

## TECHNICAL DOCUMENT

Community Network of Reference Laboratories (CNRL) for Human Influenza in Europe

# Influenza virus characterisation

Summary Europe, June 2012

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### Summary

Since 01 January 2012, influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B/Victoria- and B/Yamagata-lineage viruses have been detected in ECDC-affiliated countries.

- Type A viruses have predominated over type B.
- A(H3N2) viruses have predominated over A(H1N1)pdm09 viruses.
- A(H1N1)pdm09 viruses continue to show genetic drift from the vaccine virus, A/California/07/2009, but the vast majority are antigenically similar to A/California/07/2009.
- During this time period, all A(H3N2) viruses sequenced fell within five genetic groups. Test viruses isolated in mammalian cells show low titres with post-infection ferret antisera raised against egg-propagated viruses, including the new vaccine virus A/Victoria/361/2011. They react well with post-infection ferret antisera raised against A/Victoria/361/2011 and other current reference viruses exclusively propagated in tissue culture.
- Recent B/Victoria lineage viruses fell within the B/Brisbane/60/2008 genetic clade and were antigenically similar to reference cell-propagated viruses of the B/Brisbane/60/2008 genetic clade.
- Recent B/Yamagata-lineage viruses fell into two genetic clades, the B/Bangladesh/3333/2007 and B/Wisconsin/1/2010 genetic clade or into the B/Brisbane/3/2007 genetic clade; viruses in these clades are antigenically distinguishable.

Table 1 shows a summary of viruses from EU and EAA countries received by the WHO Collaborating Centre for Reference and Research on Influenza at the MRC National Institute for Medical Research in London from 1 January 2012. Viruses and/or clinical samples were submitted by 23 EU/EAA countries. Table 1 is an update of the table shown in the previous report (March 2012). The majority (72%) of viruses received were influenza A(H3N2) viruses. Influenza B viruses of the B/Yamagata lineage have predominated over those of the B/Victoria lineage at a ratio of approximately 3:2; influenza A(H1N1)pdm09 viruses were received from only a minority of countries.

### Influenza A(H1N1)pdm09 virus analyses

Influenza A(H1N1)pdm09 influenza viruses from Norway, Sweden and England have been analysed by HI assay since the previous report; the results are shown in Table 2. The analysed viruses show generally good reactivity with post-infection ferret antisera raised against the panel of reference viruses, including antiserum raised against the vaccine virus (A/California/7/2009); only two of the sixteen viruses analysed showed a reduction of eight-fold or more in reactivity with antiserum raised against A/California/7/2009, compared with the HI titre of the homologous virus.

Phylogenetic analysis of the HA1 coding region of a subset of the test viruses has been carried out (Figure 1), and further gene sequence analysis is underway. The HA genes of H1N1 viruses from EU/EAA countries cluster into two of

eight genetic groups that have been described previously. These viruses fall into genetic groups 6 and 7, which have the following amino acid substitutions in HA1:

- Group 6: **D97N and S185T**, e.g. A/St Petersburg/27/2011
- Group 7: **S143G, S185T and A197T**, e.g. A/St Petersburg/100/2011

The NA genes of the most recently analysed viruses fall into similar genetic groups (Figure 2).

## Influenza A(H3N2) virus analyses

As described [before](#), A(H3N2) viruses have continued to be difficult to characterise antigenically by HI assay due to variable agglutination of red blood cells from guinea pigs, turkeys and humans. Approximately 70% of viruses gave sufficient titre in HA assays to be analysed by HI assay using guinea pig red blood cells in the presence of 20nM oseltamivir, added to circumvent the NA-mediated binding of H3N2 viruses to red blood cells ([Lin et al. 2010](#)).

The results of the HI assays carried out since the last report are shown in Tables 3 to 6. HI assays using post-infection ferret antiserum raised against the vaccine virus recommended for the 2011/2012 northern hemisphere influenza vaccine, A/Perth/16/2009, showed that nearly 90% of the test viruses had a reduction in HI titre of eight-fold or more compared with the titre of the homologous virus.

All tables show results using post infection antiserum raised against the newly recommended, egg-propagated vaccine virus for the northern hemisphere 2012/2013, A/Victoria/361/2011. With this antiserum, only three viruses of the 143 tested gave HI titres within four-fold of that of the homologous virus. Notably, of these three test viruses, two had been propagated in hens' eggs. In contrast, with antiserum raised against the cell-culture propagated A/Victoria/361/2011 only two of 80 test viruses showed a reduced reactivity of eight-fold or more compared with the titre of the homologous cell-propagated virus (Tables 5 and 6). The test viruses also showed good reactivity with post-infection ferret antisera raised against other reference viruses propagated exclusively in cell culture: only nine of the 143 viruses tested showed a reduction in titres of eight-fold or more with any of the antisera compared with the titres of the homologous viruses. These post-infection ferret antisera were against cell-propagated A/Alabama/5/2010, A/Hong Kong/3969/2011, A/Stockholm/18/2011, A/Finland/190/2011, A/Norway/1789/2011, A/Berlin/93/2011, and A/Athens/112/2012.

The results of HI analysis of the test viruses using antisera raised against other egg-propagated reference viruses, A/Victoria/208/2009 and A/Iowa/19/2010, showed low levels of reactivity with ferret antisera compared with the reactivity of the homologous egg-propagated viruses. The low reactivity of test viruses with antisera raised against each of the egg-adapted viruses, importantly including the new vaccine virus A/Victoria/361/2011, suggests that egg adaptation of the H3N2 reference viruses influences the immune response of the ferret. In light of these observations, results of HI tests and other serological assays with currently circulating A(H3N2) viruses continue to warrant careful consideration.

Phylogenetic analysis of the HA and NA gene sequences of representative viruses has been carried out (Figures 3 and 4). Viruses from the EU/EAA collected since January have HA genes that fall into HA gene genetic groups 3A, 3B and 3C, and group 5 and group 6 (Figure 3).

The amino acid substitutions that are associated with each of these groups are:

- Group 3A: **N144D** (resulting in the loss of a glycosylation site), **N145S and V223I**, e.g. A/Stockholm/18/2011;
- Group 3B: **N145S, A198S, V223I and N312S**, e.g. A/Athens/GR112/2012;
- Group 3C: **S45N, T48I, A198S, V223I and N312S**, e.g. A/Hong Kong/3969/2011 and the prototype vaccine virus A/Victoria/361/2011, with some viruses also carrying the substitutions **D53N**, or **Q33R and N278K**;
- Group 5: **D53N, Y94H, I230V and E280A**, e.g. A/Alabama/5/2010;
- Group 6: D53N, Y94H, S199A, I230V and E280A, e.g. A/Iowa/19/2010.

Phylogenetic analysis of the NA gene (Figure 4) shows a similar pattern of grouping but with a less distinct differentiation in those viruses which carry HA genes in genetic groups 5 and 6, although clustering of recent virus NA gene sequences in these groups seems to be emerging.

## Influenza B virus analyses

### B/Victoria-lineage viruses

B/Victoria-lineage viruses were received from nine EU/EAA Member States. The results of HI analyses of influenza B viruses of the B/Victoria lineage are shown in Table 7. All but four of the 23 test viruses showed reduced reactivity (eight-fold or more reduction in titre compared with the homologous titre) with post-infection ferret antiserum raised against the egg-propagated vaccine virus recommended for the northern hemisphere 2011/2012 season, B/Brisbane/60/2008, with the other four test viruses showing four-fold reductions in titre compared with the titre of the homologous virus. In contrast, all viruses reacted well with antisera raised against viruses genetically closely related to the vaccine virus but propagated in cells. In Table 7, these antisera are raised against B/Paris/1762/2008, B/Hong Kong/514/2009 and B/Odessa/3886/2010, which are surrogate cell-propagated antigens for the egg-propagated vaccine virus. The reactivity of test viruses with antiserum raised against B/Malta/MV636714/2011, another egg isolate, was low and similar to their reactivities with antiserum raised against B/Brisbane/60/2008.

Phylogenetic analysis of the HA1 coding region of the HA gene of representative B/Victoria lineage viruses is shown in Figure 5. The HA genes of all recently collected viruses from EU and EAA laboratories fell into Clade 1, the B/Brisbane/60 clade. The NA gene of recently isolated viruses cluster similarly with the exception of the NA gene of B/Norway/710/2012, which was representative of viruses in a group that has an intra-clade reassortment of the HA and NA genes (Figure 6).

## B/Yamagata-lineage viruses

Influenza B viruses of the B/Yamagata lineage were received from eight EU/EAA Member States. Table 8 shows the results of HI assays of the propagated viruses examined since the last report. Only five of 18 test viruses reacted within a four-fold titre of that of the homologous virus, with the post-infection ferret antiserum raised against the recommended egg-propagated vaccine virus for the northern hemisphere 2012/2013, B/Wisconsin/1/2010. However, all but one of the test viruses reacted well with post-infection ferret antiserum raised against the egg-propagated virus B/Stockholm/12/2011. Of the 18 test viruses, 12 showed good reactivity, within four-fold of the homologous titre, with post-infection ferret antiserum raised against B/Estonia/55669/2011, a virus from a distinct genetic clade.

Figure 7 shows a phylogenetic analysis of the HA1 coding region of B/Yamagata lineage viruses. The HA genes of these viruses fall into two genetic clades, one defined as Clade 3, represented by B/Bangladesh/3333/2007 (and includes B/Wisconsin/1/2010 and B/Stockholm/12/2011), and the other defined as Clade 2, represented by the reference strains B/Brisbane/3/2007 and B/Estonia/55669/2011. Viruses falling within these two clades are antigenically distinguishable.

The two clades are differentiated by substitutions at HA residues 48, 108, 150, 165, 181 and 229. The HA gene of viruses of Clade 2 encodes **K48, A108, S150, N165, A181** and **G229**; the HA gene of viruses in Clade 3 encodes **R48, P108, I150, Y165, T181** and **D229**.

Clade 2 seems genetically homogenous, but Clade 3 can be sub-divided into four genetic groups:

- a group defined by the amino acid substitution **N202S** similar to B/Wisconsin/1/2010;
- a group defined by the substitution **T181K** (e.g. B/Ireland/M1522/2012);
- a group defined by the substitution **M251V** with the substitutions **T181A** and **K253R** (e.g. B/Serbia/1894/2011);
- a group defined by the substitution **M251V** with the substitutions **V29A** and **L172Q** (e.g. B/Stockholm/12/2011).

