

SURVEILLANCE REPORT

Influenza virus characterisation

Summary Europe, March 2016

Summary

From week 40/2015, the start of weekly reporting on influenza activity in the WHO European Region, to week 13/2016, over 120 000 influenza detections across the Region have been reported. Influenza type A viruses are prevailing over type B but, unlike the situation in the 2014–15 season, A(H1N1)pdm09 viruses are prevailing over A(H3N2) and the proportion of B/Victoria-lineage detections has risen substantially, representing ~94% of those assigned to a lineage.

To date, 24 EU/EEA countries have shared 472 influenza-positive specimens with the Francis Crick Institute, London, for detailed characterisation: one additional country and 48 specimens since the February 2016 report. Since the latter report, 67 viruses have been characterised antigenically and genetic analyses are ongoing.

The 35 A(H1N1)pdm09 viruses characterised antigenically were similar to the vaccine virus A/California/7/2009. Worldwide, new genetic sub-clusters of viruses within the 6B clade have emerged, with two being designated as subclades 6B.1 defined by HA1 amino acid substitutions S162N and I216T and 6B.2 defined by HA1 amino acid substitutions V152T and V173I. Of the 178 viruses characterised genetically for the 2015–16 season, 24 (13%) were clade 6B, 147 (83%) were subclade 6B.1 and seven (4%) were subclade 6B.2.

The six A(H3N2) test viruses characterised by haemagglutination inhibition (HI) assay were poorly recognised by reference antiserum raised against egg-propagated A/Switzerland/9715293/2013, the vaccine virus recommended for use in the 2015–16 northern hemisphere influenza season, despite at least three of the test viruses falling in the same subclade (3C.3a) as the vaccine virus. The test viruses were recognised somewhat better by antisera raised against egg-propagated A/Hong Kong/4801/2014, the virus recommended for use in 2016 southern hemisphere and 2016–17 northern hemisphere influenza vaccines. Of 55 A(H3N2) viruses characterised genetically for the 2015–16 season: one (2%) was clade 3C.3, 32 (58%) were subclade 3C.2a and 22 (40%) were subclade 3C.3a.

The 23 B/Victoria-lineage viruses were antigenically similar to tissue culture-propagated surrogates of B/Brisbane/60/2008. All 56 viruses characterised genetically for the 2015–16 season fell in genetic clade 1A as do recently collected viruses worldwide.

Three B/Yamagata viruses have been characterised since the previous report; all reacted well with post-infection ferret antiserum raised against egg-propagated B/Phuket/3073/2013, the recommended vaccine virus for the northern hemisphere 2015–16 influenza season and for quadrivalent vaccines in the 2016 southern hemisphere and 2016–17 northern hemisphere seasons. All 10 viruses characterised genetically for the 2015–16 season fell in genetic clade 3.

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Table 1 shows a summary of influenza virus detections in the WHO European Region reported to TESSy for the first 27 weeks (weeks 40/2015 – 13/2016) of reporting for the 2015–16 season. A total of over 120 000 detections had been made with type A viruses prevailing over type B at a ratio of 2.8:1; this compares to a ratio of 5.8:1 to week 7/2016, indicating a surge in influenza type B circulation over the last six weeks. So far, of the type A viruses subtyped ($n = 61\,723$) and the type B viruses ascribed to lineage ($n = 5\,846$), A(H1N1)pdm09 have prevailed over A(H3N2) and B/Victoria over B/Yamagata by ratios of 11:1 and 15:1, respectively.

Since the start of weekly reporting for the 2015–16 influenza season (week 40/2015), 44 shipments of specimens have been received at the Crick Worldwide Influenza Centre (WIC), from 24 countries in the EU/EEA (Table 2). Of the 472 specimens received, a mix of clinical samples and virus isolates, the majority (82.8%) were type A viruses, and A(H1N1)pdm09 outnumbered A(H3N2) at a ratio of 4.8:1. Of the 81 type B specimens received (17.2% of the specimens), 66 were B/Victoria-lineage and 10 B/Yamagata-lineage. A number of specimens are still in the process of being characterised. The antigenic and genetic properties of influenza virus isolates characterised since the February 2016 report¹ are presented and discussed in this report.

Table 1. Influenza virus detections in the WHO European Region since the start of reporting for the 2015–16 season (weeks 40/2015 – 13/2016)

Virus type/subtype	Cumulative number of detections			Totals*	
	Sentinel sources	Non-sentinel sources	Totals	%	Ratios
Influenza A	10021	81267	91288	73.7	2.8:1
A(H1N1)pdm09	8293	48102	56395	91.4	10.6:1
A(H3N2)	1253	4075	5328	8.6	
A not subtyped	475	29090	29565		
Influenza B	6965	25629	32594	26.3	
Victoria lineage	3353	2128	5481	93.8	15.1:1
Yamagata lineage	90	275	365	6.2	
Lineage not ascribed	3522	23226	26748		
Total detections (total tested)	16986 (45816)	106896 (461151)	123882 (506967)		

* Percentages are shown for total detections (types A & B, and for viruses ascribed to subtype/lineage). Ratios are given for type A:B, A(H1N1)pdm09: A(H3N2) and Victoria:Yamagata lineages.

¹ European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, February 2016. Stockholm: ECDC; 2016. Available from: <http://ecdc.europa.eu/en/publications/Publications/influenza-virus-characterisation-february-2016.pdf>

Table 2. Summary of clinical samples and virus isolates received from EU/EEA Member States: packages received since the start of the 2015–16 reporting period (week 40/2015)

MONTH*	TOTAL RECEIVED	A		H1N1pdm09		H3N2			B		B Victoria lineage		B Yamagata lineage	
		Number received	Number propagated	Number received	Number propagated ¹	Number received	Number propagated ²	Number received	Number propagated	Number received	Number propagated ¹	Number received	Number propagated ¹	
2015														
SEPTEMBER														
Iceland	1			1	1									
Poland	1					1	0	0						
Spain	1			1	1									
Sweden	1			1	1									
United Kingdom	3					3	3	0						
OCTOBER														
Austria	1			1	1									
Belgium	1			1	1									
France	2			2	2									
Germany	2			1	1									
Italy	2			1	1								1	1
Latvia	1			1	1								1	1
Netherlands	1			1	1									
Norway	11			8	6	2	2	0			1	1		
Portugal	1			1	1									
Romania	1			1	1									
Slovenia	2	1	0	1	1									
Spain	2			2	1									
Sweden	1					1	0	1						
United Kingdom	8			7	7						1	1		
NOVEMBER														
Austria	9			5	5	4	4	0						
Belgium	11			2	1	1	0	1			6	6	2	2
Denmark	1			1	1									
Estonia	3			3	0									
Finland	4			2	2	2	1	1						
France	5			1	1	1	1	0			3	3		
Germany	14			11	11	2	0	2			1	1		
Italy	2					1	1	0			1	1		
Netherlands	7			5	5						2	2		
Norway	11			7	6	1	1	0			1	1	2	2
Poland	1	1	0											
Portugal	8			8	7									
Slovenia	3					2	0	2	1	0				
Spain	5	2	0	2	1	1	1	0						
Sweden	11			7	7	4	4	0						
United Kingdom	7			7	5									
DECEMBER														
Austria	3					3	2	1						
Czech Republic	2			2	2									
Denmark	7			7	7									
Estonia	6			1	0				1	0	4	3		
Finland	8			7	6	1	1	0						
France	24			7	7	2	2	0			15	15		
Germany	21			17	17	3	3	0			1	1		
Greece	6			5	3	1	0	1						
Iceland	3			1	1	1	0	1			1	1		
Ireland	4			2	2	1	0	1			1	1		
Italy	8			3	3	5	2	3						
Latvia	4			3	3						1	in process		
Netherlands	5			5	5									
Norway	5			3	3	2	1	1						
Poland	12	10	0	1	1						1	0		
Portugal	14			10	7	3	2	1					1	1
Romania	1					1	0	1						
Slovenia	5					5	1	3						
Spain	14			8	7	2	0	1			4	4		
United Kingdom	3			3	3									
2016														
JANUARY														
Cyprus	15			9	in process	1	1	0			5	in process		
Czech Republic	3			3	3									
Estonia	3			2	0						1	1		
Germany	24			11	11	3	3	0			8	8	2	2
Greece	27			27	in process									
Hungary	7			4	4						3	3		
Iceland	6			5	5								1	1
Ireland	10			9	9						1	1		
Italy	1			1	1									
Netherlands	2			2	2									
Portugal	6			6	6									
Romania	8			7	7	1	0	1						
Slovenia	8			3	3	3	0	3	2	0				
Spain	19			16	in process	1	0	1	1	in process	1	1		
FEBRUARY														
Cyprus	9			8	in process						1	in process		
Greece	4			4	in process									
Latvia	2			2	in process									
Netherlands	1			1	1									
Spain	17			15	in process									
	472	14	0	312	209	65	36	26	5	0	66	57	10	10
24 Countries				66.1%		13.8%					14.0%		2.1%	
				82.8%							17.2%			

