

Influenza Updates

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

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News and Events

Thank you and happy holidays

As the year draws to a close we would like to thank all of the laboratories who have sent us influenza samples during 2014. It has been a busy year and we have been pleased to have received and processed over 5000 samples this year. We wish you all the best for the holiday season and look forward to working with you again in 2015.

WHO continues funding for shipping samples

WHO GISRS has announced the continuation of the WHO Shipping Fund Project (SFP), which covers the cost of shipping samples by National Influenza Laboratories to WHO Collaborating Centres. Of especial note, the new funding allows for an increased number (up to 3) of shipments per laboratory each year. Please contact us at whoflu@influenzacentre.org if you have any questions about shipping samples.

Shipments financially supported by the SFP:

1. All countries can send a maximum of three shipments per year of surveillance (September to August for the Southern Hemisphere or February to January for the Northern Hemisphere). The recommended timing of the three shipments is as follows: one between the end of December to mid-January, and one between the end of June and mid-August, to support the WHO vaccine composition recommendation-making for each hemisphere; the third shipment can be used at your own judgement.
2. Low and lower-middle income countries can be supported by the SFP for one extra shipment per year of surveillance, i.e. a maximum of four shipments per year of surveillance. The list of low and lower-middle income countries can be found at the World Bank website at: http://data.worldbank.org/about/country-classifications/country-and-lending-groups#Low_income.
3. In unusual situations, when more shipments are required, the laboratory can contact the WHO GISRS team at gisrs-who@who.int or Christian Fuster at fuster@who.int. This will be managed on a case-by-case basis.

Visitors to the Centre



Ms Nurwendy Ashikin Abdullah Lim (left) and Ms Mazmah Ahmad Morshidi (right) from the Biomedical Science Research Unit, Bandar Seri Begawan, Brunei, visited the Centre 6-17 October 2014. They undertook training in serology, molecular biology, rapid tests and influenza surveillance techniques.



Ms Pham Thi Thu Hang (left), from the National Institute of Hygiene and Epidemiology, Hanoi, Vietnam, and Ms Nguyen Thu Ngoc (right), from the Pasteur Institute, Ho Chi Minh City, Vietnam, visited the Centre for training in high throughput HI assays and microneutralisation assays, 2-12 December 2014.



Australian Influenza Symposium

The 10th Australian Influenza Symposium was held at the Peter Doherty Institute for Infection and Immunity on 12-13 November 2014 and was attended by over 220 delegates from Australia, the USA, Hong Kong, Singapore and Cambodia. Attendees enjoyed a wide variety of talks and a lively panel discussion about mandatory influenza vaccination for health care workers. First-time visitors to the Doherty Institute also had an opportunity to see the Institute's facilities and tour the Centre's new laboratories.

If you would like to stay informed about the 11th Australian Influenza Symposium in 2015 please email us at symposium@influenzacentre.org.



Publication in *Science*

Staff members from the Centre were co-authors with collaborators in the United Kingdom, the Netherlands and Vietnam on a paper recently published in the journal *Science*. The publication describes the use of antibody landscapes to develop immune system profiles of individuals previously exposed to influenza and how this analysis could be applied to improve influenza vaccine selection processes and hence increase influenza vaccine effectiveness.

Fonville JM, Wilks SH, James SL, Fox A, Ventresca M, **Aban M**, **Xue L**, Jones TC, Le NMH, Pham QT, Tran ND, Wong Y, Mosterin A, Katzelnick LC, Labonte D, Le TT, van der Net G, Skepner E, Russell CA, Kaplan TD, Rimmelzwaan GF, Masurel N, de Jong JC, Palache A, Beyer WEP, Le QM, Nguyen TH, Wertheim HFL, **Hurt AC**, Osterhaus ADME, **Barr IG**, Fouchier RAM, Horby PW and Smith DJ. Antibody landscapes after influenza virus infection or vaccination. *Science*. 2014 Nov 21; 346(6212):996-1000. doi: 10.1126/ science.1256427. PubMed link: <http://www.ncbi.nlm.nih.gov/pubmed/?term=25414313>