Phylogenetic analysis of the NA gene of recently analysed and representative influenza B viruses of the B/Yamagata lineage are shown in Figure 8. The clustering of the NA gene is similar to that seen in the HA gene.

*The official 'Report prepared for the WHO annual consultation on the composition of influenza vaccine for the Northern Hemisphere', which presents the results of the WHO Vaccine Composition Meeting held at WHO Geneva from 20 to 22 February 2012, can be found at: <http://www.nimr.mrc.ac.uk/documents/about/interim-report-feb-2012.pdf>*

**Note on figures**

The phylogenetic trees were constructed using RAxML and drawn using FigTree. The bars indicate the proportion of nucleotide changes in the sequence. Reference strains are viruses to which post-infection ferret antisera have been raised. The colours indicate the date of sample collection. Isolates from WHO NICs in ECDC countries are highlighted by an orange box. Sequences for some of the viruses from non-EU/EAA countries were recovered from GISAID, and we acknowledge all laboratories which submitted sequences directly to the London WHO CC.

**Table 1. Summary of clinical samples and isolates received from ECDC-affiliated countries, collection dates from 1 January 2012**

MONTH Country	A Untyped *	H1N1pdm09		H3N2		B Untyped *	B Yamagata lineage		B Victoria lineage	
		Number received	Number propagated	Number received	Number propagated		Number received	Number propagated	Number received	Number propagated
<b>JANUARY</b>										
Austria				4	4		1	1	1	1
Bulgaria				4	3					
Denmark				2	1					
Estonia				1	0					
Finland				3	2					
France				4	4					
Germany				14	13					
Greece				8	7	5	1	1	1	4
Iceland				9	7					
Ireland				7	2		1	1	1	1
Italy				13	12				1	1
Latvia				6	5		1	1		
Netherlands				2	2					
Norway	5	2		11	11					
Portugal				7	4					
Romania				3	3					
Slovenia				3	3					
Spain	1	0		18	10		2	2		
Sweden	2	2		8	7		1	1		
United Kingdom				3	3		1	1		
<b>FEBRUARY</b>										
Bulgaria				8	8					
Denmark				7	4		3	3	2	2
Estonia				18	2					
Finland				4	2					
Greece				14	13	4	4	4	1	1
Iceland				11	11					
Ireland	1	1		1	1				1	1
Italy				6	5		5	5	1	1
Norway	10	6		14	14		3	3	1	1
Portugal				1	1		2	1		
Slovenia	1	1		9	7		1	0	1	0
Sweden	3	3		5	4		1	1	1	1
United Kingdom							1	1	1	1
<b>MARCH</b>										
Denmark	3	0		8	7		2	1	1	0
Estonia				11	7					
Finland				1	1					
Iceland				3	2					
Ireland				4	4					
Italy				4	1		6	6	1	0
Norway									1	0
Portugal				6	4		3	2	1	1
Slovenia	1	0		9	7		2	0	4	1
Sweden				1	1		1	1		
United Kingdom	1	1		3	3		1	1	1	1
<b>APRIL</b>										
Denmark				4	3		1	0	1	1
Estonia				7	3		1	1		
Iceland				1	1					
Ireland				10	2					
Slovenia				1	1					
Sweden				4	3					
United Kingdom	1	1		4	4		1	1	2	2
<b>MAY</b>										
Finland									1	1
<b>Total Received = 426</b>	<b>0</b>	<b>29</b>	<b>17</b>	<b>309</b>	<b>229</b>	<b>10</b>	<b>46</b>	<b>39</b>	<b>32</b>	<b>25</b>
				<b>7%</b>	<b>72.5%</b>	<b>2%</b>		<b>11%</b>		<b>7.5%</b>

**Table 2. Antigenic analysis of A(H1N1)pdm viruses by HI (turkey RBCs)**

Viruses	Collection date	Passage History	Haemagglutination inhibition titre <sup>1</sup>							
			Post infection ferret sera							
			A/Cal 7/09 F29/11	A/Bayern 69/09 F11/11	A/Lviv N6/2009 C4/34/09	A/C'church 16/2010 F30/10	A/HK 3934/2011 F21/11	A/Astrak 1/2011 F22/11	A/St. P'burg 27/11 F23/11	A/St. P'burg 100/11 F24/11
<b>REFERENCE VIRUSES</b>										
A/California/7/2009	2009-04-09	E1/E2	1280	2560	1280	1280	1280	1280	1280	2560
A/Bayern/69/2009	2009-07-01	MDCK5	160	640	320	160	80	160	160	80
A/Lviv/N6/2009	2009-10-27	M4/S1/MDCK2	1280	2560	1280	320	160	320	320	320
A/Christchurch/16/2010	2010-07-12	E2/E1	5120	5120	5120	5120	5120	5120	5120	5120
A/Hong Kong/3934/2011	2011-03-29	MDCK2/MDCK2	2560	640	640	1280	2560	2560	2560	5120
A/Astrakhan/1/2011	2011-02-28	MDCK1/MDCK5	2560	1280	1280	1280	2560	2560	2560	5120
A/St. Petersburg/27/2011	2011-02-14	E1/E2	2560	2560	2560	1280	2560	2560	2560	5120
A/St. Petersburg/100/2011	2011-03-14	E1/E2/E1	2560	1280	2560	2560	2560	2560	2560	5120
<b>TEST VIRUSES</b>										
A/Slovenia/421/2012	20/02/2012	Mx/MDCK3	1280	640	640	640	1280	1280	640	2560
A/Norway/418/2012	02/02/2012	MDCK1/MDCK1	2560	1280	1280	2560	2560	2560	5120	5120
A/Norway/421/2012	01/02/2012	MDCK1/MDCK2	5120	2560	2560	2560	5120	5120	5120	5120
A/Norway/446/2012	02/02/2012	MDCK2/MDCK2	5120	2560	5120	2560	5120	5120	5120	5120
A/Norway/560/2012	02/02/2012	MDCK2/MDCK2	640	320	640	640	640	1280	1280	2560
A/Norway/716/2012	17/02/2012	MDCK1/MDCK2	1280	640	1280	1280	2560	2560	2560	5120
A/Norway/717/2012	19/02/2012	MDCK1/MDCK2	640	320	640	640	1280	1280	1280	2560
A/Norway/771/2012	29/01/2012	MDCK1/MDCK1	5120	2560	5120	5120	5120	5120	5120	5120
A/Norway/301/2012	18/01/2012	MDCK1/MDCK3	1280	640	1280	640	2560	1280	2560	5120
A/Ireland/12M17525/2012	29/02/2012	C1/SIAT1	1280	1280	1280	1280	1280	1280	1280	2560
A/Stockholm/9/2012	2012-01-05	C2/MDCK2	640	640	1280	640	1280	640	640	1280
A/Stockholm/18/2012	2012-02-27	C3/MDCK3	80	640	160	80	40	40	80	80
A/Stockholm/17/2012	2012-02-17	C2/MDCK2	160	160	160	160	320	160	160	320
A/Stockholm/16/2012	2012-02-21	C2/MDCK2	640	320	640	640	640	640	640	2560
A/Stockholm/25/2012	2012-04-07	C2/MDCK2	40	160	80	40	<	<	<	<
A/England/344/2012	2012-03-01	SIAT2/MDCK2	1280	640	640	640	1280	1280	1280	2560

1. &lt; = &lt;40

Vaccine virus

Sequence in phylogenetic tree

Figure 1. Phylogenetic comparison of influenza A(H1N1)pdm HA genes (HA1 coding region)