* Month indicates the months in which the clinical specimens were collected

1. Propagated to sufficient titre to perform HI assay

2. Propagated to sufficient titre to perform HI assay in presence of 20nM oseltamivir; numbers in red indicate viruses recovered but with insufficient HA titre to permit HI assay

Influenza A(H1N1)pdm09 virus analyses

Haemagglutination inhibition (HI) analyses of viruses that have been performed since the February 2016 report are shown in Tables 3-1 and 3-2. All 35 A(H1N1)pdm09 viruses from EU/EEA countries were antigenically similar to the vaccine virus, A/California/7/2009. Generally, the test viruses were recognised by the panel of antisera at titres within fourfold of the titres for the homologous viruses, with the exception of the antiserum raised against A/Christchurch/16/2010. This antiserum recognised only 7/35 (20%) test viruses at a titre within fourfold of the titre for the homologous virus. In addition, antiserum raised against A/Lviv/N6/2009 showed eightfold reduced titres with 12 of the test viruses, compared to the homologous titre. Reference viruses carrying HA1 G155E amino acid substitutions, A/Bayern/69/2009 and A/Lviv/N6/2009, showed reduced recognition by the antisera raised against A/California/7/2009 and reference viruses in genetic clades 4, 5, 6, 7 and subclades 6A, 6B, 6B.1 and 6B.2.

While sequencing is still in process for the majority of test viruses indicated in Tables 3-1 and 3-2, the eight viruses from the Netherlands all fell in subclade 6B.1 (Table 3-1). Since 2009, the HA genes have evolved, and nine clades have been designated. For well over a year, viruses in clade 6, represented by A/St Petersburg/27/2011 and carrying amino acid substitutions of **D97N**, **S185T** and **S203T** in **HA1** and **E47K** and **S124N** in **HA2** compared with A/California/7/2009, have predominated worldwide with a number of subclades emerging. All EU/EEA viruses characterised since the September 2014 report² carry HA genes in subclade 6B, which is characterised by additional amino acid substitutions of **K163Q**, **A256T** and **K283E** in **HA1** and **E172K** in **HA2** compared with A/California/7/2009, e.g. A/South Africa/3626/2013. A number of virus clusters have emerged within clade 6B and two of these have been designated as subclades: viruses in subclade 6B.1 are defined by **HA1** amino acid substitutions **S84N**, **S162N** (which results in the formation of a new potential glycosylation motif at residues 162-164 of HA1) and **I216T**, while those in subclade 6B.2 are defined by **HA1** amino acid substitutions **V152T** and **V173I** (Figure 1).

² European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, September 2014. Stockholm: ECDC; 2014. Available from: <http://ecdc.europa.eu/en/publications/Publications/Influenza-ERLI-Net-report-Sept-2014.pdf>

Table 3-1. Antigenic analysis of A(H1N1)pdm09 viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre														
				Post-infection ferret antisera														
				A/Cal F06/16 ¹	A/Bayern F09/15 ¹	ALviv F14/13 ¹	A/Chch F15/14 ¹	A/Astrak F22/13 ¹	A/St. P F26/14 ¹	A/St. P F24/11 ¹	A/HK F30/12 ¹	A/Sth Afr F03/14 ¹	A/Slov F02/16 ²	A/Israel Q-504/15				
REFERENCE VIRUSES				4	5	6	7	6A	6B	6B.1	6B.2							
A/California/7/2009		2009-04-09	E4/E3	1280	640	640	1280	1280	1280	640	5120	2560	1280	2560	1280	2560	1280	1280
A/Bayern/69/2009		2009-07-01	MDCk5/MDCk1	40	320	320	160	40	80	80	80	80	80	80	80	80	<	<
A/Lviv/N6/2009		2009-10-27	MDCk4/SIAT1/MDCk3	160	1280	1280	320	160	160	160	160	320	160	320	160	320	160	160
A/Christchurch/16/2010		2010-07-12	E1/E3	1280	1280	1280	5120	2560	1280	1280	2560	2560	1280	1280	1280	2560	1280	1280
A/Astrakhan/1/2011		2011-02-28	MDCk1/MDCk5	1280	1280	640	2560	1280	1280	1280	2560	2560	1280	1280	1280	2560	2560	2560
A/St. Petersburg/7/2011		2011-02-14	E1/E3	1280	1280	640	1280	1280	1280	1280	2560	2560	1280	1280	1280	2560	2560	2560
A/St. Petersburg/100/2011		2011-03-14	E1/E3	320	160	160	320	640	320	640	640	640	640	640	640	640	640	320
A/Hong Kong/5659/2012		2012-05-21	MDCk4/MDCk1	640	640	640	640	1280	1280	1280	2560	2560	1280	1280	1280	2560	1280	1280
A/South Africa/3626/2013		2013-06-06	E1/E3	640	640	640	640	1280	1280	1280	2560	2560	1280	1280	1280	2560	2560	2560
A/Slovenia/2903/2015	clone 37	2015-10-26	E4	1280	640	640	640	1280	1280	640	2560	2560	1280	1280	1280	2560	1280	1280
A/Israel/Q-504/2015		2015-12-15	C1/MDCk2	1280	640	640	1280	2560	640	640	5120	2560	2560	2560	2560	2560	2560	2560
TEST VIRUSES																		
A/Netherlands/2916/2015		2015-11-06	SIAT3/MDCk1	1280	640	640	1280	1280	1280	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Netherlands/2941/2015		2015-11-30	SIAT3/MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	5120	2560	2560	2560
A/Netherlands/2942/2015		2015-12-02	SIAT3/MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Netherlands/3078/2015		2015-12-14	MDCk2/MDCk1	640	320	320	640	640	320	320	1280	1280	640	1280	1280	1280	1280	1280
A/Netherlands/3027/2015		2015-12-15	MDCk3/MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/2407/2015		2015-12-28	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/2421/2015		2015-12-30	MDCk1	1280	320	320	640	1280	1280	1280	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/19/2016		2016-01-04	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Netherlands/051/2016	6B.1	2016-01-05	MDCk2/MDCk1	1280	320	320	640	1280	1280	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Netherlands/050/2016	6B.1	2016-01-06	MDCk2/MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/76/2016		2016-01-08	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/71/2016		2016-01-09	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/75/2016		2016-01-10	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Athens/141/2016		2016-01-12	MDCk1	1280	640	640	1280	1280	640	640	2560	1280	1280	1280	2560	2560	2560	2560
A/Netherlands/056/2016	6B.1	2016-02-01	MDCk2/MDCk1	1280	320	320	640	1280	1280	640	2560	1280	1280	1280	2560	2560	2560	2560
				Vaccine														

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)

