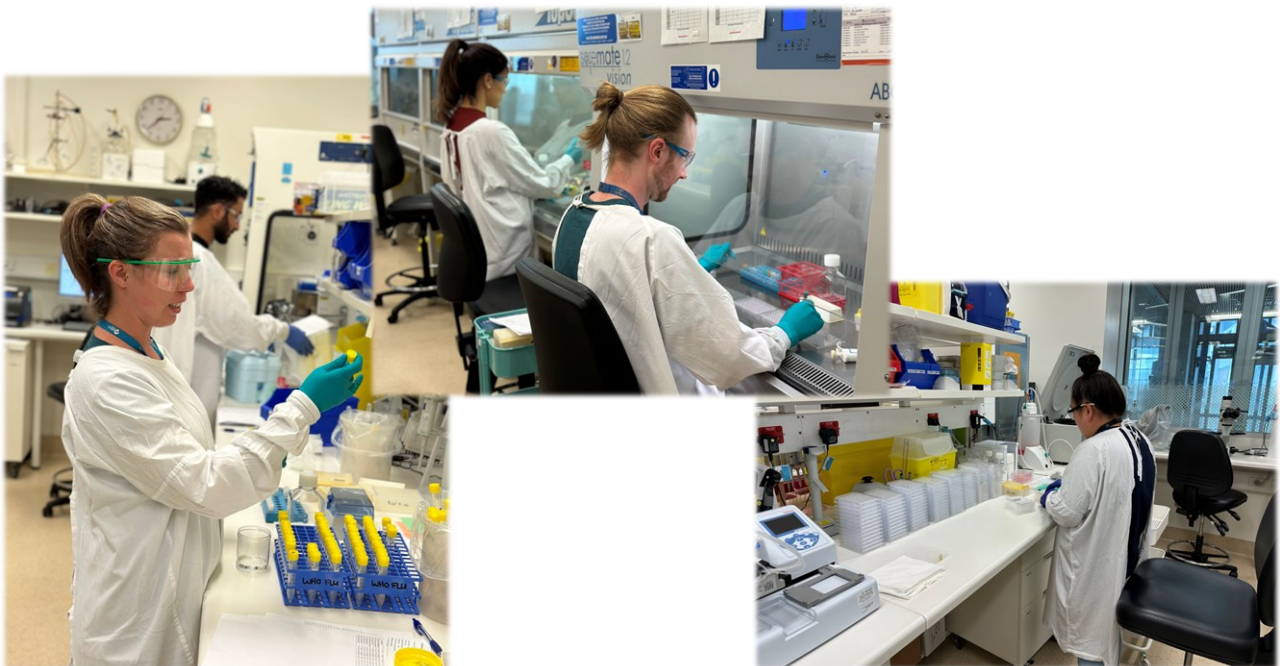
**SINGAPORE:** National Public Health Laboratory

**SRI LANKA:** Medical Research Institute

**TIMOR-LESTE:** Laboratorio Nacional Da Saude

### Isolation of viruses in eggs:

The Centre undertakes primary isolation of selected viruses in eggs to obtain potential vaccine strains. From 1 January to 30 April 2026, 3 A(H3N2) and 1 viruses A(H1N1) were successfully isolated in eggs at the Centre.





## Recent activities at the Centre (1 January — 30 April 2026) continued

### Antigenic analysis

1015 viruses analysed by haemagglutination inhibition (HI) assay

### Antiviral drug susceptibility

476 viruses analysed by neuraminidase inhibition (NAI) assay

### Sequencing

767 viruses analysed  
767 HA genes  
767 NA genes  
725 MP genes  
71 NS genes

Country of submitting laboratory	No. of viruses analysed by HI assay*			No. of viruses tested by NAI assay*			No. of viruses sequenced by NGS (ONT or Illumina)		
	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria	A(H1N1)pdm09	A(H3N2)	B/Victoria
Australia	58	574	45	20	124	10	44	542	21
Cambodia	6	30	11	6	30	11	6	12	11
India	1	8	1	1	8	1			
Indonesia	9	3	2	1	2	2	4	3	2
Nepal	1	10	3	1	10	3	1	10	3
New Caledonia	2	87	10	2	87	10	2	48	10
Papua New Guinea	0	41	0	0	41	0	0	22	0
Singapore	20	42	16	19	41	16			
Sri Lanka	0	26	3	0	26	3	0	21	3
Timor-Leste	0	3	3	0	1	0	0	1	1
<b>Total</b>	<b>97</b>	<b>824</b>	<b>94</b>	<b>50</b>	<b>370</b>	<b>56</b>	<b>57</b>	<b>659</b>	<b>51</b>

\*Subtypes and lineages are based on analysis of HA and in some cases confirmed by genetic analysis of NA.