**Vaccine virus****Reference viruses**

Collection date

Jan 2012

Feb 2012

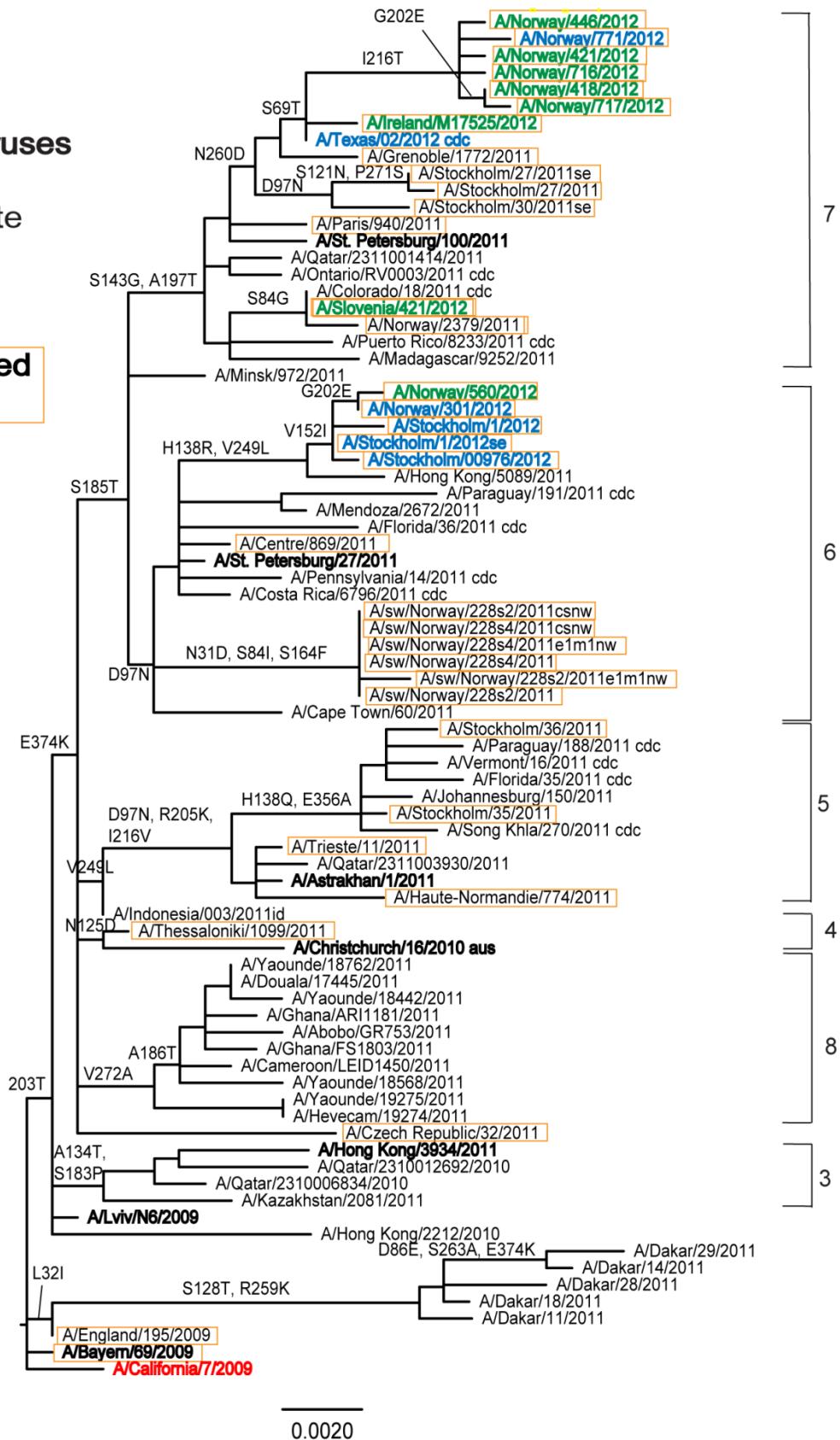
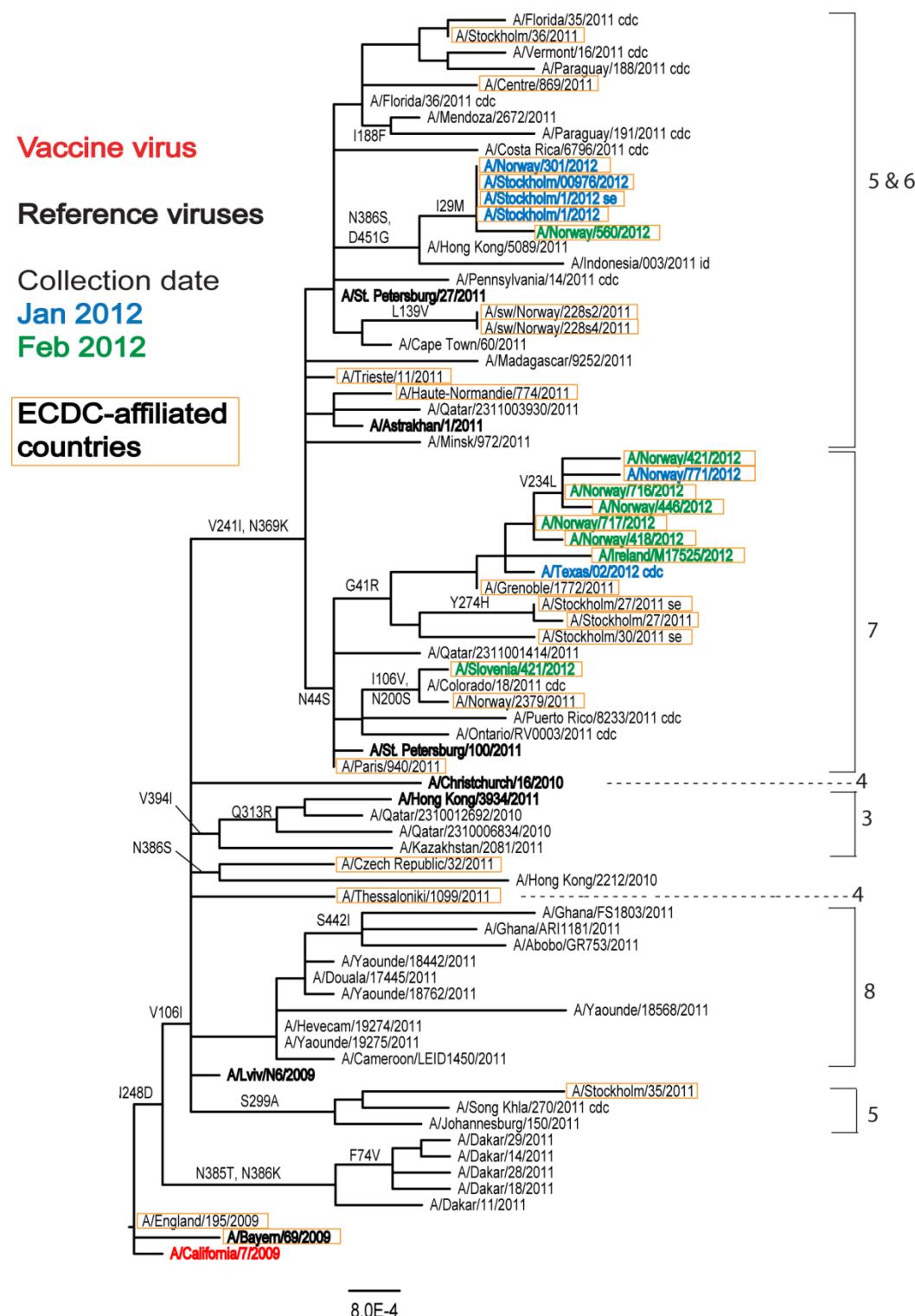
**ECDC-affiliated countries**

Figure 2. Phylogenetic comparison of influenza A(H1N1)pdm NA genes



**Table 3. Antigenic analysis of A(H3N2) viruses by HI (guinea pig RBCs with 20nM oseltamivir)**

Viruses	Collection Date	Passage History	Haemagglutination inhibition titre <sup>1</sup>												
			Post infection ferret sera												
			A/Perth/16/2009 F35/11	A/Vic/208/09 F7/10	A/Ala/5/10 F27/10	A/HK/3969/11 F27/11	A/Stock/18/11 F28/11	A/Iowa/19/10 F15/11	A/Fin/190/11 F01/12	A/Norway/1789/11 F03/12	Egg F05/12	T/C F11/12	A/Vic/361/11 group 3C	A/Berlin/93/11 group 3C	
<b>Genetic group</b>															
<b>REFERENCE VIRUSES</b>															
A/Perth/16/2009	2009-07-04	E3/E2	1280	80	160	640	160	160	160	320	80	320			
A/Victoria/208/2009	2009-06-02	E3/E1	1280	2560	1280	2560	1280	5120	2560	2560	2560	5120			
A/Alabama/5/2010	2010-07-13	MK1/C2/SIAT2	40	<	160	320	80	160	80	160	40	160			
A/Hong Kong/3969/2011	2011-05-19	MDCK2/SIAT4	160	160	160	640	320	320	640	640	160	1280			
A/Stockholm/18/2011	2011-03-28	MDCK2/SIAT3	40	40	80	320	320	160	160	320	80	320			
A/Iowa/19/2010	2010-12-30	E3/E1	640	2560	1280	2560	1280	5120	2560	2560	1280	5120			
A/Finland/190/2011	2011-11-25	Cx/SIAT1	160	160	320	640	320	320	1280	640	160	1280			
A/Norway/1789/2011	2011-08-02	Cx/SIAT1	160	160	160	640	160	320	640	640	640	160			
A/Victoria/361/2011	2011-10-24	E3/E1	320	1280	320	1280	160	1280	1280	1280	5120	1280			
A/Berlin/93/2011	2011-12-07	NVD3/S2	160	160	320	1280	320	640	640	1280	320	1280			
<b>TEST VIRUSES</b>															
A/Glasgow/407664/2012	2012-04-03	SIAT2	80	160	160	640	320	320	640	640	80	1280			
A/Glasgow/407665/2012	2012-04-03	SIAT2	160	160	320	640	320	320	640	640	160	1280			
A/Norway/326/2012	2012-01-30	SIAT1/SIAT1	80	80	160	640	160	160	640	640	160	1280			
A/Norway/337/2012	2012-01-30	SIAT1/SIAT2	80	80	160	320	160	160	320	320	160	640			
A/Norway/399/2012	2012-01-30	SIAT1/SIAT1	80	160	160	640	320	320	640	640	160	1280			
A/Norway/428/2012	2012-01-31	SIAT1/SIAT1	160	160	320	1280	320	640	1280	1280	320	1280			
A/Norway/433/2012	2012-02-05	SIAT1/SIAT1	160	160	320	1280	640	640	1280	1280	320	1280			
A/Norway/479/2012	2012-02-08	MDCK2/SIAT2	80	80	160	320	160	160	640	320	160	640			
A/Norway/528/2012	2012-02-13	SIAT1/SIAT1	80	160	320	640	640	320	640	1280	160	1280			
A/Norway/531/2012	2012-02-13	SIAT1/SIAT1	160	160	320	1280	320	640	1280	640	320	1280			
A/Norway/547/2012	2012-01-24	SIAT1/SIAT2	80	80	160	320	320	160	320	320	160	640			
A/Norway/606/2012	2012-02-20	SIAT1/SIAT1	60	160	320	640	320	320	640	640	160	1280			
A/Norway/624/2012	2012-02-20	SIAT1/SIAT1	160	160	320	640	320	320	640	640	160	1280			
A/Slovenia/94/2012	2012-01-16	MDCKx/SIAT2	80	160	320	640	320	320	640	640	160	640			
A/Slovenia/326/2012	2012-02-13	MDCKx/SIAT2	80	160	160	320	320	160	320	320	80	640			
A/Slovenia/663/2012	2012-03-05	MDCKx/SIAT2	80	160	160	640	320	320	640	640	160	640			
A/Slovenia/910/2012	2012-03-19	MDCKx/SIAT2	40	80	160	640	160	160	640	640	80	640			
A/Slovenia/913/2012	2012-03-19	MDCKx/SIAT2	40	80	160	640	160	160	320	640	80	640			
A/Glasgow/407581/2012	2012-03-30	SIAT2	80	80	160	320	320	160	320	320	80	640			
A/Slovenia/646/2012	2012-03-05	MDCKx/SIAT3	40	80	160	640	160	160	320	160	40	640			
A/Norway/342/2012	2012-01-26	SIAT1/SIAT2	80	160	320	640	320	160	640	640	320	640			
A/Norway/410/2012	2012-02-01	SIAT2/SIAT2	40	80	80	320	160	80	320	320	80	640			
A/Norway/564/2012	2012-02-10	SIAT1/SIAT2	80	80	160	320	640	160	320	320	80	640			
A/Norway/596/2012	2012-02-09	SIAT2/SIAT2	80	80	160	320	160	160	320	320	80	640			
A/Norway/625/2012	2012-02-20	SIAT2/SIAT2	80	80	320	320	160	320	320	320	160	640			
A/Norway/657/2012	2012-02-22	SIAT2/SIAT2	80	80	320	320	160	320	320	320	160	640			
A/Norway/722/2012	2012-02-15	SIAT1/SIAT2	80	80	160	320	160	160	320	320	160	640			
A/Slovenia/274/2012	2012-02-06	P1/SIAT1	40	160	160	160	160	160	160	640	80	640			
A/Estonia/6073/2012	2012-03-06	MDCK2/SIAT1	40	80	40	80	160	80	320	320	160	640			
A/Estonia/6678/2012	2012-03-27	MDCK1/SIAT1	160	160	320	320	320	640	320	640	320	1280			
A/Estonia/66234/2012	2012-03-09	MDCK2/SIAT1	160	160	320	640	320	640	1280	1280	640	1280			
A/Estonia/66837/2012	2012-03-28	MDCK1/SIAT1	40	40	80	160	80	320	160	320	160	320			
A/Ireland/12M28404/2012	2012-04-11	SIAT3	160	320	160	640	640	320	640	640	160	640			
A/Estonia/66103/2012	2012-03-07	MDCK2/SIAT2	80	160	160	1280	640	320	640	640	640	160			
A/Estonia/66239/2012	2012-03-09	MDCK2/SIAT2	40	160	80	640	320	160	640	320	80	640			
A/Estonia/66240/2012	2012-03-09	MDCK1/SIAT2	40	80	80	160	320	160	160	320	80	640			
A/Estonia/67179/2012	2012-04-09	MDCK1/SIAT3	160	320	640	1280	640	640	1280	1280	160	2560			
A/Estonia/67238/2012	2012-04-10	MDCK1/SIAT3	160	160	640	1280	640	640	1280	1280	160	1280			
A/Estonia/67221/2012	2012-04-11	MDCK1/SIAT2	160	320	640	1280	640	640	1280	640	160	1280			