1 < = <40

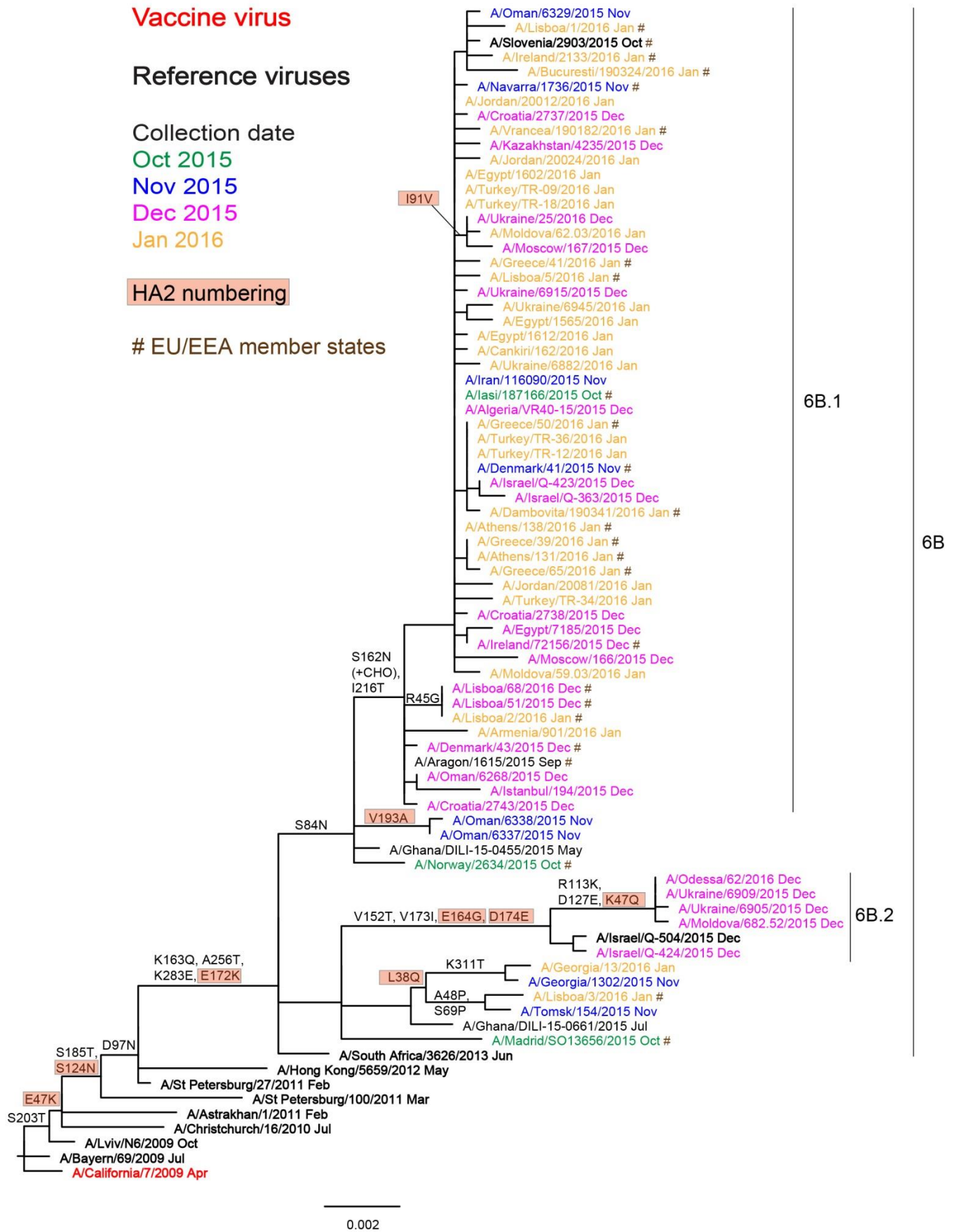
2 < = <80

Table 3-2. Antigenic analysis of A(H1N1)pdm09 viruses by HI

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre																
				Post-infection ferret antisera																
				A/Cal 7/09 Egg F06/16 ¹	A/Bayern 69/09 MDCK F09/15 ¹	A/Lviv N6/09 MDCK F14/13 ¹	A/Chch 16/10 Egg F15/14 ¹	A/Astrak 1/11 MDCK F22/13 ¹	A/St. P 27/11 Egg F26/14 ¹	A/St. P 100/11 Egg F24/11 ¹	A/HK 5659/12 MDCK F30/12 ¹	A/Sth Afr 3626/13 Egg F03/14 ¹	A/Slov 2903/2015 Egg F02/16 ²	A/Israel Q-504/15 MDCK F08/16 ²	A/Sth Afr 3626/13 Egg F03/14 ¹	A/HK 5659/12 MDCK F30/12 ¹	A/St. P 100/11 Egg F24/11 ¹	A/Sth Afr 3626/13 Egg F03/14 ¹	A/Slov 2903/2015 Egg F02/16 ²	A/Israel Q-504/15 MDCK F08/16 ²
REFERENCE VIRUSES																				
A/California/7/2009 Clones38-32		2009-04-09	E9/E2	1280	640	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	
A/Bayern/69/2009		2009-07-01	MDCK5/MDCK1	40	320	320	80	40	40	40	40	40	40	40	40	40	40	40	80	<
A/Lviv/N6/2009		2009-10-27	MDCK4/SIAT1/MDCK3	160	1280	1280	320	80	160	160	160	160	160	160	160	160	160	160	320	160
A/Christchurch/16/2010		2010-07-12	E1/E3	1280	1280	1280	2560	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	2560
A/Astrakhan/1/2011		2011-02-28	MDCK1/MDCK5	1280	640	640	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	1280
A/St. Petersburg/27/2011		2011-02-14	E1/E3	1280	640	640	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	2560
A/St. Petersburg/100/2011		2011-03-14	E1/E3	1280	640	640	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	2560
A/Hong Kong/5659/2012		2012-05-21	MDCK4/MDCK2	320	160	160	160	320	320	320	320	320	320	320	320	320	320	320	640	640
A/South Africa/3626/2013		2013-06-06	E1/E3	640	640	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	1280
A/Slovenia/2903/2015	clone 37	2015-10-26	EA/E1	2560	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280	2560	2560
A/Israel/Q-504/2015		2015-12-15	C1/MDCK2	1280	320	320	640	640	640	640	640	640	640	640	640	640	640	640	2560	2560
TEST VIRUSES																				
A/Athens/2395/2015		2015-12-22	MDCK2	640	320	160	320	640	640	320	1280	1280	640	640	640	640	640	640	1280	1280
A/Athens/82/2016		2016-01-11	MDCK2	1280	320	320	640	1280	1280	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/16352866NS/2016		2016-01-18	C0/MDCK1	640	320	160	320	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/6590S/2016		2016-01-25	C0/MDCK1	1280	320	320	640	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Greece/188/2016		2016-01-25	MDCK1	640	320	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Greece/87/2016		2016-01-26	C2/MDCK1	640	320	320	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8610S/2016		2016-01-27	C0/MDCK1	1280	640	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8608S/2016		2016-01-27	C0/MDCK1	1280	640	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8607S/2016		2016-01-27	C0/MDCK1	640	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8621S/2016		2016-01-27	C0/MDCK1	640	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/160626710S/2016		2016-02-02	C0/MDCK1	1280	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/160626718S/2016		2016-02-02	C0/MDCK1	1280	320	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8664S/2016		2016-02-03	C0/MDCK1	1280	320	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/8687S/2016		2016-02-04	C0/MDCK1	1280	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/163529394NS/2016		2016-02-05	C0/MDCK1	640	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Greece/239/2016		2016-02-06	MDCK1	1280	320	320	640	1280	1280	640	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/163529493NS/2016		2016-02-07	C0/MDCK1	1280	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/163529479NS/2016		2016-02-07	C0/MDCK1	1280	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Catalonia/163529538NS/2016		2016-02-09	C0/MDCK1	640	320	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	1280
A/Greece/249/2016		2016-02-09	MDCK2	640	160	160	320	640	640	320	1280	1280	1280	1280	1280	1280	1280	1280	1280	640

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)
 1 <= <40
 2 <= <80

Figure 1. Phylogenetic comparison of influenza A(H1N1)pdm09 HA genes



Influenza A(H3N2) virus analyses

As described in many previous reports³, influenza A(H3N2) viruses continue to be difficult to characterise antigenically by HI assay due to variable agglutination of red blood cells (RBCs) from guinea pigs, turkeys and humans or the loss of the ability of viruses to agglutinate any of the RBCs. This is a particular problem for most viruses that fall in genetic subgroup 3C.2a as was highlighted first in the November 2014 report⁴.

Results of HI tests performed with guinea pig RBCs in the presence of 20nM oseltamivir, added to circumvent NA-mediated binding of A(H3N2) viruses to the RBCs, are shown in Table 4. Of the six test viruses that retained sufficient HA titre to be analysed by HI assay, four have been analysed genetically with three (from Germany) falling in subclade 3C.3a and one in subclade 3C.2a.