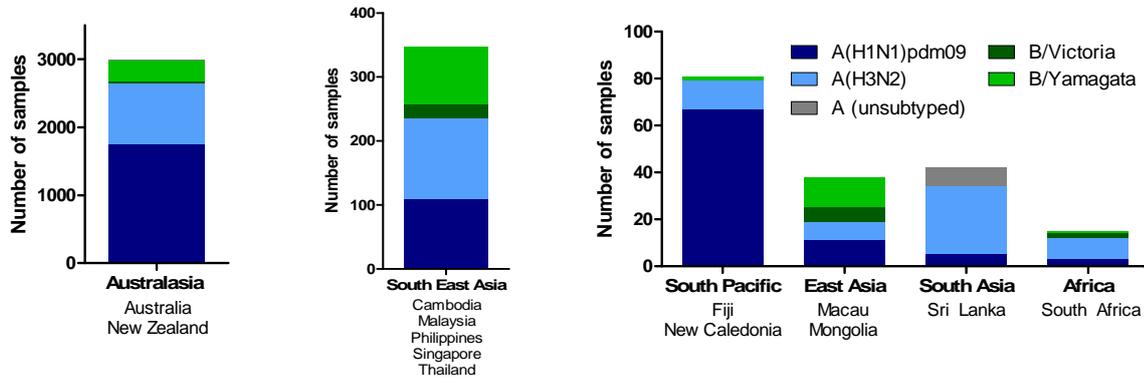


Surveillance update: Virus activity 1 January–31 October

The data below are results for viruses collected between 1 January and 31 October 2014 that have been analysed at the Centre as of 9 December 2014.

Virus types/subtypes[†]

The type and subtype/lineage of 3507 viruses have been determined. The predominant type/subtype amongst viruses analysed to date is A(H1N1)pdm09 (55.3%); however, A(H3N2) remains prominent in some countries.

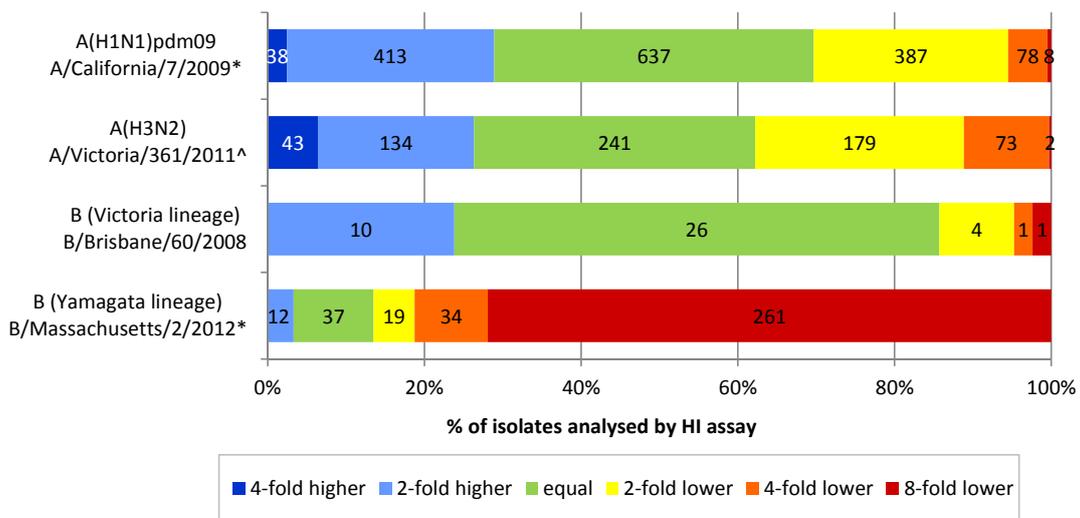


[†] Subtypes and lineages are based on analysis of the HA and in some cases confirmed by genetic analysis of NA.

Antigenic analysis

Haemagglutination inhibition (HI) assays indicate that most A(H1N1)pdm09, A(H3N2) and B/Victoria isolates are antigenically similar to the 2014-2015 Northern Hemisphere vaccine strains. A large proportion of B/Yamagata isolates are low reactors to B/Massachusetts/2/2012. Detection of low reactors with specific antisera may be due to several different factors, so further analyses are performed to determine whether antigenic drift has occurred.