1. &lt; = &lt;40

Vaccine virus

Vaccine virus

Sequence in phylogenetic tree

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

Viruses	Collection Date	Passage History	Haemagglutination inhibition titre <sup>1</sup>									
			Post infection ferret sera									
			A/Perth/16/09 F35/11	A/Vic 208/09 F7/10	A/Ala 5/10 F27/10	A/HK 3969/11 F27/11	A/Stock 18/2011 F28/11	A/Iowa 19/2010 F15/11	A/Fin 190/11 F01/12	A/Norway 1789/11 F03/12	A/Vic 361/11 Egg F05/12	A/Berlin 93/11 TC F11/12
<b>REFERENCE VIRUSES</b>												
A/Perth/16/2009	2009-07-04	E3/E1	1280		160	640	320	320	320	640	160	640
A/Victoria/208/2009	2009-06-02	E3/E1	1280	5120	2560	5120	2560	5120	5120	5120	5120	5120
A/Alabama/5/2010	2010-07-13	MK1/M2/SIAT1	40	40	160	320	160	160	160	320	40	320
A/Hong Kong/3969/2011	2011-05-19	MDCK3	160	160	160	640	320	320	640	1280	320	1280
A/Stockholm/18/2011	2011-03-28	MDCK2/SIAT2	40	80	80	320	320	80	160	320	160	640
A/Iowa/19/2010	2010-12-30	E3/E1	640	2560	1280	2560	2560	5120	5120	5120	2560	5120
A/Finland/190/2011	2011-11-25	Cx/SIAT3	160	160	160	640	320	320	1280	1280	320	1280
A/Norway/1789/2011	2011-08-02	Cx/SIAT3	160	320	160	1280	640	640	1280	1280	320	2560
A/Victoria/361/2011	2011-10-24	E3/E1	640	2560	320	1280	320	1280	2560	1280	5120	2560
A/Victoria/361/2011	2011-10-24	E3/E1S2	320	1280	160	640	160	640	1280	640	5120	1280
A/Berlin/93/2011	2011-12-07	NVD3/E3	160	640	160	640	160	640	1280	640	5120	2560
A/Berlin/93/2011	2011-12-07	NVD3/S2	160	640	160	640	320	640	1280	1280	320	2560
<b>TEST VIRUSES</b>												
A/Bulgaria/41/2012	2012-01-18	C3/SIAT1	40	160	80	320	160	80	160	320	80	640
A/Bulgaria/42/2012	2012-01-18	C3/SIAT1	40	160	40	160	160	80	160	320	40	320
A/Bulgaria/43/2012	2012-01-18	C3/SIAT1	80	160	160	320	160	160	640	640	160	1280
A/Bulgaria/217/2012	2012-02-09	C3/SIAT1	40	320	80	320	160	160	320	640	80	640
A/Bulgaria/218/2012	2012-02-09	C3/SIAT1	40	320	80	160	160	160	320	320	80	640
A/Bulgaria/280/2012	2012-02-20	C3/SIAT1	80	160	320	320	320	320	640	640	160	1280
A/Bulgaria/182/2012	2012-02-02	C3/SIAT1	80	640	320	640	320	640	640	640	160	1280
A/Bulgaria/311/2012	2012-02-24	C3/SIAT1	40	320	160	320	160	160	320	320	80	1280
A/Bulgaria/312/2012	2012-02-24	C3/SIAT1	80	320	160	320	320	160	640	640	160	1280
A/Bulgaria/313/2012	2012-02-24	C3/SIAT1	80	320	160	640	320	320	640	640	160	1280
A/Bulgaria/314/2012	2012-02-24	C3/SIAT1	80	320	320	640	320	320	640	640	160	1280
A/Stockholm/32/2011	2011-11-27	NVD3	320	640	640	1280	640	640	2560	1280	320	2560
A/Stockholm/32/2011	2011-11-27	E3	160	640	160	640	160	640	1280	1280	5120	1280
A/Stockholm/32/2011	2011-11-27	E4	160	320	160	640	160	640	1280	640	2560	1280
A/Slovenia/118/2012	2012-01-09	Mx/SIAT1	40	80	40	160	80	80	320	320	40	640
A/Slovenia/402/2012	2012-02-20	Mx/SIAT1	40	160	80	320	160	160	640	640	160	640
A/Slovenia/435/2012	2012-02-20	Mx/SIAT1	40	160	80	640	160	160	640	640	80	1280
A/Slovenia/459/2012	2012-02-20	Mx/SIAT1	160	320	320	640	640	640	2560	1280	320	2560
A/Slovenia/566/2012	2012-02-27	Mx/SIAT1	40	160	80	320	160	160	320	640	80	640
A/Slovenia/599/2012	2012-02-27	Mx/SIAT1	80	320	320	640	640	640	1280	1280	320	2560
A/Slovenia/637/2012	2012-03-05	Mx/SIAT1	160	640	320	1280	640	640	1280	1280	320	2560
A/Slovenia/815/2012	2012-03-12	Mx/SIAT1	40	160	80	320	160	160	640	640	160	1280
A/Slovenia/879/2012	2012-03-19	Mx/SIAT1	160	320	160	1280	640	640	1280	1280	160	2560
A/Slovenia/1049/2012	2012-04-02	Mx/SIAT1	160	320	160	640	320	320	640	1280	160	1280