The test viruses, propagated in MDCK-SIAT1 cells, reacted poorly in HI assays with the panel of post-infection ferret antisera relative to the titres of the antisera with their respective homologous viruses (shown in red: Table 4). However, in terms of absolute titres, antisera raised against A/Stockholm/6/2014 (3C.3a: tissue culture- and egg-propagated), tissue culture-propagated A/Hong Kong/5738/2014 (3C.2a), tissue culture-propagated A/Georgia/532/2015 and A/Hong Kong/4801/2014 (3C.2a: tissue culture- and egg-propagated), gave consistent reactivity with all test viruses. In terms of absolute titre, the antiserum raised against the northern hemisphere 2015–16 vaccine component, egg-propagated A/Switzerland/9715293/2013 (3C.3a) reacted with test viruses at titres equivalent to (two viruses) or at least twofold-reduced (four viruses) compared to titres achieved with egg-propagated A/Hong Kong/4801/2014, the virus recommended for use in vaccines for the southern hemisphere 2016 and northern hemisphere 2016–17 influenza seasons.

Since 2009, seven genetic groups based on the HA gene have been defined for A(H3N2) viruses. Phylogenetic analysis of the HA genes of representative A(H3N2) viruses with recent collection dates is shown in Figure 2. The HA genes fall within clade 3C. This clade has three subdivisions: 3C.1 (represented by A/Texas/50/2012, the vaccine virus recommended for use in the 2014–15 northern hemisphere season), 3C.2 and 3C.3. Viruses in these three subdivisions had been antigenically similar. In 2014, three new subclades emerged, one in subdivision 3C.2, 3C.2a, and two in 3C.3, 3C.3a and 3C.3b, with subclade 3C.2a viruses dominating in recent months (Figure 2). While viruses in subclades 3C.2a and 3C.3a are antigenic drift variants, those in 3C.3b have remained antigenically similar to previously circulating viruses in the 3C.3 subdivision. Amino acid substitutions that define these subdivisions and subclades are:

- (3C.2) **N145S** in **HA1**, and **D160N** in **HA2**, e.g. A/Hong Kong/146/2013
- (3C.2a) Those in 3C.2 plus **L3I**, **N144S** (resulting in the loss of a potential glycosylation site), **F159Y**, **K160T** (in the majority of viruses, resulting in the gain of a potential glycosylation site), **N225D** and **Q311H** in **HA1**, e.g. A/Hong Kong/5738/2014
- (3C.3) **T128A** (resulting in the loss of a potential glycosylation site), **R142G** and **N145S** in **HA1**, e.g. A/Samara/73/2013
- (3C.3a) those in 3C.3 plus **A138S**, **F159S** and **N225D** in **HA1**, many with **K326R**, e.g. A/Switzerland/9715293/2013
- (3C.3b) those in 3C.3 plus **E62K**, **K83R**, **N122D** (resulting in the loss of a potential glycosylation site), **L157S** and **R261Q** in **HA1** with **M18K** in **HA2**, e.g. A/Stockholm/28/2014.

Based on results available at the time of the February 2015 vaccine composition meeting showing cross-reactivity of antisera raised against subclade 3C.3a and 3C.2a viruses, but with changes acquired on egg-adaptation of genetic subgroup 3C.2a viruses and, at that time, the lack of a suitable 3C.2a vaccine candidate, the World Health Organization recommendation was to use an A/Switzerland/9715293/2013-like virus as the A(H3N2) component of vaccines for the northern hemisphere 2015–16 influenza season [1]. After February 2015, a new subclade designated 3C.3b emerged, these three subclades being antigenically distinguishable, but subclade 3C.2a viruses became prevalent and have remained so. While ferret antisera raised against 3C.3a and 3C.2a subclade viruses showed some cross-reactivity with viruses in all three subclades, antisera raised against 3C.3b viruses were subclade-specific. With the availability of new subclade 3C.2a vaccine candidates and the continued cross-reactivity of antisera raised against viruses in subclades 3C.3a and 3C.2a viruses, the World Health Organization recommendation for the A(H3N2) component of influenza vaccines for the southern hemisphere 2016 [2] and northern hemisphere 2016–17 [3] influenza seasons was for an A/Hong Kong/4801/2014-like (3C.2a) virus.

³ For example, the September 2013 report: European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, September 2013. Stockholm: ECDC; 2013. Available from: <http://www.ecdc.europa.eu/en/publications/Publications/influenza-virus-characterisation-sep-2013.pdf>

⁴ European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe, November 2014. Stockholm: ECDC; 2014. Available from: http://www.ecdc.europa.eu/en/publications/Publications/ERLI-Net_report_November_2014.pdf

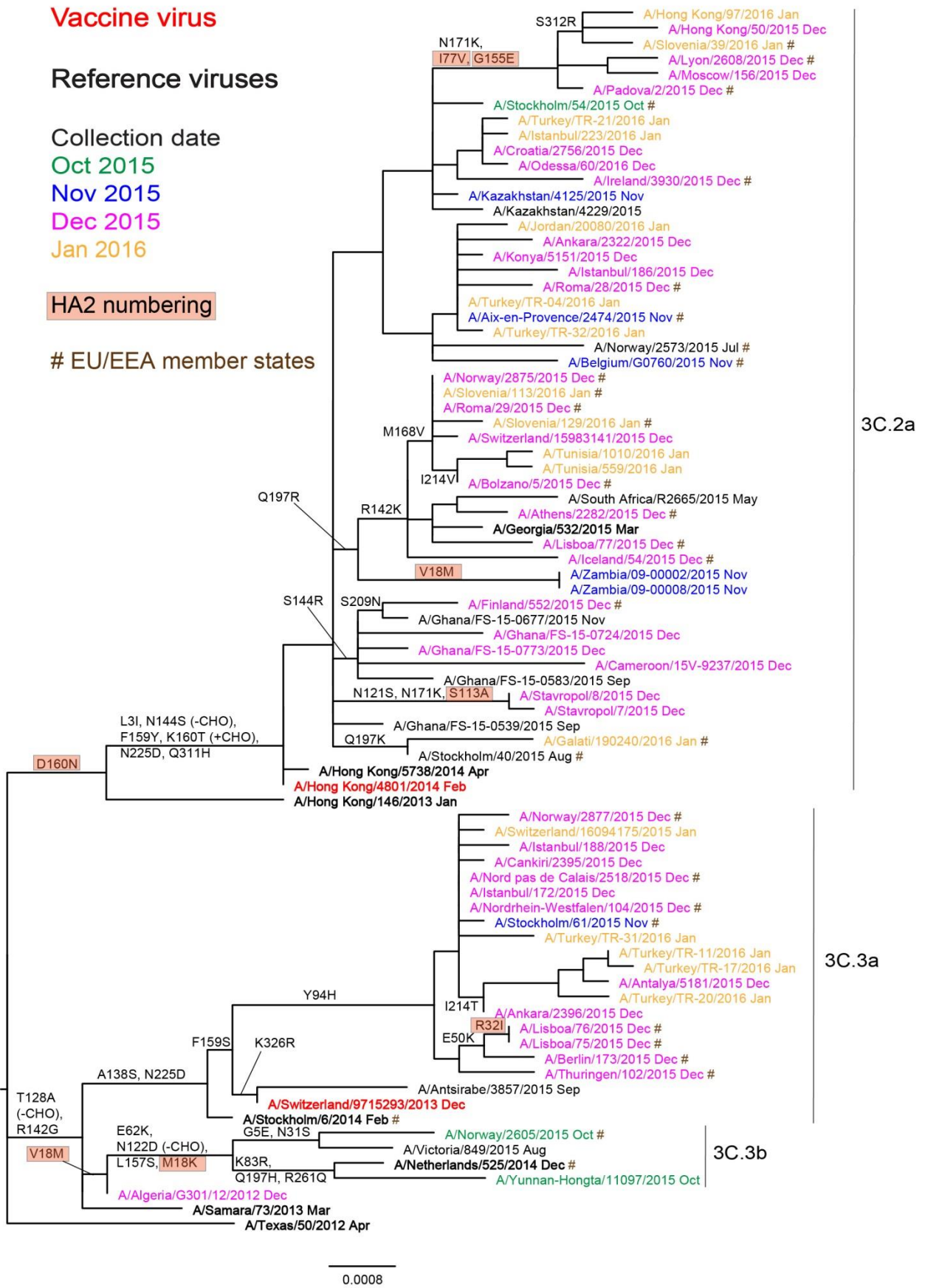
Table 4. Antigenic analysis of A(H3N2) viruses by HI (guinea pig RBC with 20nM oseltamivir)