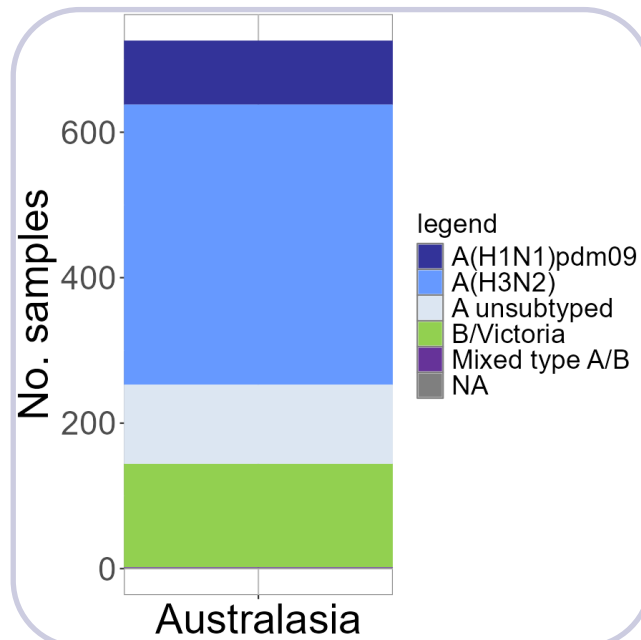
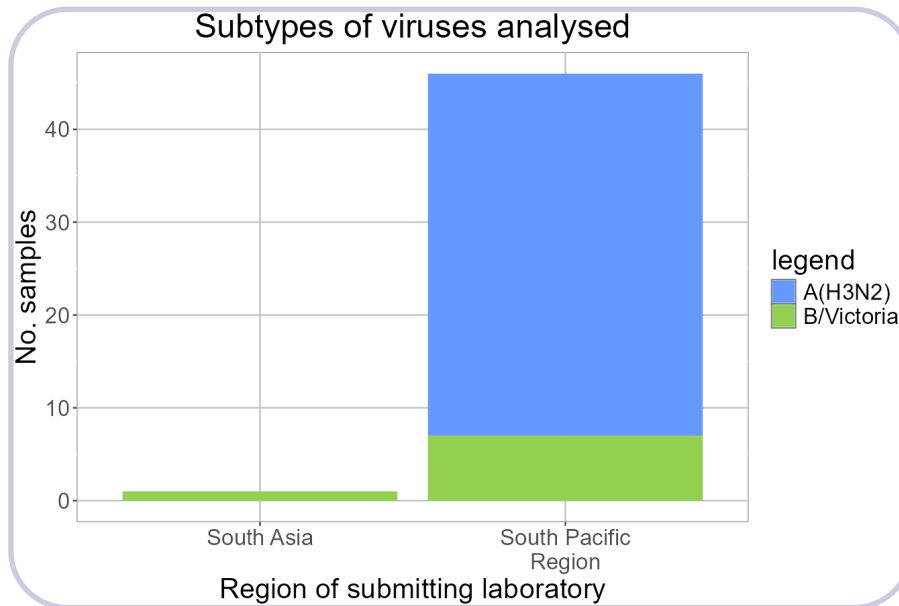
## Surveillance update: Virus activity 1 January—30 April 2026

The data below are results for viruses collected or sampled between 1 January and 30 April 2026 that have been analysed at the Centre as of 6 May 2026.

### Virus types/subtypes<sup>†</sup>

The type and subtype/lineage of 754 viruses have been determined.