Vaccine

Vaccine

**Table 5. Antigenic analysis of A(H3N2) viruses by HI (guinea pig RBCs with 20nM oseltamivir)**

Viruses	Collection Date	Passage History	Haemagglutination inhibition titre <sup>1</sup>													
			Post infection ferret sera													
			A/Perth 16/09	A/Vic 208/09	A/Ala 5/10	A/HK 3969/11	A/Stock 18/11	A/Iowa 19/10	A/Vic 361/11	A/Berlin 93/11	A/Vic 361/11	A/Berlin 93/11	A/Vic 361/11	A/Athens 112/12		
			F35/11	F7/10	F27/10	F27/11	F28/11	F15/11	Egg F05/12	T/C F11/12	T/C F15/12	T/C F11/12	T/C F15/12	F16/12		
<b>Genetic group</b>																
<b>REFERENCE VIRUSES</b>																
A/Perth/16/2009	2009-07-04	E3/E2	1280	80	320	1280	320	320	320	640	640	1280				
A/Victoria/208/2009	2009-06-02	E3/E1	1280	5120	2560	5120	2560	5120	5120	5120	5120	5120	5120	5120		
A/Alabama/5/2010	2010-07-13	MK1/C2/SIAT2	40	40	160	640	160	160	80	320	160	640				
A/Hong Kong/3969/2011	2011-05-19	MDCK2/SIAT4	80	160	320	1280	320	320	640	1280	2560	1280				
A/Stockholm/1/8/2011	2011-03-28	MDCK2/SIAT4	40	40	80	640	160	80	160	320	160	640				
A/Iowa/19/2010	2010-12-30	E3/E1	640	5120	1280	5120	1280	5120	2560	5120	5120	5120	5120	5120		
A/Victoria/361/2011	2011-10-24	E3/E2	320	640	320	1280	160	640	5120	640	640	320				
A/Berlin/93/2011	2011-12-07	NVD3/S2	160	160	320	1280	320	320	320	1280	640	1280				
A/Victoria/361/2011	2011-10-24	M2/S2	160	160	320	1280	320	320	320	1280	640	1280				
A/Athens/112/2012	2012-02-01	SIAT4	80	160	320	1280	320	320	320	1280	640	1280				
<b>TEST VIRUSES</b>																
A/Denmark/38/2012	2012-03-05	SIAT2	160	320	640	1280	320	640	320	1280	1280	2560				
A/Iceland/66/2011	2011-12-07	MDCK1/SIAT1	80	160	320	640	160	320	160	640	320	640				
A/Iceland/67/2011	2011-12-08	MDCK2/SIAT1	80	160	320	640	320	320	160	640	640	640				
A/Iceland/68/2011	2011-12-13	MDCK3/SIAT1	40	80	160	160	80	160	80	160	160	320				
A/Iceland/69/2011	2011-12-22	MDCK3/SIAT1	320	160	640	1280	320	640	320	1280	640	1280				
A/Iceland/70/2011	2011-12-28	MDCK2/SIAT1	80	160	320	640	320	320	160	1280	640	640				
A/Iceland/02/2012	2012-01-13	MDCK2/SIAT1	80	160	320	640	160	320	160	640	640	320				
A/Iceland/04/2012	2012-01-16	MDCK3/SIAT1	<	80	80	160	80	80	80	320	160	320				
A/Iceland/05/2012	2012-01-18	MDCK2/SIAT1	<	40	40	160	80	80	80	320	160	320				
A/Iceland/07/2012	2012-01-24	MDCK2/SIAT1	160	320	640	1280	640	640	640	1280	1280	1280				
A/Iceland/1/2012	2012-02-08	MDCK2/SIAT1	40	80	160	640	160	160	160	640	320	640				
A/Iceland/1/2012	2012-02-08	MDCK3/SIAT1	<	40	80	80	80	80	80	320	160	320				
A/Iceland/1/2012	2012-02-09	MDCK2/SIAT1	40	160	160	160	320	160	160	1280	640	1280				
A/Iceland/13/2012	2012-02-09	MDCK2/SIAT1	40	80	160	160	320	160	160	1280	320	1280				
A/Iceland/14/2012	2012-02-12	MDCK2/SIAT1	40	80	80	160	320	<	160	1280	320	1280				
A/Iceland/15/2012	2012-02-13	MDCK1/SIAT1	40	80	80	160	160	80	160	640	320	6340				
A/Iceland/16/2012	2012-02-13	MDCK2/SIAT1	40	160	80	160	320	160	160	640	640	320				
A/Iceland/17/2012	2012-02-17	MDCK2/SIAT1	320	320	640	2560	320	1280	640	2560	640	1280				
A/Iceland/18/2012	2012-02-23	MDCK3/SIAT1	<	40	80	320	80	80	80	320	160	320				
A/Iceland/19/2012	2012-02-24	MDCK2/SIAT1	40	80	160	320	160	160	160	640	160	640				
A/Iceland/20/2012	2012-02-27	MDCK2/SIAT1	160	160	160	320	160	160	320	640	160	1280				
A/Iceland/21/2012	2012-03-02	MDCK2/SIAT1	80	160	320	640	320	320	160	1280	320	1280				
A/Iceland/23/2012	2012-03-27	MDCK3/SIAT1	80	80	160	320	160	320	160	640	160	640				
A/Iceland/24/2012	2012-04-14	MDCK2/SIAT1	<	<	<	80	40	40	40	160	40	160				
A/Lisboa/23/2012	2012-02-07	SIAT1/SIAT1	40	80	160	160	160	160	160	320	320	160				
A/Lisboa/30/2012	2012-01-27	SIAT1/SIAT1	40	160	320	640	160	160	160	640	320	640				
A/Lisboa/31/2012	2012-01-27	SIAT1/SIAT1	80	160	320	640	320	320	160	640	640	1280				
A/Lisboa/32/2012	2012-01-27	SIAT1/SIAT1	<	160	160	640	160	320	160	640	320	640				
A/Lisboa/38/2012	2012-03-15	SIAT1/SIAT1	<	80	160	320	160	160	160	640	320	320				
A/Lisboa/58/2012	2012-03-20	SIAT1/SIAT1	<	80	160	320	160	160	160	640	320	320				
A/Lisboa/59/2012	2012-03-27	SIAT1/SIAT1	<	80	160	320	160	160	160	640	320	320				
A/Lisboa/61/2012	2012-03-05	SIAT1/SIAT1	40	160	320	640	320	320	320	640	640	640				
A/Stockholm/11/2012	2012-01-21	C2/SIAT1	80	160	320	640	320	1280	320	1280	640	640				
A/Stockholm/6/2012		C1/SIAT1	80	160	640	1280	320	640	320	1280	1280	1280				
A/Stockholm/14/2012	2012-03-16	C2/SIAT1	80	160	160	1280	320	320	320	640	640	640				
A/Stockholm/19/2012	2012-04-14	C1/SIAT1	80	160	320	1280	320	320	320	640	640	1280				
A/England/524/2012	2012-04-12	SIAT1/SIAT3	40	80	160	160	320	160	80	640	320	320				
A/Iceland/65/2011	2011-11-19	MDCK3/SIAT2	<	80	40	160	80	80	80	320	160	320				
A/Iceland/06/2012	2012-01-24	MDCK2/SIAT2	<	40	80	160	80	80	80	320	160	160				

1. &lt; = &lt;40

Vaccine

Vaccine

Vaccine

**Table 6. Antigenic analysis of A(H3N2) viruses by HI (guinea pig RBCs with 20nM oseltamivir)**

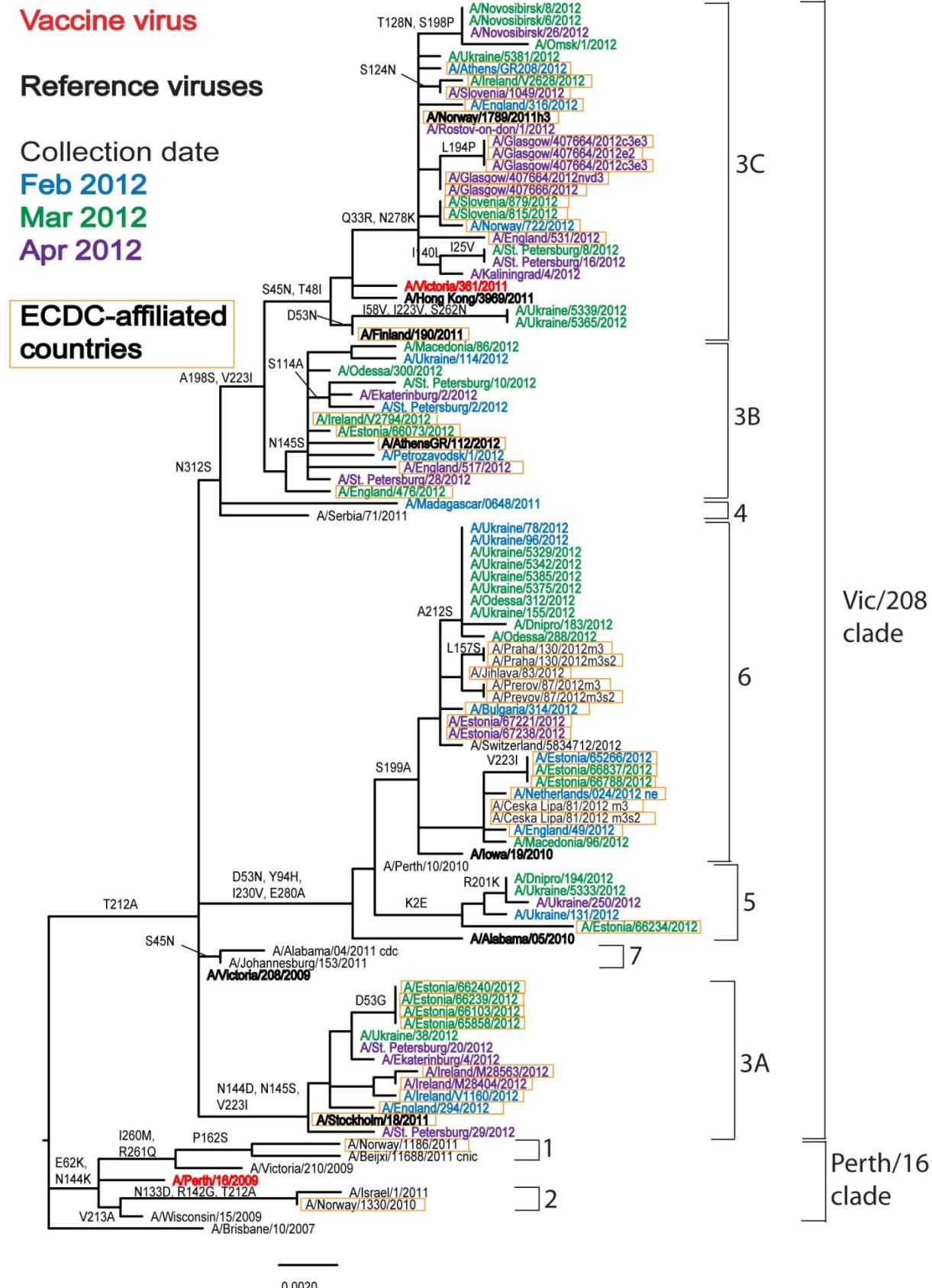
Viruses	Collection Date	Passage History	Haemagglutination inhibition titre <sup>1</sup>										
			Post infection ferret sera										
			A/Perth/16/2009 F35/09	A/Vic/208/09 F7/10	A/Ala/5/10 F27/10	A/HK/3969/11 F27/11	A/Stock/18/11 F28/11	A/Iowa/19/10 F15/11	A/Vic/361/11 Egg F05/12	A/Berlin/93/11 T/C F17/12	A/Vic/361/11 T/C F15/12	A/Athens/112/12 F16/12	
Genetic group			group 5	group 3C	group 3A	group 6	group 3C	group 3C	group 3C	group 3C	group 3C	group 3B	
<b>REFERENCE VIRUSES</b>													
A/Perth/16/2009	2009-07-04	E3/E2	640	80	160	640	160	160	160	640	640	640	640
A/Victoria/208/2009	2009-06-02	E3/E1	2560	5120	1280	5120	2560	5120	5120	5120	5120	5120	5120
A/Alabama/5/2010	2010-07-13	MK1/C2/SIAT2	40	40	160	640	160	160	80	640	320	640	640
A/Hong Kong/3969/2011	2011-05-19	MDCK2/SIAT4	320	320	640	1280	640	640	640	2560	1280	2560	2560
A/Stockholm/18/2011	2011-03-28	MDCK2/SIAT4	40	80	80	640	320	80	160	640	320	640	640
A/Iowa/19/2010	2010-12-30	E3/E1	1280	5120	2560	5120	5120	5120	5120	5120	5120	5120	5120
A/Victoria/361/2011	2011-10-24	E3/E1	160	640	320	640	160	640	5120	1280	320	640	640
A/Berlin/93/2011	2011-12-07	NVD3/SIAT2	160	160	320	1280	640	640	640	1280	1280	1280	1280
A/Victoria/361/2011	2011-10-24	M2/S2	80	160	160	640	160	320	160	640	640	640	640
A/Athens/112/2012	2012-02-01	SIAT3	80	160	160	640	160	160	160	640	640	640	1280
<b>TEST VIRUSES</b>													
A/Pardubice/7/2012		MDCK5/SIAT2	160	160	640	1280	320	640	320	2560	1280	1280	1280
A/Ceska Lipa/83/2012		MDCK3/SIAT2	160	160	640	1280	320	640	320	1280	1280	1280	1280
A/Jihlava/83/2012		MDCK3/SIAT2	160	160	640	1280	320	640	320	1280	1280	1280	1280
A/Vsetin/85/2012		MDCK3/SIAT2	160	320	640	1280	640	640	320	2560	1280	1280	1280
A/Prerov/87/2012		MDCK3/SIAT2	160	160	320	640	320	320	160	1280	1280	640	640
A/Praha/130/2012		MDCK3/SIAT2	160	320	640	2560	640	1280	640	2560	2560	2560	2560
A/England/294/2012	2012-02-20	SIAT2/SIAT1	80	160	160	640	160	160	160	640	320	640	640
A/England/49/2012	2012-02-26	SIAT1/SIAT1	160	320	640	1280	640	640	320	2560	1280	1280	1280
A/England/316/2012	2012-02-28	SIAT1/SIAT1	160	320	320	1280	640	640	320	2560	1280	1280	1280
A/England/392/2012	2012-03-13	SIAT1/SIAT1	80	320	160	640	640	320	160	640	640	640	640
A/England/476/2012	2012-03-19	SIAT1/SIAT1	160	320	320	1280	640	640	640	2560	1280	1280	1280
A/England/517/2012	2012-04-05	SIAT1/SIAT1	80	160	160	640	320	320	160	1280	640	640	640
A/England/531/2012	2012-04-16	MDCK1/SIAT1	40	40	40	320	80	80	80	320	320	320	320
A/Iceland/09/2012	2012-01-30	MDCK3/SIAT3	80	80	160	640	160	320	160	640	320	640	640
A/Ireland/12M28563/2012	2012-04-10	SIAT4	160	160	320	1280	640	320	320	2560	640	1280	1280
A/Denmark/2/2012	2012-01-30	SIAT3/SIAT1	80	160	160	640	320	160	160	1280	320	640	640
A/Denmark/3/2012	2012-02-06	SIAT1/MDCK2/SIAT1	40	160	80	640	320	160	160	1280	320	640	640
A/Denmark/5/2012	2012-02-07	SIAT1/MDCK2/SIAT1	160	320	640	1280	320	640	320	2560	640	1280	1280
A/Denmark/6/2012	2012-02-07	SIAT1/MDCK2/SIAT1	40	80	80	320	160	160	160	640	320	320	320
A/Denmark/12/2012	2012-02-14	SIAT1/MDCK2/SIAT1	40	80	80	160	160	80	80	640	160	160	160
A/Denmark/24/2012	2012-03-11	SIAT1/MDCK1/SIAT1	80	320	160	640	640	320	320	1280	640	640	1280
A/Denmark/25/2012	2012-03-13	SIAT1/MDCK2/SIAT1	80	160	160	640	320	160	160	1280	640	640	640
A/Denmark/26/2012	2012-03-18	SIAT1/MDCK3/SIAT1	80	160	160	640	160	160	160	1280	640	640	640
A/Denmark/28/2012	2012-03-14	SIAT1/MDCK1/SIAT1	80	160	160	640	160	160	160	1280	320	640	640
A/Denmark/31/2012	2012-03-21	SIAT1/MDCK2/SIAT1	160	320	320	640	640	320	320	2560	640	1280	1280
A/Denmark/36/2012	2012-03-26	SIAT1/MDCK2/SIAT1	320	640	640	1280	1280	640	640	5120	1280	2560	2560
A/Denmark/41/2012	2012-04-10	SIAT1/MDCK2/SIAT1	80	320	320	1280	640	320	320	2560	640	640	640
A/Denmark/42/2012	2012-04-21	SIAT1/MDCK1/SIAT1	160	160	320	640	320	320	320	2560	640	640	640
A/Denmark/45/2012	2012-04-24	SIAT1/MDCK2/SIAT1	640	1280	1280	2560	1280	1280	1280	5120	2560	2560	2560
A/Karlovy Vary/46/2012		MDCK5/SIAT3	40	80	80	320	80	160	80	640	320	320	320
A/Decin/42/2012		MDCK5/SIAT3	40	80	80	320	80	160	80	640	320	320	320
A/Cercany/96/2012		MDCK3/SIAT3	40	80	160	320	160	160	160	640	640	640	320
A/Praha/98/2012		MDCK3/SIAT3	40	80	80	320	160	160	160	640	320	320	320
A/England/354/2012	2012-02-28	SIAT2/SIAT2	40	80	80	320	160	160	80	320	160	320	320
A/Scotland/1/2012	2012-03-30	SIAT3/SIAT2	< 40	40	40	160	160	40	80	320	80	160	160
A/England/509/2012	2012-04-04	SIAT1/SIAT2	40	80	80	320	160	160	160	640	640	640	640
A/Ireland/V1160/2012	2012-02-01	C2/SIAT1	80	80	80	320	320	160	160	160	640	320	640
A/Ireland/12V2608/2012	2012-03-22	C1/SIAT1	40	80	80	320	320	160	160	160	640	320	640
A/Ireland/12V2628/2012	2012-03-22	C1/SIAT1	160	160	320	1280	320	640	320	2560	1280	1280	1280
A/Ireland/12V2734/2012	2012-03-26	C1/SIAT1	40	80	80	640	320	160	160	640	320	640	640
A/Ireland/12V2794/2012	2012-03-28	C1/SIAT1	40	40	40	320	160	80	160	640	160	6340	