Note about A(H3N2): Evolutionary changes in A(H3N2) viruses have made it difficult to detect recent antigenic change using HI assays. Some laboratories have detected antigenic changes in recent viruses using HI assays that incorporate oseltamivir carboxylate. This was not done at the Centre and hence little antigenic change has been observed in our analyses. The change in recommended vaccine strain at the most recent WHO Consultation on the Composition of Influenza Virus Vaccines was based on antigenic and genetic data (see page 4, Genetic Analysis) collated from all WHO Collaborating Centres.



* indicates strains included in the 2014-2015 Northern Hemisphere WHO vaccine recommendation.

[^] A/Texas/50/2012, which is included in the 2014-2015 Northern Hemisphere WHO vaccine recommendation, is an A/Victoria/361/2011-like virus.



Surveillance update: Virus activity 1 January–31 October 2014 (continued)

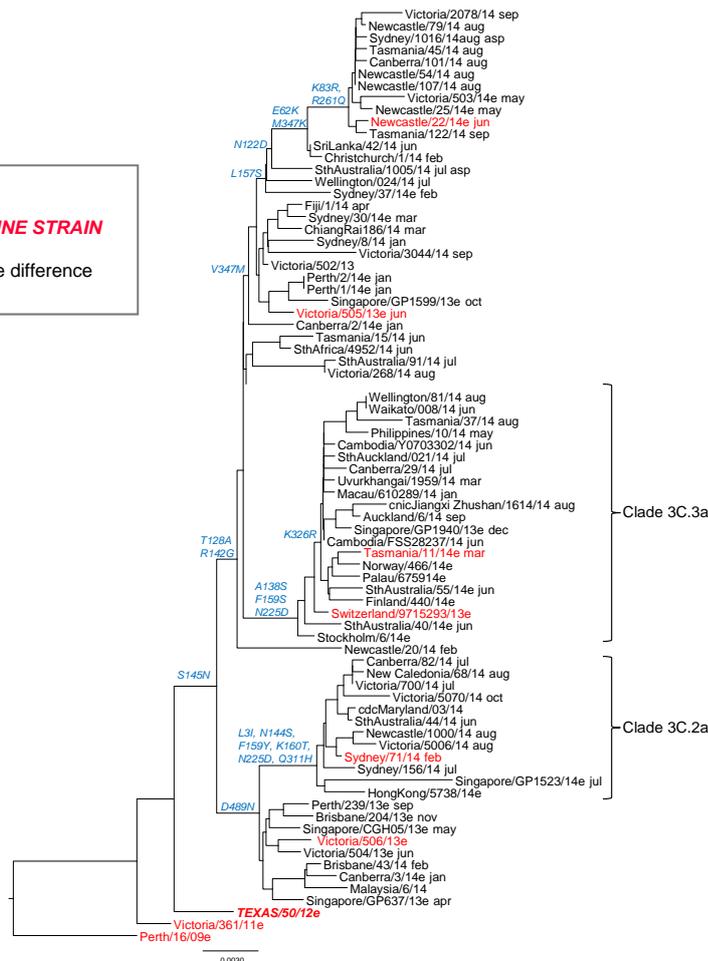
The data presented are for viruses collected between 1 January and 31 October 2014 that have been analysed at the Centre as of 9 December 2014.

Genetic analysis: focus on A(H3N2)

Sequencing and phylogenetic analysis of haemagglutinin (HA) genes indicate that viruses circulating during January–October 2014 have undergone genetic change compared to A/Texas/50/2012, consistent with the antigenic and genetic changes observed by other WHO Collaborating Centres and warranting a change in recommended vaccine strain. The antigenic variants fall into clades 3C.2a and 3C.3a — viruses from these clades are genetically distinct but antigenically indistinguishable from each other. The new recommended vaccine strain, A/Switzerland/9715293/2013, is in clade 3C.3a.