9.8% A(H1N1)pdm09  
54.8% A(H3N2)  
18.7% B/Victoria  
16.7% A untyped



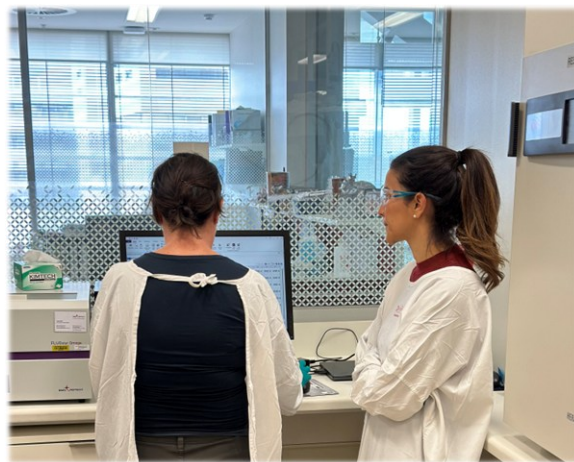
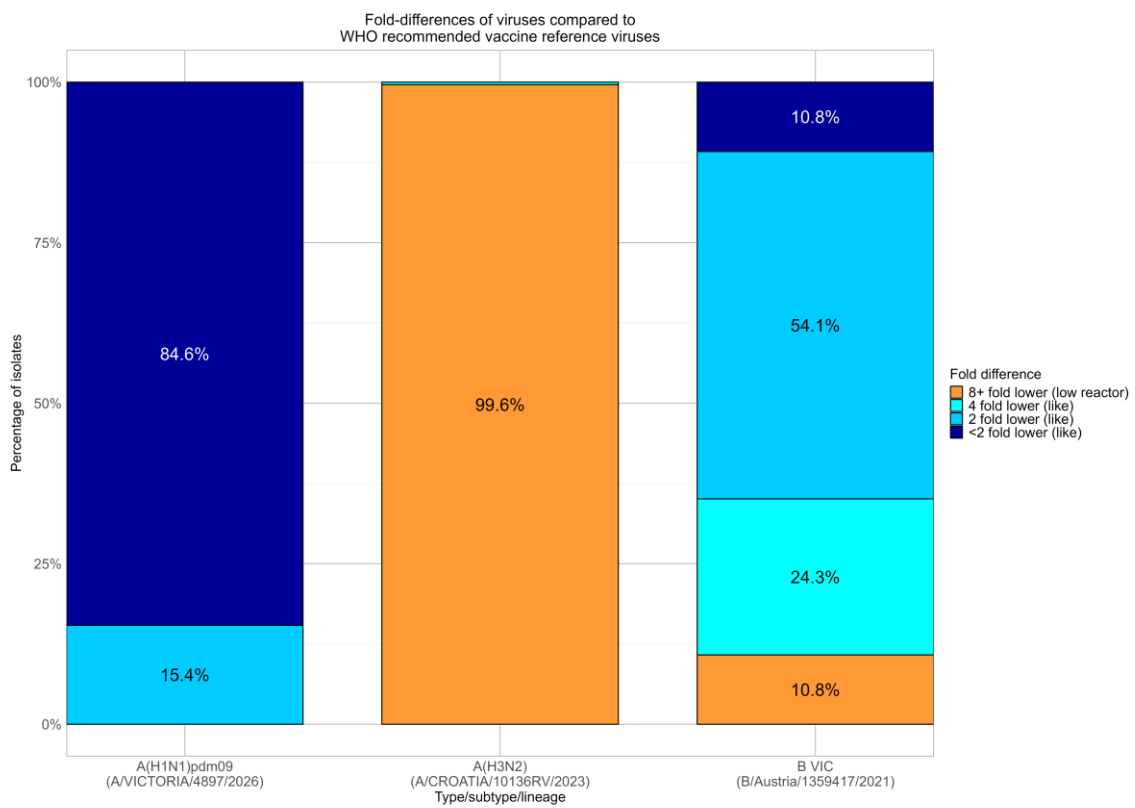
<sup>†</sup> Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.



### Antigenic analysis\*

A total of 1015 viruses were tested using the haemagglutination inhibition (HI) assay.

Viruses were identified as low-reactors if their titre against reference antiserum was at least 8-fold lower than the titre of the reference virus. All A(H1N1)pdm09 viruses were antigenically similar to their respective reference strains. A small proportion (10.8%) of B Victoria viruses were low reactors to the reference strain B/Austria/1359417/2021. Almost all (99.6%) A(H3N2) viruses were low reactors to the reference strain A/Croatia/10136RV/2023.



\*Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.