1. &lt; = &lt;40

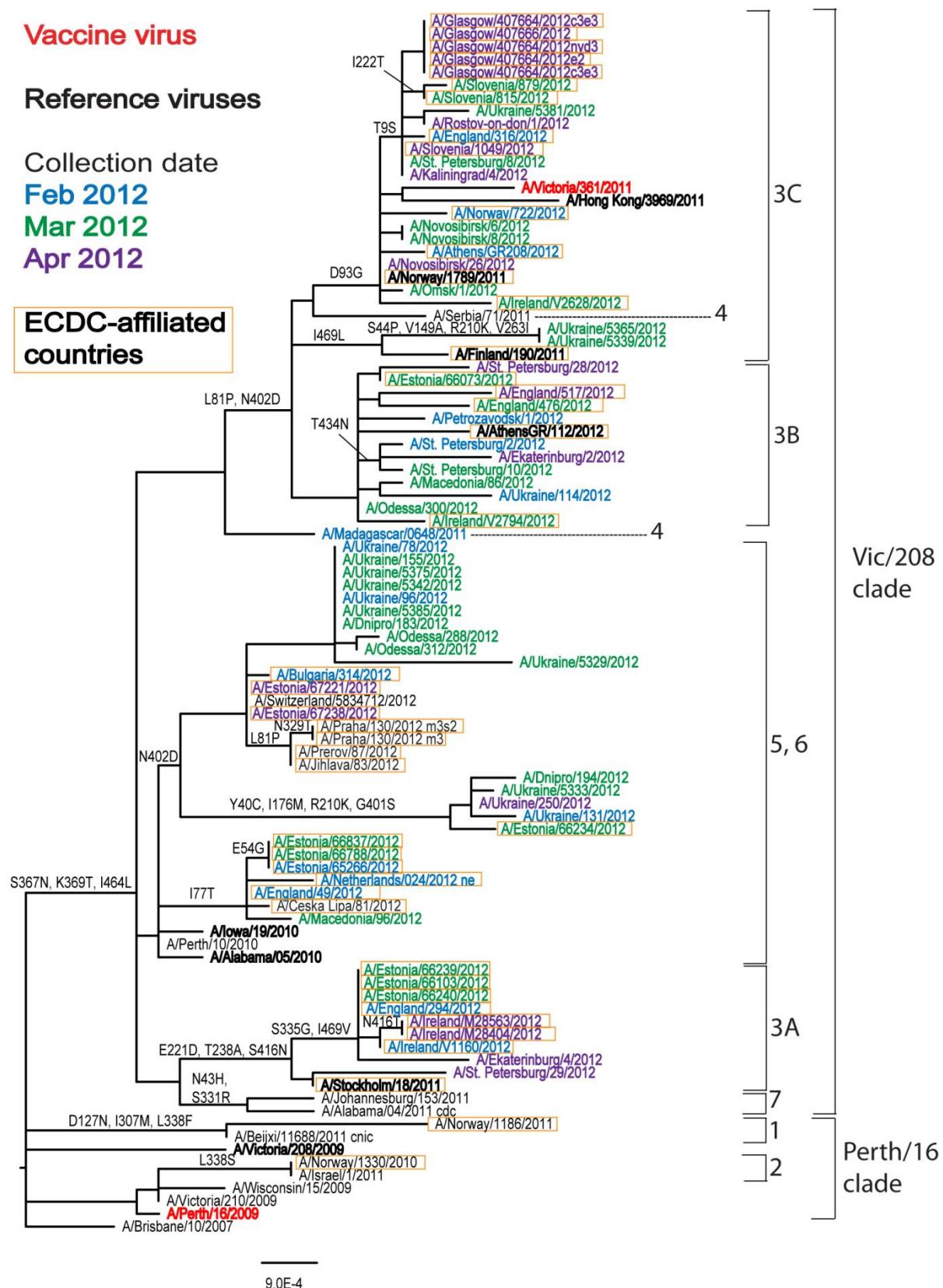
Vaccine virus

Vaccine virus

Vaccine virus

**Figure 3. Phylogenetic comparison of influenza A(H3N2) HA genes (HA1 coding region)**

#### Figure 4. Phylogenetic comparison of influenza A(H3N2) NA genes



**Table 7. Antigenic analysis of influenza B/Victoria-lineage viruses by HI (turkey RBCs)**

Antigenic analyses of influenza B viruses (Victoria lineage)