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre											
				Post-infection ferret antisera											
				A/Texas 5/0/12 Egg F36/12 ¹	A/Samara 73/13 SIAT F35/15 ¹	A/Stock 6/14 SIAT F14/14 ¹	A/Stock 6/14 Egg F20/14 ¹	A/Switz 9715233/13 SIAT F18/15 ¹	A/Switz 9715233/13 Egg F32/14 ¹	A/Neth 525/14 SIAT F23/15 ¹	A/HK 146/13 Egg F10/15 ¹	A/HK 5738/14 MDCK F30/14 ¹	A/HK 4801/14 MDCK F43/15 ¹	A/HK 4801/14 Egg F12/15 ¹	A/Georgia 532/15 SIAT F33/15 ¹
				3C.1	3C.3	3C.3a	3C.3a	3C.3a	3C.3a	3C.3b	3C.2	3C.2a	3C.2a	3C.2a	
REFERENCE VIRUSES															
A/Texas/50/2012		2012-04-15	E5/E2	2560	640	160	640	640	80	640	320	160	320	80	320
A/Samara/73/2013		2013-03-12	C1/SIAT3	2560	640	640	640	160	160	640	640	640	640	320	320
A/Stockholm/6/2014		2014-02-06	SIAT1/SIAT2	160	80	320	160	160	80	80	40	80	160	80	160
A/Stockholm/6/2014	Isolate 2	2014-02-06	E4/E1	640	80	160	320	160	640	80	160	160	320	80	80
A/Switzerland/9715233/2013		2013-12-06	SIAT1/SIAT2	80	40	320	160	160	80	80	40	80	80	80	80
A/Switzerland/9715233/2013	clone 123	2013-12-06	E4/E1	640	160	160	320	160	80	640	80	320	320	80	160
A/Netherlands/525/2014		2014-12-17	SIAT2/SIAT3	640	160	160	160	160	40	80	640	80	160	80	160
A/Hong Kong/146/2013		2013-01-11	E6	2560	640	80	640	640	80	640	320	320	640	160	320
A/Hong Kong/5738/2014		2014-04-30	MDCK1/MDCK2/SIAT2	160	40	160	160	160	80	80	40	160	320	160	160
A/Hong Kong/4801/2014		2014-02-26	MDCK4/MDCK1/SIAT1	80	40	160	160	160	80	80	<	160	320	160	160
A/Hong Kong/4801/2014	Isolate 1	2014-02-26	E6/E2	80	160	160	80	80	40	80	80	320	640	320	640
A/Georgia/532/2015	plaq 20	2015-03-09	SIAT1/SIAT3	160	80	160	160	160	80	80	<	160	320	160	640
TEST VIRUSES															
A/Italy-FVG/105/2015		2015-11-25	SIAT3/SIAT2	40	<	80	40	40	40	<	40	80	80	40	40
A/Catalonia/8396S/2015		2015-11-25	C0/MDCK3	40	<	160	40	40	<	<	<	40	80	40	40
A/Cyprus/F16/2016		2016-01-15	SIAT1	40	<	160	40	40	40	<	40	80	160	80	80
A/Berlin/7/2016		2016-01-18	C2/SIAT1	160	80	640	320	160	160	80	40	160	160	160	160
A/Sachsen/2/2016		2016-01-18	C2/SIAT1	160	80	640	320	160	160	160	40	160	160	160	160
A/Berlin/11/2016		2016-01-25	C2/SIAT1	160	40	640	320	160	80	40	80	160	160	160	160
* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)															
1 < = <40															

Vaccine SH 2016 NH 2016-17

Vaccine NH 2015-16

Figure 2. Phylogenetic comparison of influenza A(H3N2) HA genes



Influenza B virus analyses

Eighty-one influenza type B viruses have been received from EU/EEA countries of which 76 were ascribed to a lineage: 66 B/Victoria-lineage and 10 B/Yamagata-lineage (Table 2).

Influenza B – Victoria lineage

Since the February 2016 report, 23 viruses of this lineage from EU/EEA countries have been characterised antigenically. HI results are shown in Table 5; as observed throughout the previous season, those test viruses for which gene sequencing was completed carried HA genes of clade 1A.

The test viruses showed similar HI reactivity patterns to those from the 2014–15 influenza season: greater than eightfold reductions in HI titres compared with the titre for the homologous virus with post-infection ferret antisera raised against the recommended vaccine virus for quadrivalent live and inactivated vaccines for the northern hemisphere 2015–16 influenza season, B/Brisbane/60/2008. Similarly, they were poorly recognised by post-infection ferret antisera raised against the reference viruses propagated in eggs B/Malta/636714/2011, B/Johannesburg/3964/2013 and B/South Australia/81/2012. In contrast, all but one test virus (B/Catalonia/8514S/2016) showed reactivity within fourfold, the majority within twofold, of the titres for the corresponding homologous viruses with antisera raised against viruses that are considered to be surrogate tissue culture-propagated antigens representing the egg-propagated B/Brisbane/60/2008 prototype virus; these antisera were raised against B/Paris/1762/2009, B/Odessa/3886/2010 and B/Hong Kong/514/2009.

Phylogenetic analysis of the HA gene of representative B/Victoria lineage viruses is shown in Figure 3. Worldwide, recent viruses have HA genes that fall into the B/Brisbane/60/2008 clade (clade 1A) and remain antigenically similar to the recommended vaccine virus, B/Brisbane/60/2008, for use in quadrivalent vaccines. The great majority of viruses, with collection dates since October 2015, fall in a major sub-cluster defined by amino acid substitutions N129D, V146I and I117V within clade 1A.

These results, linked with the rise in the proportion of B/Victoria-lineage viruses seen in the 2015 southern hemisphere and 2015–16 northern hemisphere influenza seasons, support the recommendations made to include B/Brisbane/60/2008 in trivalent influenza vaccines for the southern hemisphere 2016 [2] and northern hemisphere 2016–17 [3] influenza seasons.

Influenza B – Yamagata lineage

HI results for three B/Yamagata-lineage test viruses analysed since the February 2016 report, all of which fell in HA genetic clade 3, are shown in Table 6.

The homologous titres of the ten post-infection ferret antisera, shown in red, ranged from 160 to 640 and the test viruses show similar reactivity patterns though B/Italy-FVG/19/2015 was generally inhibited slightly better (Table 6). This virus carried HA1 K116R and V263M amino acid substitutions compared to the other two test viruses.

Antisera raised against egg-propagated clade 3 viruses B/Phuket/3073/2013 (the virus recommended for inclusion in trivalent influenza vaccines for the northern hemisphere 2014–15 season) and B/Hong Kong/3417/2014 recognised all test viruses at titres within twofold of their respective homologous titres, as did that raised against egg-propagated B/Wisconsin/1/2010 (a previous vaccine virus). However, the antisera raised against egg-propagated B/Stockholm/12/2011 and tissue culture-propagated B/Phuket/3073/2013 showed somewhat reduced reactivity (up to fourfold) with the test viruses. The test viruses also consistently showed fourfold reductions in HI titres compared to the homologous titre for the antiserum raised against egg-propagated B/Massachusetts/02/2012, the clade 2 vaccine virus recommended for use in the 2014–15 northern hemisphere influenza season.

Figure 4 shows a phylogenetic analysis of the HA genes of representative B/Yamagata-lineage viruses. Worldwide, the vast majority of HA genes from recently collected viruses have fallen in the B/Wisconsin/1/2010–B/Phuket/3073/2013 clade (clade 3) with the great majority falling in a subgroup defined by L172Q amino acid substitution in HA1. A few viruses, annotated in the phylogenetic trees, are reassortants carrying NA genes normally associated with the B/Victoria-lineage: none was from an EU/EEA country.