Legend

Reference strains
NORTHERN HEMISPHERE 2014-2015 VACCINE STRAIN
Changes in amino acid sequence
 Scale bar represents 0.3% nucleotide sequence difference between viruses



Neuraminidase inhibitor susceptibility

Viral isolates are routinely tested for their susceptibility to the antiviral drugs oseltamivir (Tamiflu), zanamivir (Relenza), peramivir and laninamivir using the neuraminidase inhibition (NAI) assay. Of 2826 viruses tested, only a small number showed highly reduced inhibition by the neuraminidase inhibitors.

Viruses that demonstrate reduced inhibition by antiviral drugs in the NAI assay undergo genetic analysis of the neuraminidase gene to detect known or novel 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.

Type/subtype	A(H1N1) pdm09	A(H3N2)	B/Victoria	B/Yamagata
No. viruses tested	1599	760	51	416
Number of viruses with highly reduced inhibition				
Oseltamivir	6 (0.4%)	0	1 (2.0%)	0
Peramivir	5 (0.3%)	0	2 (3.9%)	2 (0.5%)
Zanamivir	0	0	1 (2.0%)	0
Laninamivir	0	0	1 (2.0%)	0



Recent activity at the Centre (1 Aug–30 Nov 2014)

Below is a summary of surveillance activities at the Centre from 1 August to 30 November. This encompasses the busiest period of the year for us, with the WHO Consultation on the Composition of Influenza Virus Vaccines held in September.

Samples received

The Centre received 2905 influenza samples from the laboratories and institutions listed below during the period 1 August–30 November, 2014.

AUSTRALIA: Alfred Hospital; Austin Health; Canberra Hospital; SA Pathology; John Hunter Hospital; Monash Medical Centre; Pathwest QEII Medical Centre; Prince of Wales Hospital; Queensland Health Forensic and Scientific Services; Royal Children's Hospital (Virology Laboratory); Royal Children's Hospital (Molecular Microbiology Department); Royal Darwin Hospital; Royal Hobart Hospital; Royal Prince Alfred Hospital; Victorian Infectious Diseases Reference Laboratory; Westmead Hospital

MALAYSIA: Institute for Medical Research

NEW CALEDONIA: Institut Pasteur du Cambodge

NEW ZEALAND: Auckland Hospital; Canterbury Health Services; Institute of Environmental Science and Research

PHILIPPINES: Research Institute for Tropical Medicine

	Antigenic analysis: A total of 1790 influenza isolates were analysed by HI assay.				Genetic analysis: Sequencing was performed on 473 HA, 456 NA, 335 MP and 240 NS genes from 473 viruses. In total, 481 sequences from 167 human viruses were deposited with the GISAID EpiFlu™ database (http://www.gisaid.org).				Neuraminidase inhibitor susceptibility: A total of 1858 influenza isolates were tested by neuraminidase inhibition (NAI) assay for susceptibility to oseltamivir, zanamivir, peramivir and laninamivir.			
Country of submitting laboratory	No. of viruses analysed by HI assay*				No. of viruses with gene sequences deposited with GISAID				No. of viruses tested by NAI assay			
	A(H1N1) pdm09	A(H3N2)	B/Vic	B/Yam	A(H1N1) pdm09	A(H3N2)	B/Vic	B/Yam	A(H1N1) pdm09	A(H3N2)	B/Vic	B/Yam
Australia	695	378	5	99	44	44	5	22	717	401	7	101
Cambodia	26	43		3	7			1	26	43		3
Fiji						1						
Macau SAR					2	2		2				
Malaysia	12	5		11	3	3	2	4	12	5		11
Mongolia					1	1	4	3				
New Caledonia	8	9							9	9		
New Zealand	133	64	1	84		4		1	145	54	2	97
Philippines	1	10	3	2					1	10	3	2
Singapore	49	56	15	63		1			49	57	15	63
South Africa	4	8		3					4	8		3
Sri Lanka					1	1				1		
Thailand					2	1	1	4				
Total	928	573	24	265	60	58	12	37	963	588	27	280

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

Isolation of viruses in eggs

The Centre undertakes primary isolation of selected viruses in eggs to obtain potential vaccine strains. From 1 August to 30 November 2014, 7 A(H1N1)pdm09 and 4 A(H3N2) viruses have been successfully isolated in eggs at the Centre.