Viruses	Collection date	Passage History	Haemagglutination inhibition titre <sup>1</sup>								
			Post infection ferret sera								
			B/Bris <sup>2</sup> 60/08 Sh 523	B/Mal 2506/04 F28/05	B/England 393/08 F05/11	B/Bris 60/08 F06/11	B/Paris 1762/08 F07/11	B/HK 514/09 F13/10	B/Odessa 3886/10 F19/11	B/Malta 636714/11 F33/11	
<b>REFERENCE VIRUSES</b>											
B/Malaysia/2506/2004	2004-12-06	E3/E5	2560	1280	40	80	<	40	<	160	
B/England/393/2008	2008-08-29	E1/E6	2560	160	320	640	40	40	40	320	
B/Brisbane/60/2008	2008-08-04	E4/E3	2560	160	160	320	40	40	40	320	
B/Paris/1762/2008	2009-02-09	C2/MDCK4	2560	10	20	40	80	80	80	20	
B/Hong Kong/514/2009	2009-10-11	MDCK1/MDCK3	5120	10	20	40	160	160	160	20	
B/Odessa/3886/2010	2010-03-19	C2/MDCK4	5120	20	40	80	160	160	160	40	
B/Malta/636714/2011	2011-03-07	E4/E1	2560	320	640	640	80	80	80	320	
<b>TEST VIRUSES</b>											
B/Denmark/2/2012	2012-02-15	MDCK2	5120	10	20	40	80	80	160	20	
B/Lisboa/3/2012	2012-03-13	SIAT1/MDCK1	5120	20	40	80	160	160	80	40	
B/Sweden/3/2011	2011-12-30	C2/MDCK1	5120	10	40	80	160	160	160	40	
B/Stockholm/5/2012	2012-02-09	C1/MDCK1	5120	20	40	80	80	80	80	40	
B/Denmark/5/2012	2012-02-27	MDCK2/MDCK1	2560	10	20	20	80	40	80	20	
B/Denmark/15/2012	2012-04-16	MDCK2/MDCK1	2560	20	40	40	40	40	40	40	
B/Pardubice/21/2012		MDCK4/MDCK1	1280	<	10	10	40	40	20	10	
B/Karlovy Vary/24/2012		MDCK3/MDCK2	5120	<	10	40	80	80	40	20	
B/Vsetin/51/2012		MDCK3/MDCK1	2560	<	10	20	80	80	20	20	
B/Praha/27/2012		MDCK3/MDCK1	2560	<	10	20	80	80	20	10	
B/Praha/52/2012		MDCK4/MDCK1	2560	<	10	20	80	80	20	20	
B/Praha/90/2012		MDCK3/MDCK1	2560	<	10	20	80	80	40	20	
B/Karlovy Vary/93/2012		MDCK3/MDCK1	2560	<	20	20	80	80	40	20	
B/Karlovy Vary/23/2012		MDCK3/MDCK2	2560	<	20	40	40	80	20	20	
B/Prerov/55/2012		MDCK3/MDCK2	2560	<	20	20	80	80	40	20	
B/England/322/2012	2012-02-29	SIAT1/MDCK1	2560	<	10	20	40	40	20	10	
B/England/507/2012	2012-04-04	SIAT1/MDCK1	2560	<	10	20	80	80	20	20	
B/England/537/2012	2012-04-17	SIAT2/MDCK1	2560	<	10	20	80	80	20	20	
B/Prerov/25/2012		MDCK3/MDCK3	5120	10	40	40	80	80	160	40	
B/England/345/2012	2012-03-08	SIAT1/MDCK2	5120	10	40	80	80	160	160	40	
B/Ireland/12M17522/2012	2012-02-29	C1/SIAT1	5120	<	20	40	40	40	80	20	
B/Slovenia/955/2012	2012-03-26	MDCKx/MDCK1	5120	10	10	20	80	80	80	20	
B/Norway/710/2012	2012-02-13	MDCK1/MDCK1	2560	<	10	40	40	20	40	<	

1. &lt; = &lt;10; 2. hyperimmune sheep serum

Sequence in phylogenetic tree

**Table 8. Antigenic analysis of influenza B/Yamagata-lineage viruses by HI (turkey RBCs)**

Viruses	Collection date	Passage History	Haemagglutination inhibition titre											
			Post infection ferret sera											
			B/F1 <sup>1</sup> 4/06 SH479	B/Eg <sup>1</sup> 144/05 F3/07	B/F1 <sup>1</sup> 4/06 F21/07	B/Bris <sup>2</sup> 3/07 F24/07	B/Eng <sup>2</sup> 145/08 F9/08	B/Bang <sup>2</sup> 3333/07 F21/08	B/Wis <sup>2</sup> 1/10 F26/10	B/Stock <sup>2</sup> 12/2011 F12/12	B/Estonia <sup>2</sup> 55669/2011 F26/11	B/Serbia <sup>2</sup> 1894/2011 F25/11	B/Stock <sup>2</sup> 12/2011 T/C F8/12	
<b>REFERENCE VIRUSES</b>														
B/Egypt/144/2005	2005-05-01	E3/E5	5120	640	1280	1280	320	640	640	1280	320	40	640	
B/Florida/4/2006	2006-12-15	E3/E4	5120	320	1280	1280	320	320	640	1280	320	40	320	
B/Brisbane/3/2007	2007-09-03	E2/E1	5120	160	640	640	80	320	320	640	160	10	320	
B/England/145/2008		E/x/E1	640	<	40	20	160	20	20	80	<	<	20	
B/Bangladesh/3333/2007	2007-08-07	E4/E1	5120	80	160	160	80	320	320	1280	10	20	320	
B/Wisconsin/1/2010	2007-08-07	E4/E1	2560	160	320	160	160	640	640	20	40	160		
B/Stockholm/12/2011	2007-08-07	E4/E1	5120	80	160	160	80	320	320	640	20	40	320	
B/Estonia/55669/2011	2011-03-14	MDCK2/MDCK2	2560	80	160	40	160	80	40	320	1280	80	40	
B/Serbia/1894/2011	2011-03-08	MDCK1/MDCK4	2560	80	160	40	160	160	160	640	160	320	160	
B/Stockholm/12/2011	2011-03-28	Cx/MDCK1	5120	160	320	80	640	320	320	320	320	640	320	
<b>TEST VIRUSES</b>														
B/Lisboa/1/2012	2012-02-28	SIAT2/MDCK1	2560	40	160	80	160	40	40	160	1280	80	20	
B/Lisboa/5/2012	2012-03-19	SIAT1/MDCK1	2560	40	80	40	160	160	160	320	80	160	160	
B/Lisboa/6/2012	2012-03-15	SIAT1/MDCK2	5120	160	160	80	320	320	320	640	640	640	160	
B/Stockholm/2/2012	2012-02-02	C1/MDCK1	5120	160	80	40	160	160	160	640	160	320	160	
B/Stockholm/8/2012	2012-03-06	CO/MDCK1	2560	160	80	80	80	40	40	160	1280	80	20	
B/Denmark/3/2012	2012-02-22	MDCK3/MDCK1	640	40	40	20	40	40	40	160	20	40	10	
B/Denmark/7/2012	2012-02-28	MDCK2/MDCK1	640	<	<	10	40	20	40	160	10	40	20	
B/Denmark/8/2012	2012-02-29	MDCK2/MDCK1	1280	40	40	40	80	40	80	320	80	80	40	
B/Hradec Kralove/26/2012		MDCK3/MDCK1	640	<	40	40	10	10	10	80	320	20	ND	
B/Hradec Kralove/29/2012		MDCK3/MDCK1	2560	40	160	80	80	160	80	160	640	160	ND	
B/England/267/2012	2012-02-22	SIAT1/MDCK1	2560	40	40	40	40	80	40	160	80	160	ND	
B/England/386/2012	2012-03-13	SIAT1/MDCK1	2560	80	80	80	40	40	40	160	640	40	ND	
B/England/538/2012	2012-04-10	SIAT2/MDCK1	5120	80	80	80	80	160	160	320	320	320	ND	
B/Estonia/67205/2012	2012-04-09	MDCK1/MDCK1	2560	80	160	160	80	160	160	640	160	160	ND	
B/Norway/579/2012	2012-02-14	SIAT1/MDCK1	1280	40	80	20	20	20	10	160	640	80	ND	
B/Norway/773/2012	2012-02-23	MDCK1/MDCK1	1280	40	80	20	20	20	10	160	640	80	ND	
B/Norway/777/2012	2012-02-20	MDCK1/MDCK1	2560	40	80	40	40	40	10	160	640	160	ND	
B/Athens GR/199/2012	2012-02-07	MDCK2	5120	160	80	80	320	160	80	640	1280	320	ND	

1. &lt; = &lt;40; 2. &lt; = &lt;10 ; 3. hyperimmune sheep serum

ND = not determined

Sequence in phylogenetic tree

Figure 5. Phylogenetic comparison of influenza B/Victoria-lineage HA genes (HA1 coding region)

