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CNRL

SURVEILLANCE REPORT

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

Influenza virus characterisation

Summary Europe, July 2010

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Since the June 2010 report (http://ecdc.europa.eu/en/publications/Publications/1007_Influenza_virus_characterisation_2010_JUNE.pdf) only one ECDC-affiliated country (UK, England) has sent samples to the WHO CC in London (Table 1). These were composed of five influenza B viruses - Victoria lineage, a single H3N2 virus and six H1N1 pandemic viruses; all have been propagated in tissue culture and analysis of these viruses is underway.

Table 1. Summary of specimens received in May, June and July and collected since February 2010

Collection Date (Month) Country	Viruses received									
	Pandemic A(H1N1)		H3		B-Unknown lineage		B-Victoria lineage		B-Yamagata lineage	
	Number received	Number grown	Number received	Number grown	Number received	Number grown	Number received	Number grown	Number received	Number grown
FEBRUARY										
Italy							1	1		
Latvia	3	2								
Norway	6	5					1	1		
MARCH										
Italy							8	8		
Latvia									4	2
Norway	2	1			3	0				
Slovakia	6	3								
United Kingdom	2	0*					3	0*		
APRIL										
Italy							2	2		
Latvia									1	0
Norway	1	1			2	0	1	0		
Slovakia	6	3								
United Kingdom	2	0*								
MAY										
United Kingdom	2	0*					1	0*		
JUNE										
United Kingdom			1	0*						
Total	30	15	1		5		11	11	5	2

** viruses are in culture.*

Three Victoria lineage viruses tested from Norway were antigenically closely related to the current vaccine strain B/Brisbane/60/2008 and other recently circulating Victoria lineage viruses.

All pandemic H1N1 viruses received from the ECDC-affiliated countries since the June report have been antigenically similar to the vaccine strain A/California/7/2009 in HI tests (Table 2). Genetic analysis of the HA (Figure 1) and the NA (Figure 2) genes of representative viruses confirmed that the viruses remain genetically closely related to the vaccine virus and the prototype A/California/4/2009.

In the HA phylogeny, neither substitution at position 222, which may be associated with differences in severity of disease, nor viruses resistant to oseltamivir, caused by H275Y substitution in NA, form discrete subgroups (Figure 1). However, the NA sequences from oseltamivir-resistant viruses cluster in the NA phylogeny, with the exception of A/Paris/6232/2009, which contains an H/Y amino acid mixture at position 275 (Figure 2). No oseltamivir resistance has been found among pandemic H1N1 viruses tested at the WHO CC, London for specimens collected by ECDC-affiliated countries during 2010.

Table 2. Representative examples of recent antigenic analyses of pandemic A(H1N1) influenza viruses.

			Haemagglutination inhibition titre[1]					
			Post infection ferret sera					
Viruses	**Collection date**	**Passage History**	**A/Cal 4/09 C4/F14/09**	**A/Cal 7/09 C4/31/09**	**A/Eng 195/09 NIBSC F17/09**	**A/Auck 3/09 C4/17/09**	**A/Bayern 69/09 C4/33/09**	**A/Lviv N6/2009 C4/34/09**
REFERENCE VIRUSES								
A/California/4/2009		C1,E2	**2560**	2560	2560	2560	1280	2560
A/California/7/2009		E6	1280	**1280**	1280	1280	640	1280
A/England/195/2009		MDCK3/SIAT1	1280	1280	**1280**	1280	640	1280
A/Auckland/3/2009		Ex+3	2560	1280	1280	**2560**	1280	2560
A/Bayern/69/2009		MDCK4/SIAT1	40	80	40	40	**320**	160
A/Lviv/N6/2009		MDCK4/SIAT1	160	640	80	80	1280	**1280**
TEST VIRUSES								
A/Salamanca/49/2009	16/11/2009	E2 E1	640	1280	1280	1280	640	1280
A/Zamora/50/2009	16/11/2009	E2 E1	640	1280	1280	1280	640	1280
A/Valladolid/51/2009	17/11/2009	E2 E1	1280	1280	1280	1280	640	1280
A/Slovakia/1580/2010	09/03/2010	MDCKx MDCK1	1280	1280	2560	2560	640	1280
A/Slovakia/1581/2010	09/03/2010	MDCKx MDCK1	1280	2560	2560	2560	640	1280
A/Slovakia/1584/2010	09/03/2010	MDCKx MDCK1	1280	1280	2560	2560	1280	2560
A/Slovakia/1639/2010	06/04/2010	MDCKx MDCK1	2560	2560	2560	2560	1280	2560
A/Slovakia/1694/2010	06/04/2010	MDCKx MDCK1	1280	1280	2560	2560	1280	1280
A/Slovakia/1641/2010	06/04/2010	MDCKx MDCK1	2560	2560	2560	5120	1280	5120
A/Norway/6/2010	02/01/2010	MDCK2 MDCK2	1280	1280	1280	2560	1280	1280
A/Norway83//2010	04/01/2010	MDCK2 MDCK2	1280	1280	2560	2560	640	1280
A/Norway84//2010	05/01/2010	MDCK3 MDCK2	1280	1280	2560	1280	1280	1280
A/Norway/238/2010	23/02/2010	MDCK1 MDCK2	640	640	640	1280	320	640
A/Norway252//2010	25/02/2010	MDCK3 MDCK1	2560	2560	2560	2560	2560	2560
A/Norway308//2010	18/03/2010	MDCK2 MDCK2	2560	5120	5120	5120	1280	2560
A/Norway445//2010	22/04/2010	MDCK3 MDCK1	640	640	640	2560	1280	1280

