

TECHNICAL DOCUMENT

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

Influenza virus characterisation

Summary Europe, June 2010

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Since the [May 2010](#) report, only three ECDC-affiliated countries (Norway, Slovakia and Spain) have sent specimens to the WHO CC in London (Table 1). The 128 Slovakian pandemic A(H1N1) specimens were composed of 64 virus isolates and their corresponding clinical samples. The Spanish B viruses were received as egg-grown isolates while all other virus isolates received were propagated in MDCK cells.

Table 1: Summary of specimens received in May and June 2010 and analyses conducted on them.

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
PRE-FEBRUARY										
Norway	12	0*	1	0*	10	0*				
Slovakia	104	0*								
Spain	13	13								
FEBRUARY										
Italy							1	1		
Latvia	3	2								
Norway	6	0*			1	0*				
MARCH										
Italy							8	8		
Latvia									4	2
Norway	2	0*			3	0*				
Slovakia	12	0*								
APRIL										
Italy							2	2		
Latvia									1	0
Norway	1	0*			3	0*				
Slovakia	12	0*								
Total	165	15	1		17		11	11	5	2

* viruses are in culture.

The small number of pandemic A(H1N1) viruses received from ECDC-affiliated countries since the May report have all been antigenically similar to the vaccine strain A/California/7/2009.

Sixteen B viruses have been received. Of these, the 11 Victoria-lineage viruses from Italy (Milano) were antigenically and genetically closely related to the current vaccine strain B/Brisbane/60/2008, as were other currently circulating Victoria-lineage viruses from around the world (Figure 1).

The Yamagata-lineage B viruses from Latvia were antigenically similar to B/Florida/4/2006, the most recently recommended B-Yamagata strain for inclusion in vaccine formulations (Southern Hemisphere 2009), and other reference viruses such as B/Bangladesh/3333/2007. There has been some genetic drift as shown in Figure 2. The resulting amino acid substitutions in the haemagglutinin glycoproteins of the Latvian influenza B viruses are located away from the receptor binding site but within the globular head of the haemagglutinin trimer.

The Italian (Milano) B Victoria-lineage viruses fall within a distinct genetic subgroup as do the Latvian B Yamagata-lineage viruses.

Figure 1: Phylogenetic comparison of B HA1 genes (Victoria-lineage)