Based on such results, a B/Phuket/3073/2013-like virus has been recommended for inclusion in quadrivalent vaccines for the 2016 southern hemisphere [2] and 2016–17 northern hemisphere [3] influenza seasons.

Table 5. Antigenic analysis of influenza B/Victoria-lineage viruses by HI

Viruses	Haemagglutination inhibition titre														
	Passage history	Ferret number	Genetic group	Collection date	Passage history	Post-infection ferret antisera						B/1911 ²			
						B/Bris	B/Mal	B/Bris	B/Paris	B/Malta	B/Jhb		B/For	B/Sth Aus	B/HK
<i>B/Malaysia/2506/2004</i>	Egg	539/540	1A	2004-12-06	E3/E7	640	320	<	<	80	160	80	160	10	<
<i>B/Risbane/60/2008</i>	Egg	/543/544 ^{1,3}	1A	2008-08-04	E4/E5	640	40	40	40	320	320	320	640	40	40
<i>B/Paris/1762/2009</i>	Egg		1A	2009-02-09	C2/MDCK2	640	<	80	80	40	80	80	80	40	40
<i>B/Malta/6367/2011</i>	Egg		1A	2011-03-07	E4/E1	640	40	160	40	320	320	320	640	40	40
<i>B/Johannesburg/3964/2012</i>	Egg		1A	2012-08-03	E1/E2	2560	320	640	160	1280	1280	1280	1280	160	80
<i>B/Formosa/V2367/2012</i>	Egg		1A	2012-08-06	MDCK1/MDCK3	1280	40	80	40	160	320	320	640	40	40
<i>B/South Australia/81/2012</i>	Egg		1A	2012-11-28	E4/E2	640	40	80	40	160	320	160	640	40	40
<i>B/Hong Kong/514/2009</i>	Egg		1B	2009-10-11	MDCK3	640	<	80	40	40	40	40	40	40	80
<i>B/Odesa/3886/2010</i>	Egg		1B	2010-03-19	C2/MDCK2	640	<	80	80	80	80	80	80	40	80
TEST VIRUSES															
<i>B/Belgium/2015G0749/2015</i>			1A	2015-11-03	MDCK3	160	<	40	40	20	<	40	40	20	20
<i>B/Netherlands/2928/2015</i>			1A	2015-11-23	SIAT3/MDCK1	160	<	40	40	20	<	40	40	20	20
<i>B/Rennes/2483/2015</i>			1A	2015-11-26	MDCK1/MDCK1	640	<	80	80	40	40	80	80	40	40
<i>B/Bretagne/2322/2015</i>			1A	2015-11-30	MDCK1/MDCK1	1280	<	80	80	40	40	80	80	40	40
<i>B/Champagne Ardenne/2335/2015</i>			1A	2015-11-30	MDCK1/MDCK1	1280	<	80	80	40	40	80	80	40	40
<i>B/Roma/1/2015</i>			1A	2015-11-30	SIAT1/MDCK1	1280	<	80	80	40	40	80	80	40	40
<i>B/Bretagne/2368/2015</i>			1A	2015-12-07	MDCK1/MDCK1	640	<	80	40	40	40	80	80	40	40
<i>B/Rennes/2548/2015</i>			1A	2015-12-11	MDCK1/MDCK1	1280	<	80	40	40	40	80	80	40	40
<i>B/Rennes/2547/2015</i>			1A	2015-12-13	MDCK1/MDCK1	1280	<	80	40	40	40	80	80	40	40
<i>B/Estonia/97326/2015</i>			1A	2015-12-23	MDCK2	160	<	40	40	40	<	40	40	20	20
<i>B/Estonia/97370/2015</i>			1A	2015-12-29	MDCK1	640	<	80	40	40	40	80	80	40	40
<i>B/Catalonia/8515S/2016</i>			1A	2016-01-07	C0/MDCK2	80	<	40	40	20	10	20	40	20	20
<i>B/Catalonia/8514S/2016</i>			1A	2016-01-07	C0/MDCK3	80	<	20	10	10	<	20	20	10	10
<i>B/Hungary/19/2016</i>			1A	2016-01-18	MDCK2/MDCK1	1280	<	80	40	40	40	80	80	40	40
<i>B/Nordrhein-Westfalen/2/2016</i>			1A	2016-01-18	C2/MDCK1	640	<	80	40	40	40	80	80	40	40
<i>B/Hungary/16/2016</i>			1A	2016-01-19	MDCK1/MDCK1	1280	<	80	80	80	160	160	160	40	40
<i>B/Hungary/15/2016</i>			1A	2016-01-19	MDCK1/MDCK1	1280	<	40	80	80	80	160	160	40	40
<i>B/Berlin/2/2016</i>			1A	2016-01-25	C2/MDCK1	640	<	80	40	40	80	80	80	40	40
<i>B/Thuringen/8/2016</i>			1A	2016-01-25	C2/MDCK1	1280	<	80	40	40	80	80	80	40	40
<i>B/Bayern/1/2016</i>			1A	2016-01-25	C2/MDCK1	640	<	40	20	20	<	40	40	20	40
<i>B/Bremen/1/2016</i>			1A	2016-01-25	C2/MDCK1	640	<	80	40	40	40	80	80	40	40
<i>B/Catalonia/16203880NS/2016</i>			1A	2016-02-03	C0/MDCK1	320	<	80	20	20	20	40	80	40	40
<i>B/Catalonia/8693S/2016</i>			1A	2016-02-04	C0/MDCK1	320	<	80	80	80	80	160	160	80	80

Vaccine
NH 2015-16⁴
SH 2016
NH 2016-17

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)