1. < = 40

Figure 1. Phylogenetic comparison of influenza A H1N1(2009) HA1 genes

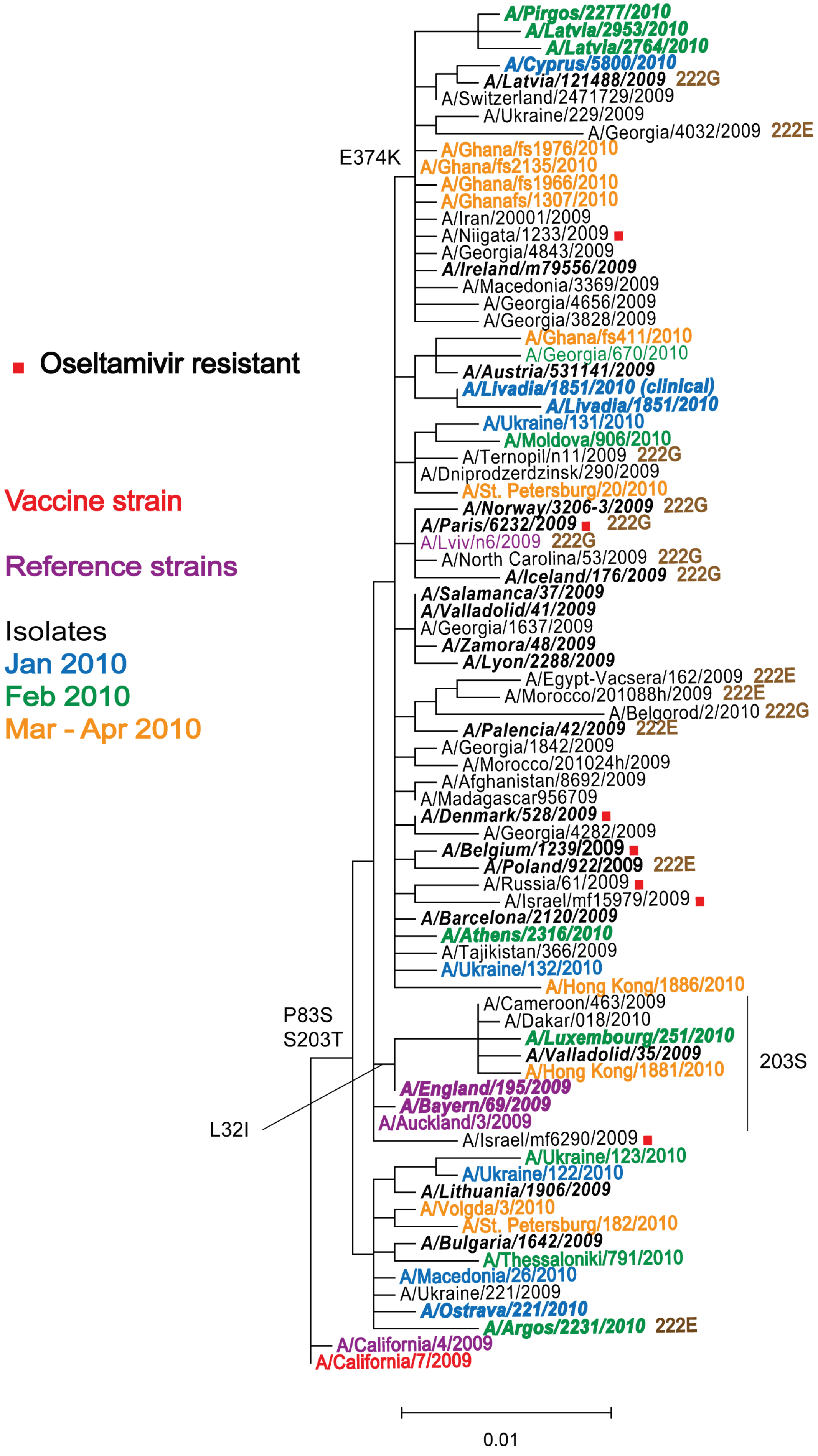
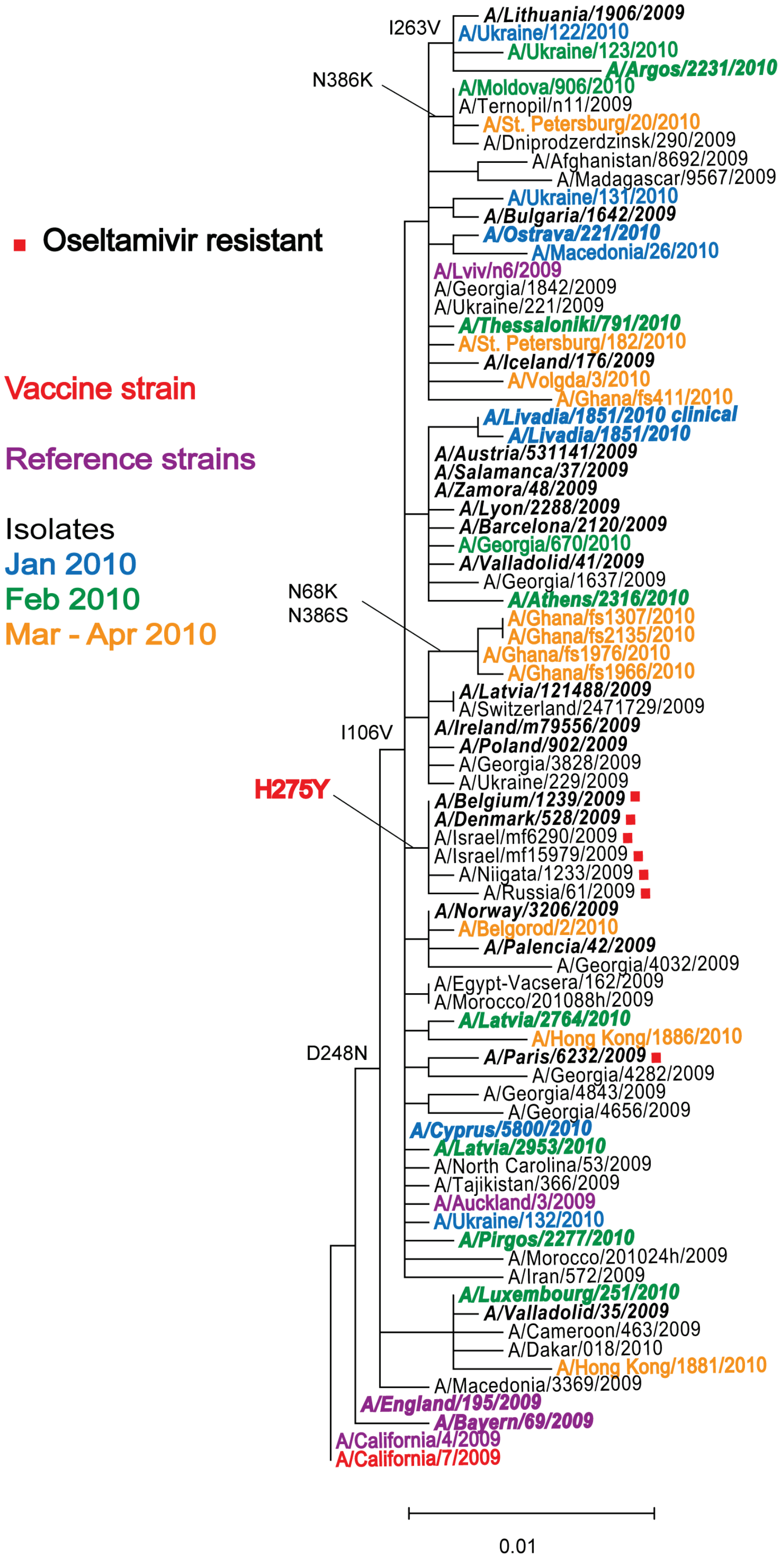


Figure 2. Phylogenetic comparison of influenza A H1N1(2009) NA genes



The phylogenetic trees were constructed using maximum parsimony in PAUP (Sinauer Associates). The bars indicate the proportion of nucleotide changes in the sequence. Reference strains are viruses to which post-infection ferret antisera have been developed. The colours indicate the date of sample collection. Isolates from ECDC countries are in italics. Sequences for some of the viruses from non-European countries were recovered from GISAID and we acknowledge all laboratories submitting sequences.