# Surveillance update (continued): Virus activity 1 January—30 April 2026

**Genetic analysis:**  
**Focus on B/Victoria**  
Sequencing of the haemagglutinin (HA) gene

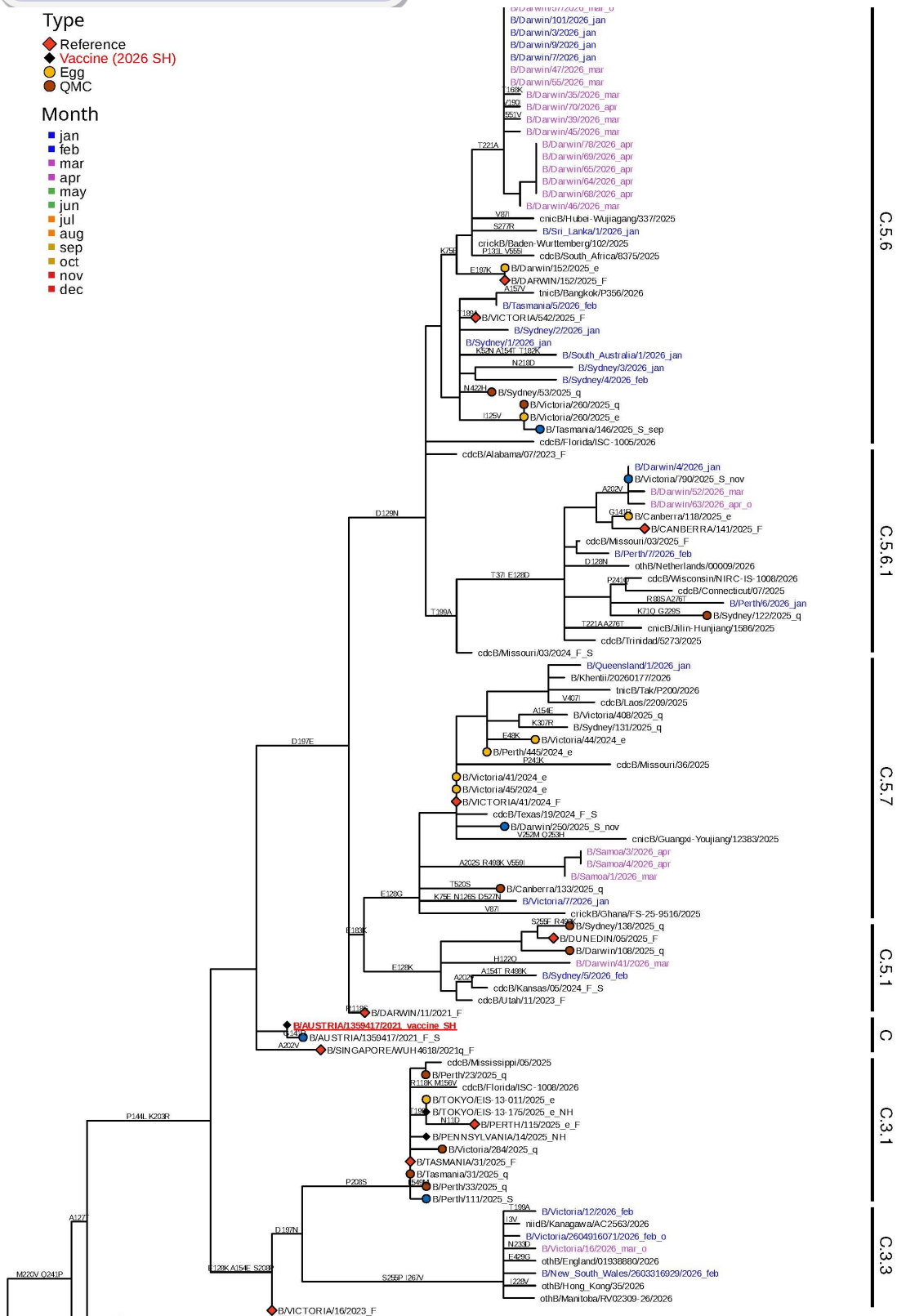
Phylogenetic analysis shows the majority of recent B/Victoria viruses belong to subclade C.5.6.

### Type

- ◆ Reference
- ◆ Vaccine (2026 SH)
- Egg
- QMC

### Month

- jan
- feb
- mar
- apr
- may
- jun
- jul
- aug
- sep
- oct
- nov
- dec





**Antiviral drug susceptibility testing:  
192 viruses tested by neuraminidase inhibition (NAI) assay**

Testing for susceptibility to the antiviral drugs oseltamivir (Tamiflu), zanamivir (Relenza), peramivir, and laninamivir showed that no virus had highly reduced inhibition by one or more of these neuraminidase inhibitors (NAI).

Type/subtype/ lineage	Oseltamivir			Peramivir			Laninamivir			Zanamivir		
	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition	Normal inhibition	Reduced inhibition	Highly reduced Inhibition
A(H1N1) pdm09	19	0	0	19	0	0	19	0	0	19	0	0
A(H3N2)	162	0	0	162	0	0	162	0	0	162	0	0
B/Victoria	11	0	0	11	0	0	11	0	0	11	0	0
<b>Total</b>	<b>192</b>	<b>0</b>	<b>0</b>	<b>192</b>	<b>0</b>	<b>0</b>	<b>192</b>	<b>0</b>	<b>0</b>	<b>192</b>	<b>0</b>	<b>0</b>

Viruses with reduced inhibition by antiviral drugs in the NAI assay undergo genetic analysis of the neuraminidase gene to detect mutations associated with the functional change. The relationship between reduced inhibition and the clinical effectiveness of a neuraminidase inhibitor is not well understood. Further studies would be required to determine whether a virus with reduced inhibition in the NAI assay is clinically resistant.

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