1 < = <40

2 < = <10

3 hyperimmune sheep serum

4 < = <20

[#] B/Victoria-lineage virus recommended for use in quadrivalent vaccines

Figure 3. Phylogenetic comparison of influenza B/Victoria-lineage HA genes

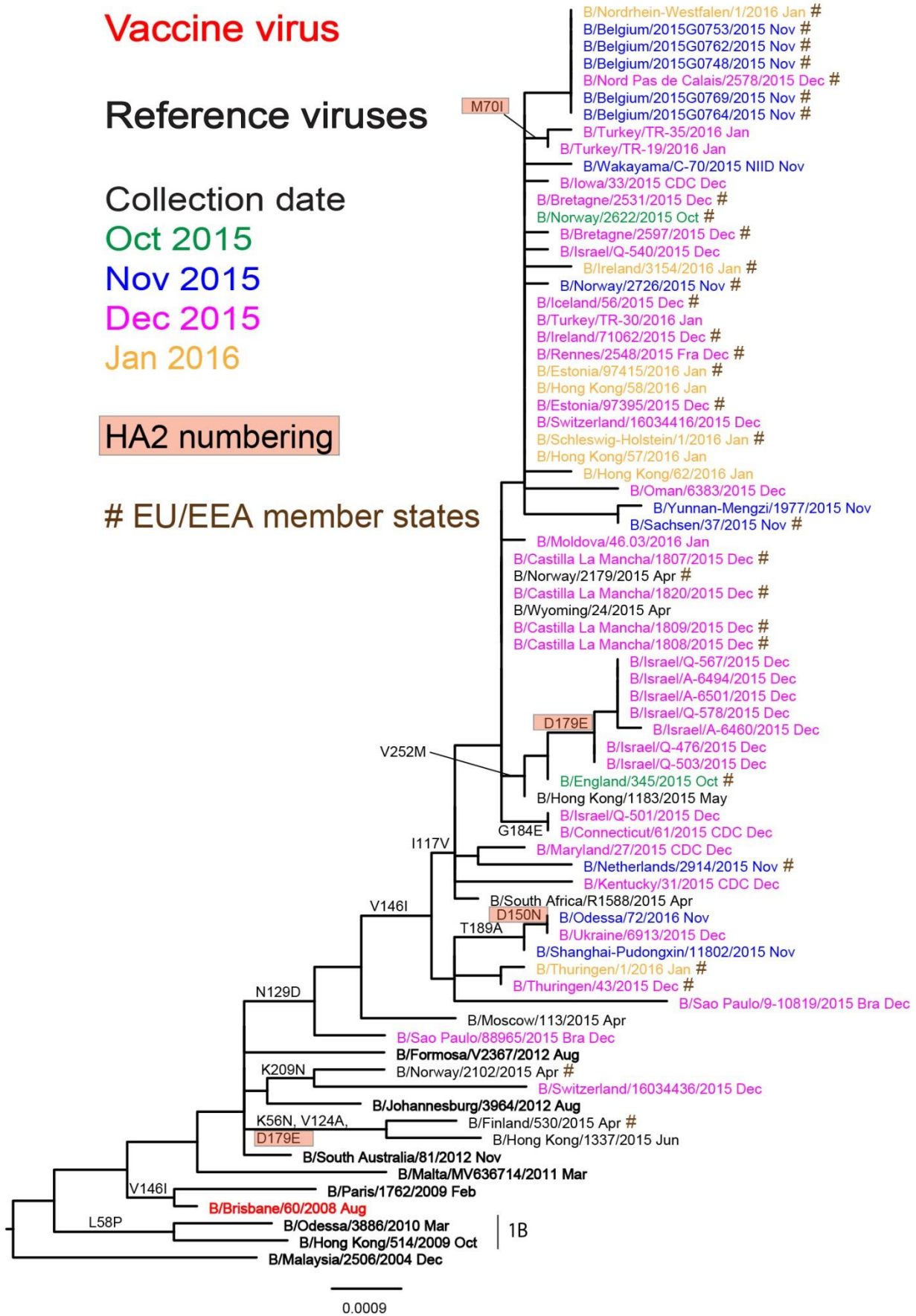


Table 6. Antigenic analysis of influenza B/Yamagata-lineage viruses by HI

Viruses	Haemagglutination inhibition titre											
	Post-infection ferret antisera											B/HK 3417/14
	B/Phuket 3073/13	B/FI 4/06	B/Bris 3/07	B/Estonia 55669/11	B/Mass 02/12	B/Mass 02/12	B/Wis 1/10	B/Stock 12/11	B/Phuket 3073/13	B/Phuket 3073/13	B/HK 3417/14	
	Passage history	Egg	Egg	MDCK	MDCK	Egg	Egg	Egg	MDCK	MDCK	Egg	Egg
	Ferret number	SH614 ^{1,3}	F/1/10 ¹	F38/14 ²	F32/12 ²	F05/15 ⁻¹	F42/14 ²	F10/13 ²	F06/15 ⁻¹	F35/14 ²	F36/14 ²	St. Jude F715/14 ^{2,4}
	Genetic Group	3	1	2	2	2	2	3	3	3	3	3
REFERENCE VIRUSES												
B/Florida/4/2006	1	2006-12-15	E7/E1	1280	640	160	640	160	160	40	320	160
B/Brisbane/3/2007	2	2007-09-03	E2/E3	1280	80	320	320	80	160	20	160	160
B/Estonia/55669/2011	2	2011-03-14	MDCK2/MDCK3	1280	160	320	80	40	20	40	80	160
B/Massachusetts/02/2012	2	2012-03-13	MDCK1/C2/MDCK3	2560	640	320	640	320	20	80	320	320
B/Massachusetts/02/2012	2	2012-03-13	E3/E3	1280	320	40	640	160	80	20	160	160
B/Wisconsin/1/2010	3	2010-02-20	E3/E3	2560	160	<	160	160	80	40	160	160
B/Stockholm/12/2011	3	2011-03-28	E4/E1	2560	160	<	160	80	160	40	160	160
B/Phuket/3073/2013	3	2013-11-21	MDCK2/MDCK2	5120	320	320	320	320	40	640	320	320
B/Phuket/3073/2013	3	2013-11-21	E4/E3	2560	320	<	160	160	160	80	320	160
B/Hong Kong/3417/2014	3	2014-06-04	E4/E1	1280	80	<	40	80	20	20	40	160
TEST VIRUSES												
B/Italy-FVG/19/2015	3	2015-10-12	SIAT2/MDCK1	5120	160	320	160	160	40	640	320	160
B/Hamburg/1/2016	3	2016-01-18	C2/MDCK1	5120	160	80	160	160	40	160	160	320
B/Rheinland-Pfalz/1/2016	3	2016-01-25	C2/MDCK1	2560	80	80	160	160	40	160	160	160

Vaccine
NH 2015-16
SH 2016[#]
NH 2016-17[#]

* Superscripts refer to antiserum properties (< relates to the lowest dilution of antiserum used)

1 < = <40

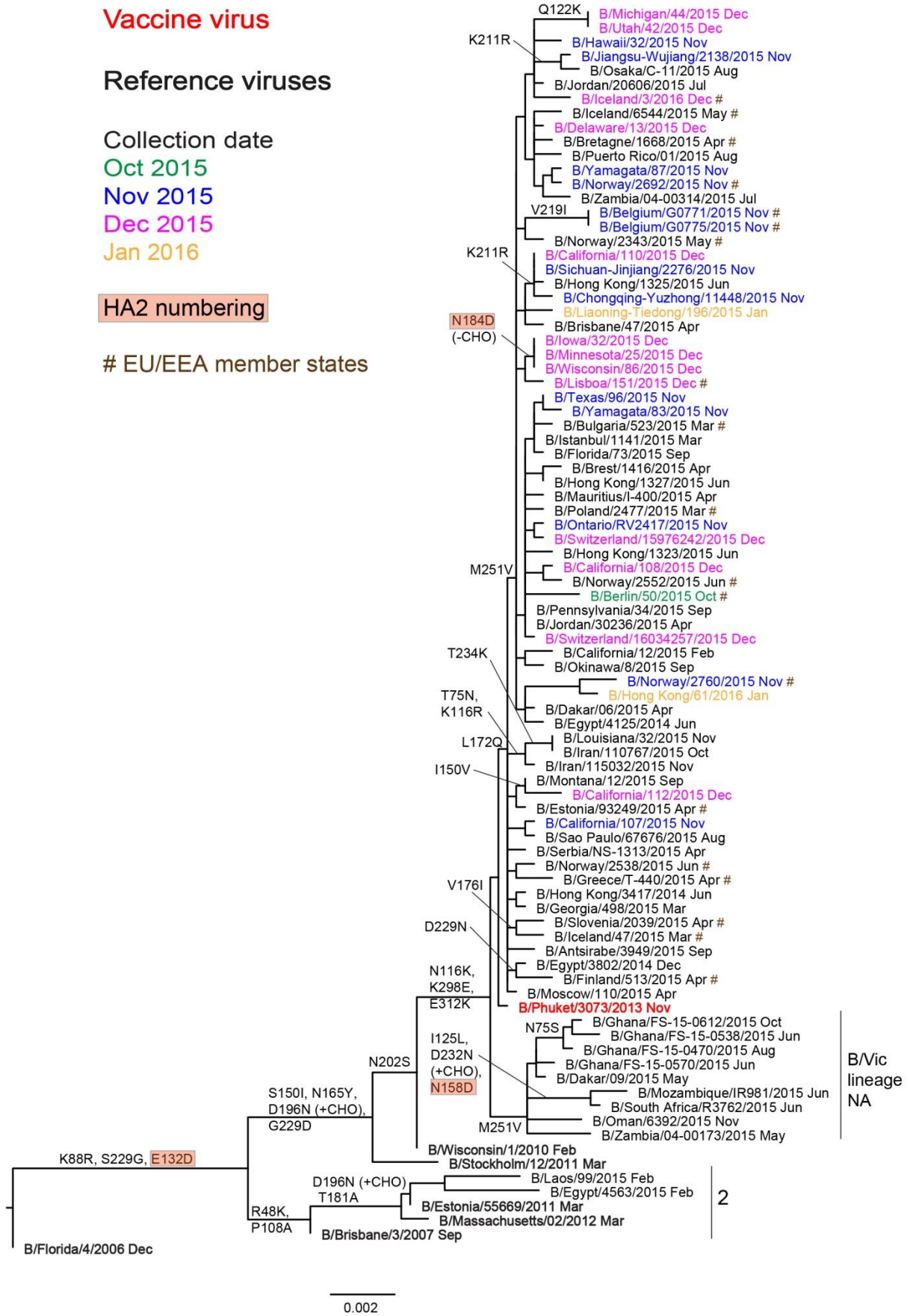
2 < = <10

3 hyperimmune sheep serum

4 RDE serum pre-absorbed with TRBC

B/Yamagata-lineage virus recommended for use in quadravalent vaccines

Figure 4. Phylogenetic comparison of influenza B/Yamagata-lineage HA genes



Summary of genetic data submitted to TESSy

For the period covering weeks 40/2015 – 13/2016, 4 314 viruses have been characterised genetically: 3 066 A(H1N1)pdm09 clade 6B represented by A/South Africa/3626/2013 (6B.1 and 6B.2 subclade designations were not available as reporting categories at the start of the 2015–16 influenza season); 315 A(H3N2) subclade 3C.2a represented by A/Hong Kong/4801/2014, 132 subclade 3C.3a represented by A/Switzerland/9715293/2013, three subclade 3C.3b represented by A/Stockholm/28/2014, and six subclade 3C.3 represented by A/Samara/73/2013; 672 B/Victoria-lineage clade 1A represented by B/Brisbane/60/2008; and 120 B/Yamagata-lineage clade 3 represented by B/Phuket/3073/2013.