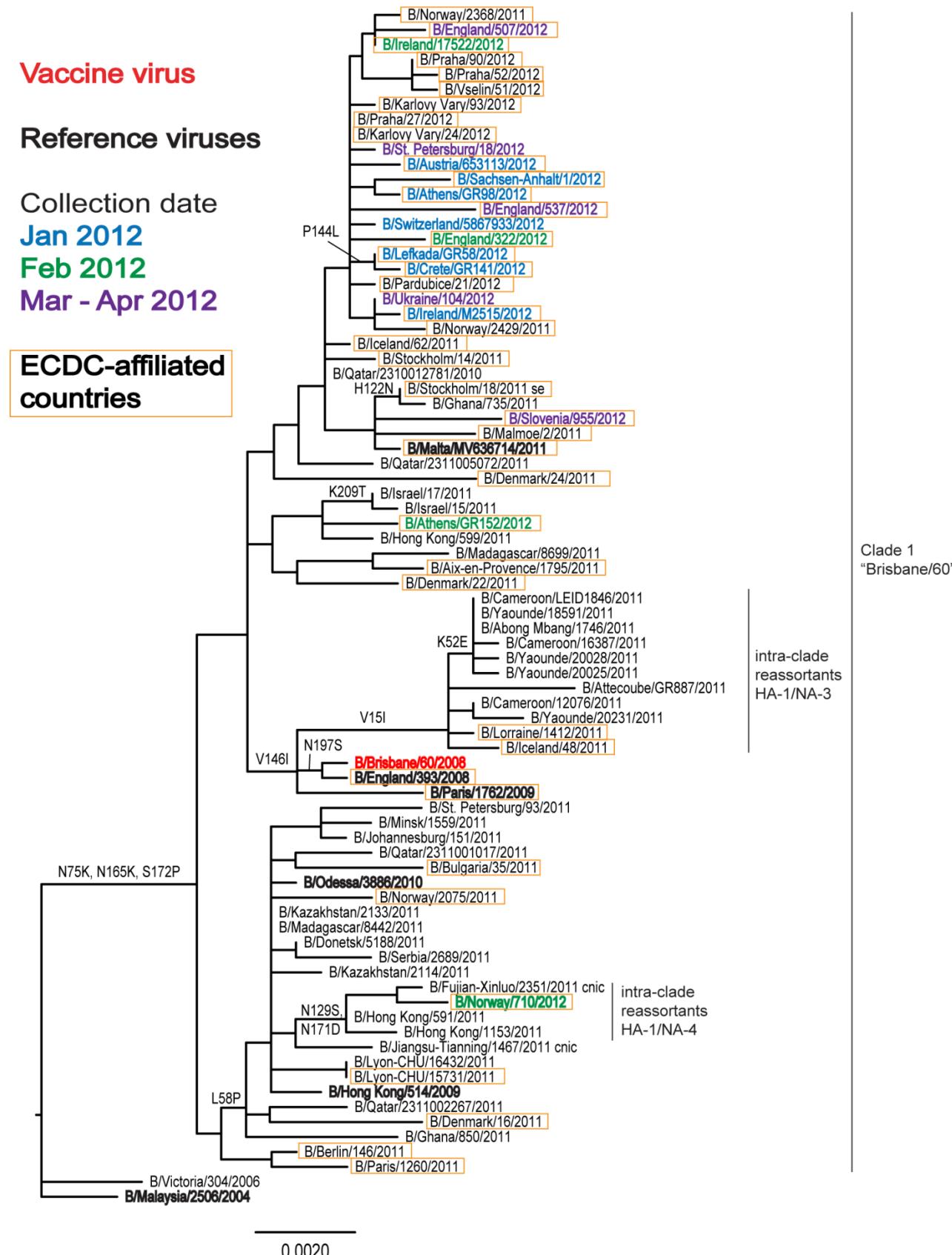


Figure 6. Phylogenetic comparison of influenza B/Victoria-lineage NA genes

## Vaccine virus

## Reference viruses

Collection date

**Jan 2012**

**Feb 2012**

**Mar - Apr 2012**

## ECDC-affiliated countries

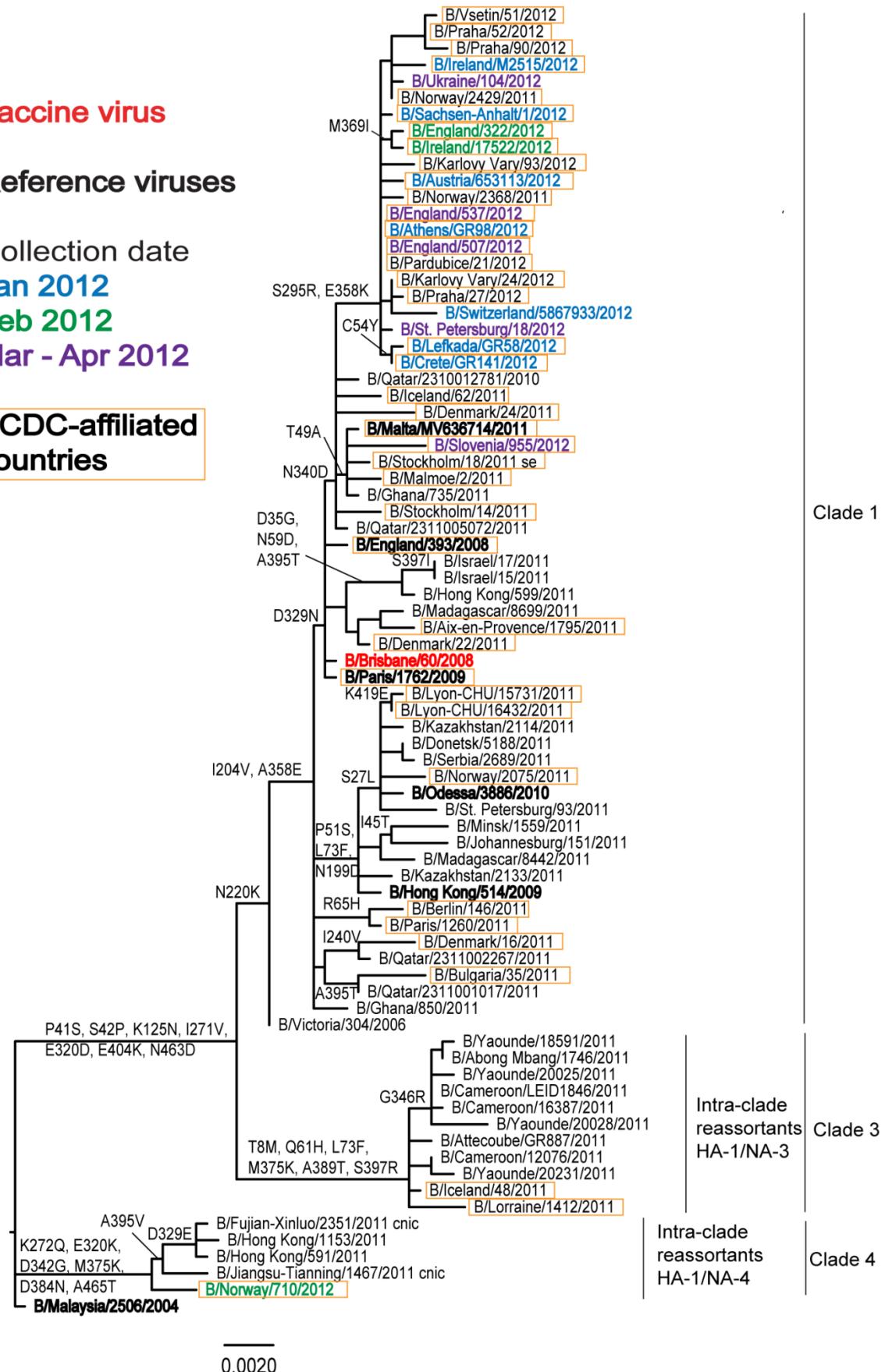


Figure 7. Phylogenetic comparison of influenza B/Yamagata-lineage HA genes (HA1 coding region)

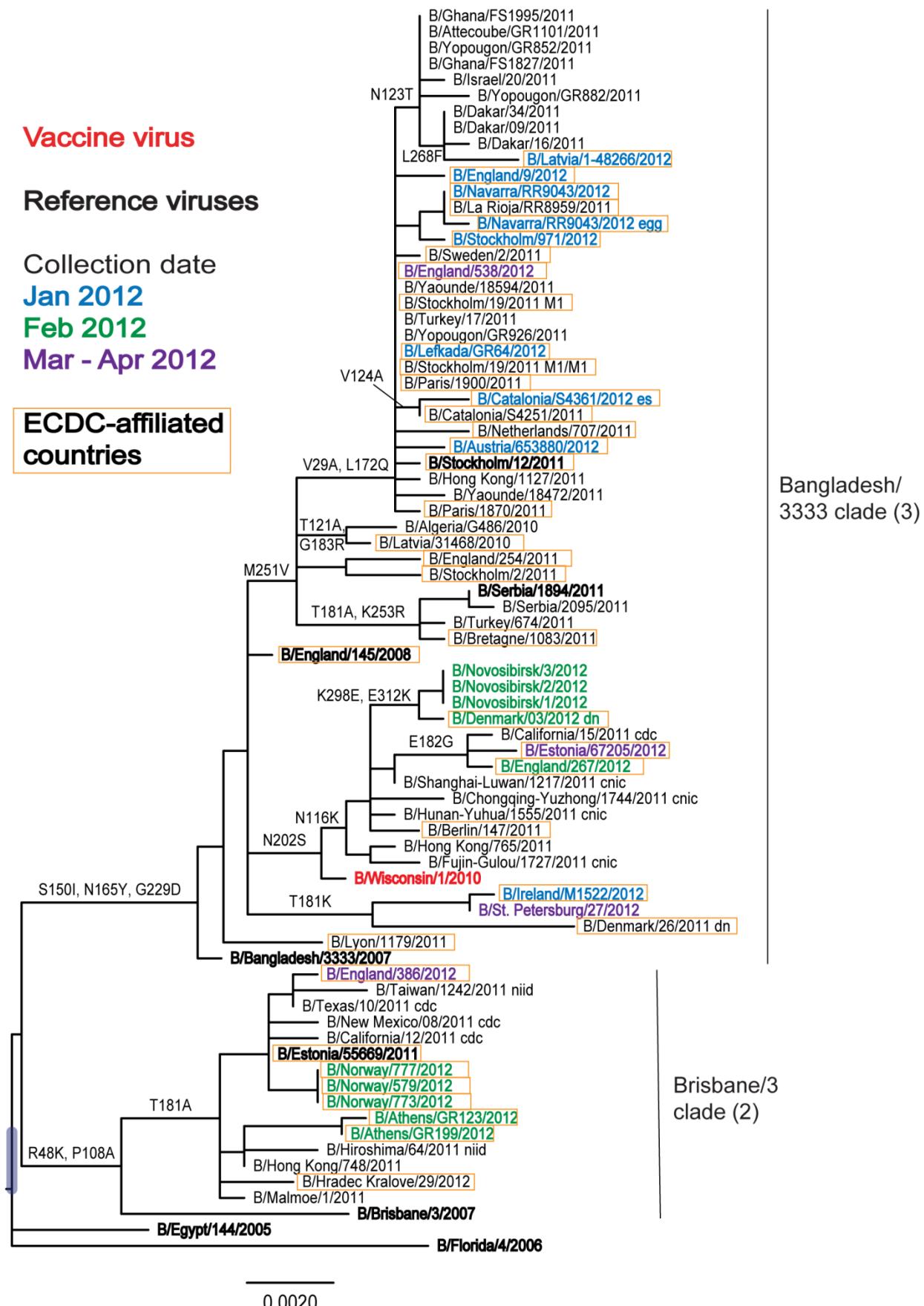


Figure 8. Phylogenetic comparison of influenza B/Yamagata-lineage NA genes