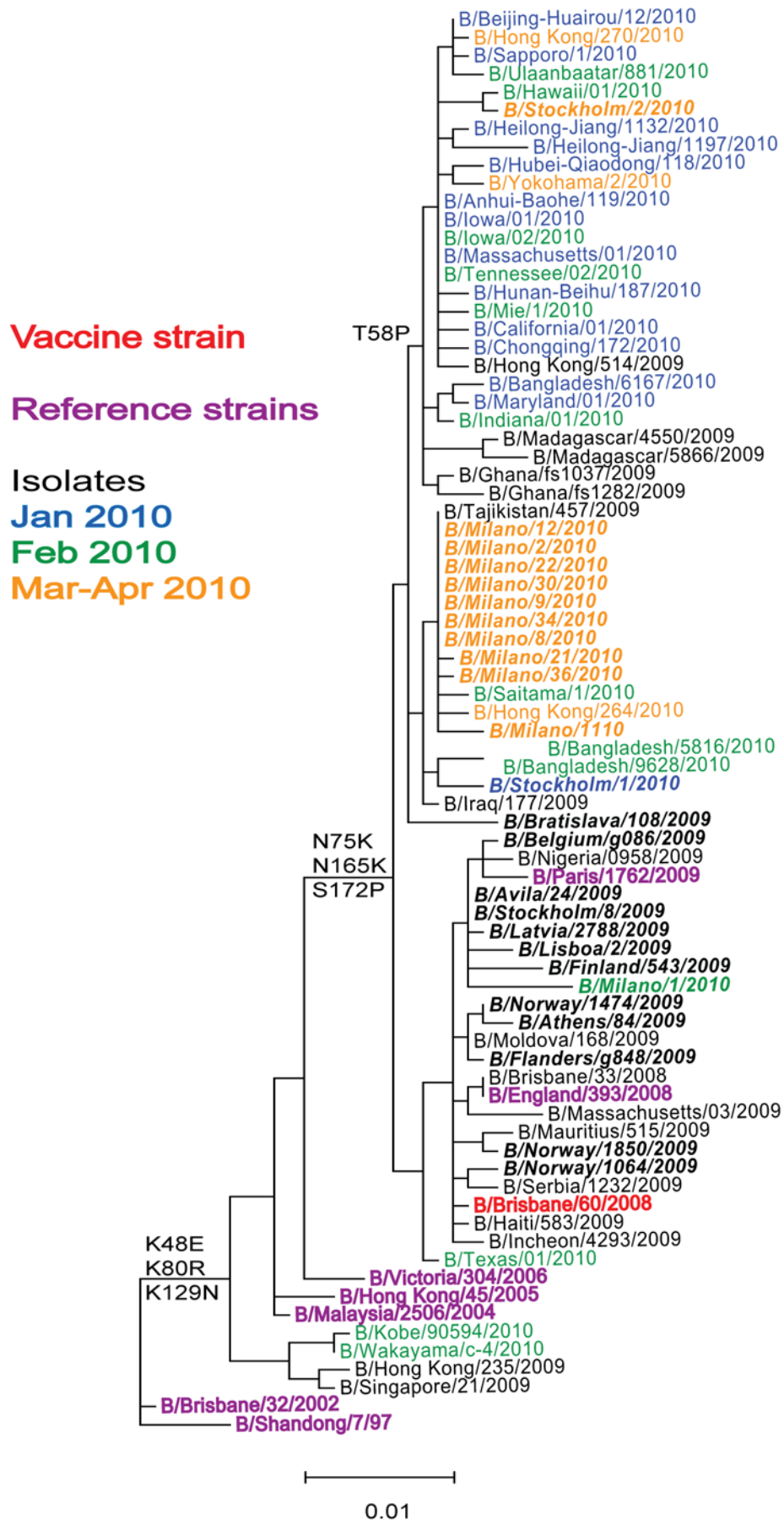
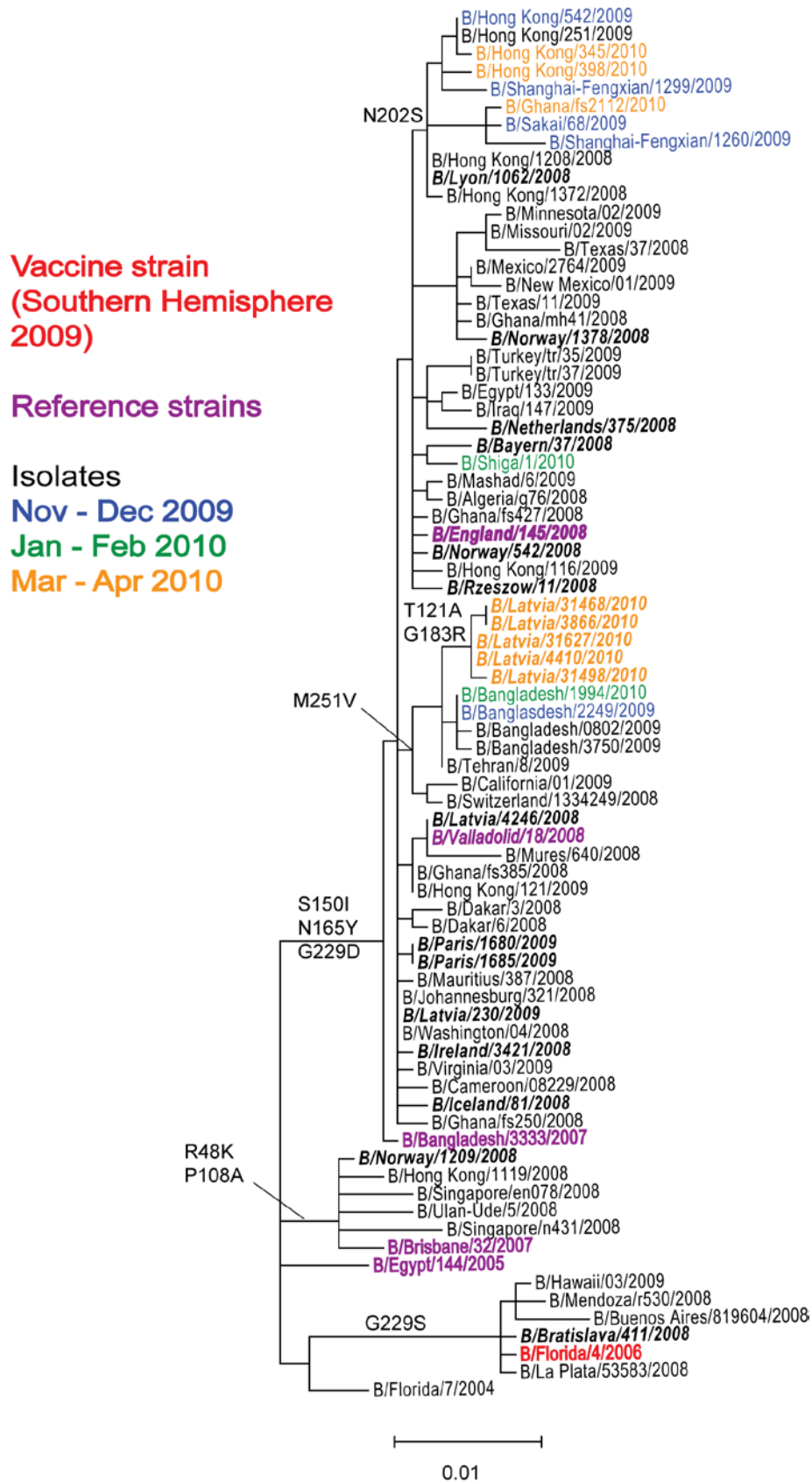


Figure 2: Phylogenetic comparison of B HA1 genes (Yamagata-lineage)



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.