Antiviral susceptibility

For weeks 40/2015 – 13/2016 of the 2015–16 influenza season, countries reported on the antiviral susceptibility of 2 041 A(H1N1)pdm09 viruses, 108 A(H3N2) viruses and 228 influenza type B viruses from sentinel and non-sentinel sources. All but 13 showed no molecular or phenotypic evidence of reduced inhibition (RI) by neuraminidase inhibitors. Twelve A(H1N1)pdm09 viruses carried NA H275Y amino acid substitution associated with highly reduced inhibition (HRI) by oseltamivir and one A(H3N2) virus showed RI by oseltamivir associated with NA-E119V amino acid substitution.

Phenotypic testing for susceptibility to oseltamivir and zanamivir has been conducted on 350 viruses at the WIC: 221 A(H1N1)pdm09, 61 A(H3N2), 58 B/Victoria-lineage and 10 B/Yamagata-lineage viruses. All showed normal inhibition (NI) by these neuraminidase inhibitors.

Influenza A(H7N9) virus

On 1 April 2013, the World Health Organization (WHO) Global Alert and Response [4] reported that the China Health and Family Planning Commission had notified the WHO of three cases of human infection with influenza A(H7N9). The cases were confirmed by laboratory testing on 29 March 2013 by the Chinese CDC. A description of the characteristics of H7N9 viruses can be found on the WHO website [5]. Increased numbers of cases were reported over the course of the 2013–14, 2014–15 and 2015–16 seasons and cases have been reported recently [6]. A revised Rapid Risk Assessment [7] for these A(H7N9) viruses was carried out by ECDC and published on 2 February 2015. WHO published a summary of human infection on 31 January 2014 [8], updated on 25 February 2016 [9] with 29 new cases since the report of 21 January 2016, and conducted a risk assessment on 23 February 2015 [10]. In light of the assessment, WHO advised that countries continue to strengthen influenza surveillance. WHO last summarised the numbers of cases of human infection related to their geographic location on 14 July 2014 [11] and has provided subsequent situation updates, with the latest being on 29 March 2016 [6].

Influenza A(H5) virus

The most recent monthly risk assessment of influenza at the human–animal interface was published by WHO on 25 February 2016 [9]. Since the last WHO Influenza update on 21 January 2016, no new laboratory-confirmed human cases of avian influenza A(H5) virus infection have been reported to WHO. ECDC published an updated rapid risk assessment on the situation in Egypt on 13 March 2015 [12] and an epidemiological update on 10 April 2015 [13]. On 2 December 2015 ECDC published a rapid risk assessment related to the identification of highly pathogenic H5 viruses in poultry in France [14].

WHO CC reports

A description of results generated by the WHO Collaborating Centre for Reference and Research on Influenza at the Crick Worldwide Influenza Centre, the Francis Crick Institute, Mill Hill Laboratory and used at the WHO Vaccine Composition Meetings held in Memphis, USA, on 21–23 September 2015 and at WHO headquarters in Geneva on 22–24 February 2016 can be found, respectively, at:

https://www.crick.ac.uk/media/273950/crick_sep2015_vcm_report_to_post.pdf and
https://www.crick.ac.uk/media/286458/crick_feb2016_vcm_report_to_post.pdf

Note on the figures

The phylogenetic trees were constructed using [RAxML](#), drawn using [FigTree](#) and annotated using Adobe Illustrator. The bars indicate the proportion of nucleotide changes between sequences. Reference strains are viruses to which post-infection ferret antisera have been raised. The colours indicate the month of sample collection. Isolates from WHO NICs in EU/EEA countries are marked (#). Sequences for some viruses from non-EU/EEA countries were recovered from GISAID. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu database which were downloaded for use in the preparation of this report (all submitters of data may be contacted directly via the [GISAID website](#)), along with all laboratories who submitted sequences directly to the London WHO Collaborating Centre.

References

1. World Health Organization. Recommended composition of influenza virus vaccines for use in the 2015–2016 northern hemisphere influenza season. [Weekly Epidemiological Record 90, 97-108.](#)
2. World Health Organization. Recommended composition of influenza virus vaccines for use in the 2016 southern hemisphere influenza season. [Weekly Epidemiological Record 90, 545-558.](#)
3. World Health Organization. Recommended composition of influenza virus vaccines for use in the 2016–2017 northern hemisphere influenza season. [Weekly Epidemiological Record 91, 121-132.](#)
4. World Health Organization. Global alert and response: Human infection with influenza A(H7N9) virus in China. 1 April 2013. Available from: http://www.who.int/csr/don/2013_04_01/en/index.html
5. World Health Organization. Avian influenza A(H7N9) virus. Available from: http://www.who.int/influenza/human_animal_interface/influenza_h7n9/en/
6. World Health Organization. Situation updates - avian influenza. Available from: <http://www.who.int/csr/don/29-march-2016-avian-ah7n9-china/en/>
7. European Centre for Disease Prevention and Control. Updated rapid risk assessment. Human infection with avian influenza A(H7N9) virus. Fourth update. 2 February 2015. Available from: <http://ecdc.europa.eu/en/publications/Publications/RRA-Influenza-A-H7N9-update-four.pdf>
8. World Health Organization. Background and summary of human infection with avian influenza A(H7N9) virus – as of 31 January 2014. Geneva: WHO; 2014. Available from: http://www.who.int/influenza/human_animal_interface/20140131_background_and_summary_H7N9_v1.pdf
9. World Health Organization. Influenza at the human-animal interface. Summary and assessment as of 25 February 2016. Available from: http://www.who.int/influenza/human_animal_interface/Influenza_Summary_IRA_HA_interface_25_02_2016.pdf
10. World Health Organization. WHO risk assessment: Human infections with avian influenza A(H7N9) virus, 23 February 2015. Available from: http://www.who.int/influenza/human_animal_interface/influenza_h7n9/RiskAssessment_H7N9_23Feb2015.pdf
11. World Health Organization. Map and epidemiological curve of confirmed human cases of avian influenza A(H7N9). Report 18- data in WHO/HQ as of 14 July 2014. Available from: http://www.who.int/influenza/human_animal_interface/influenza_h7n9/18_reportwebh7n9number_20140714.pdf
12. European Centre for Disease Prevention and Control. Rapid Risk Assessment. Human infection with avian influenza A(H5N1) virus, Egypt. Available from: <http://ecdc.europa.eu/en/publications/Publications/Rapid-Risk-Assessment-Influenza-A-H5N1-Egypt-March-2015.pdf>
13. European Centre for Disease Prevention and Control. Epidemiological update: increase in reporting of human cases of A(H5N1) influenza, Egypt. Available from: http://ecdc.europa.eu/en/press/news/layouts/forms/News_DispForm.aspx?List=8db7286c-fe2d-476c-9133-18ff4cb1b568&ID=1199
14. European Centre for Disease Prevention and Control. Rapid Risk Assessment. Situation overview: highly pathogenic avian influenza virus A of H5 type. Available from: <http://ecdc.europa.eu/en/publications/Publications/highly-pathogenic-avian-influenza-virus-A-H5-rapid-risk-assessment-2-dec-2015.pdf>