SURVEILLANCE REPORT

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

Influenza virus characterisation

Summary for Europe, September 2010

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Since the August 2010 report (click here for August report), one ECDC-affiliated country (Norway) has sent samples to the WHO CC in London (Table 1). These were composed of one H1N1 pandemic virus and nine influenza B viruses (Victoria-lineage).

The pandemic H1N1 virus received from Norway (an imported case following travel to India) was antigenically similar to the vaccine virus A/California/7/2009 in HI tests. Genetic analysis of the HA (Figure 1) and the NA genes of representative viruses collected in the same time frame from the rest of the world confirmed that the viruses remain closely related genetically to the vaccine virus (A/California/7/2009). However, a significant number of the most recently collected viruses fall within sub-groups defined by S128P, V199A and I295V (represented by A/Hong Kong/2213/2010) and by D94N, N125D and V250A (represented by A/Christchurch/16/2010). These viruses are antigenically similar to the vaccine virus.

Of the nine Victoria-lineage influenza B viruses received from Norway, seven were propagated and shown to be similar antigenically to the vaccine virus (B/Brisbane/60/2008) and other Victoria-lineage influenza B viruses currently being isolated around the world. Genetic analysis of the HA (Figure 2) and the NA genes of recent representative viruses from non-ECDC affiliated countries confirmed that the viruses remain closely related genetically to the vaccine virus.

Recently collected B/Yamagata-lineage viruses are antigenically similar to B/Bangladesh/3333/2007 and fall within the Bangladesh/3333 clade (Figure 3). Similar observations have been made for B/Yamagata-lineage viruses collected in Europe earlier in 2010.

Although no H3N2 viruses were received from ECDC-affiliated countries at the London WHOCC in September, genetic analysis of the HA (Figure 4) and NA of recently circulating viruses from other parts of the world showed the majority of viruses to cluster within the Victoria/208 clade. Notably, within the HA, a subgroup defined by D53N, Y94H, I230V, and E280A (represented by A/Hong Kong/2121/2010) has emerged recently and shows geographic spread. The isolates throughout the Victoria/208 clade that have been analysed by HI remain antigenically similar to the vaccine virus (A/Perth/16/2009).

Table 1: Summary of specimens received in May to September and collected since February 2010

Collection Month	Viruses received									
	Pandemic A(H1N1)		H3		B-Unknown lineage		B-Victoria lineage		B-Yamagata lineage	
Country	Number received	Number grown	Number received	Number grown	Number received	Number grown	Number received	Number grown	Number received	Number grown
FEBRUARY										
France	6	6								
Italy							1	1		
Latvia	3	2								
Norway	6	5					1	1		
Sweden							1	1		
MARCH										
France							2	2		
Italy							8	8		
Latvia									4	2
Norway	2	1			2	0	1	1		
Slovakia	6	3								
Sweden							1	1		
United Kingdom	2	2					3	3		
APRIL										
France							1	1		
Italy							2	2		
Latvia									1	0
Netherlands					1	1				
Norway	1	1			2	0	2	2		
Slovakia	6	3								
Sweden	1	1	2	2			2	1		
United Kingdom	2	2								
MAY										
France							1	1		
Norway							6	4		
Spain							3	3		
Sweden	1	1								
United Kingdom	2	2					1	1		
JUNE										
France			1	0			1	1		
Norway	1	1								
Spain							3	3		
United Kingdom			1	0						
JULY										
Norway							1	1		
Spain							1	0		
Total	39	30	4	2	5		42	38	5	2

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

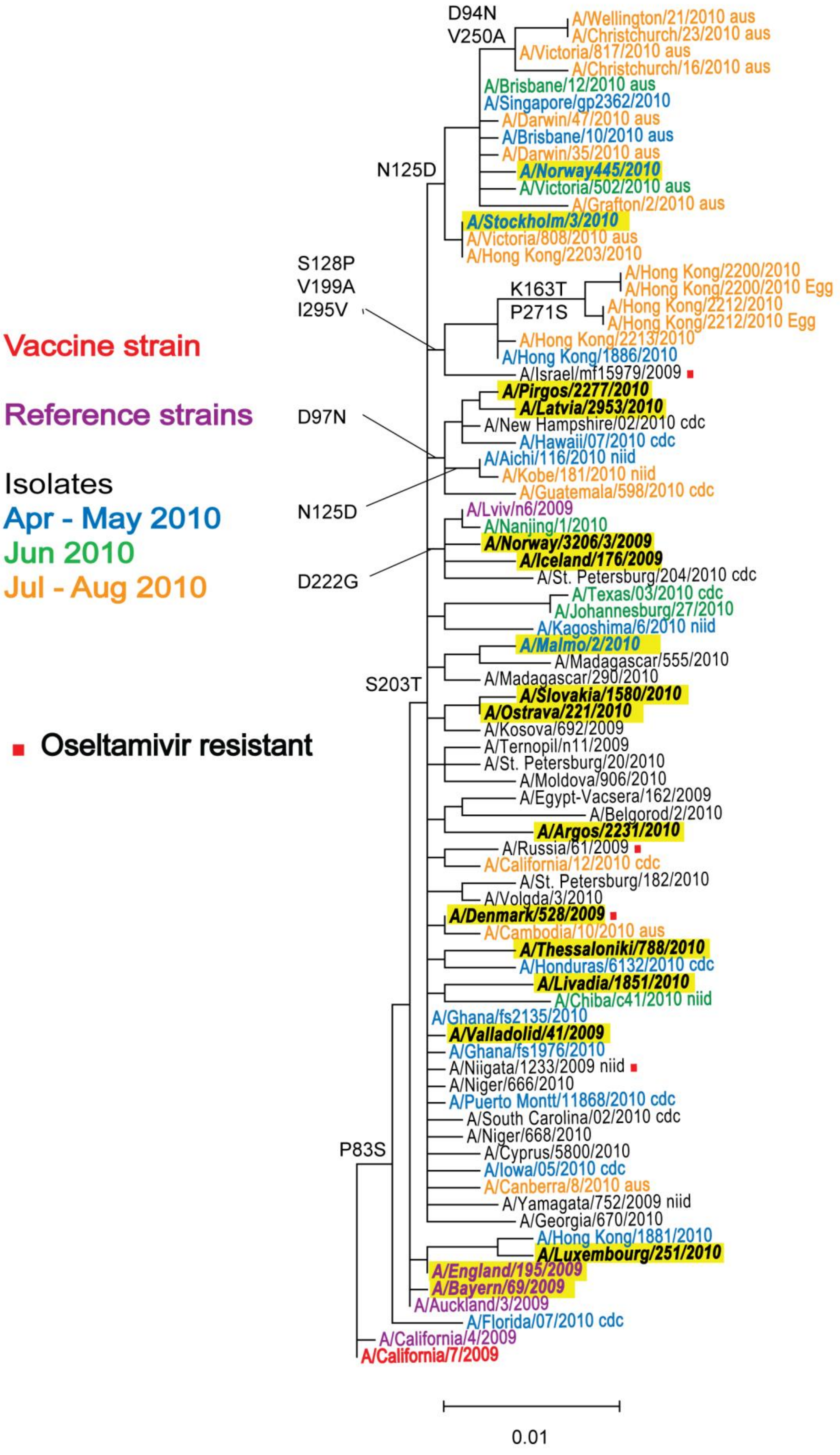


Figure 2: Phylogenetic comparison of influenza B HA1 genes (Victoria-lineage)

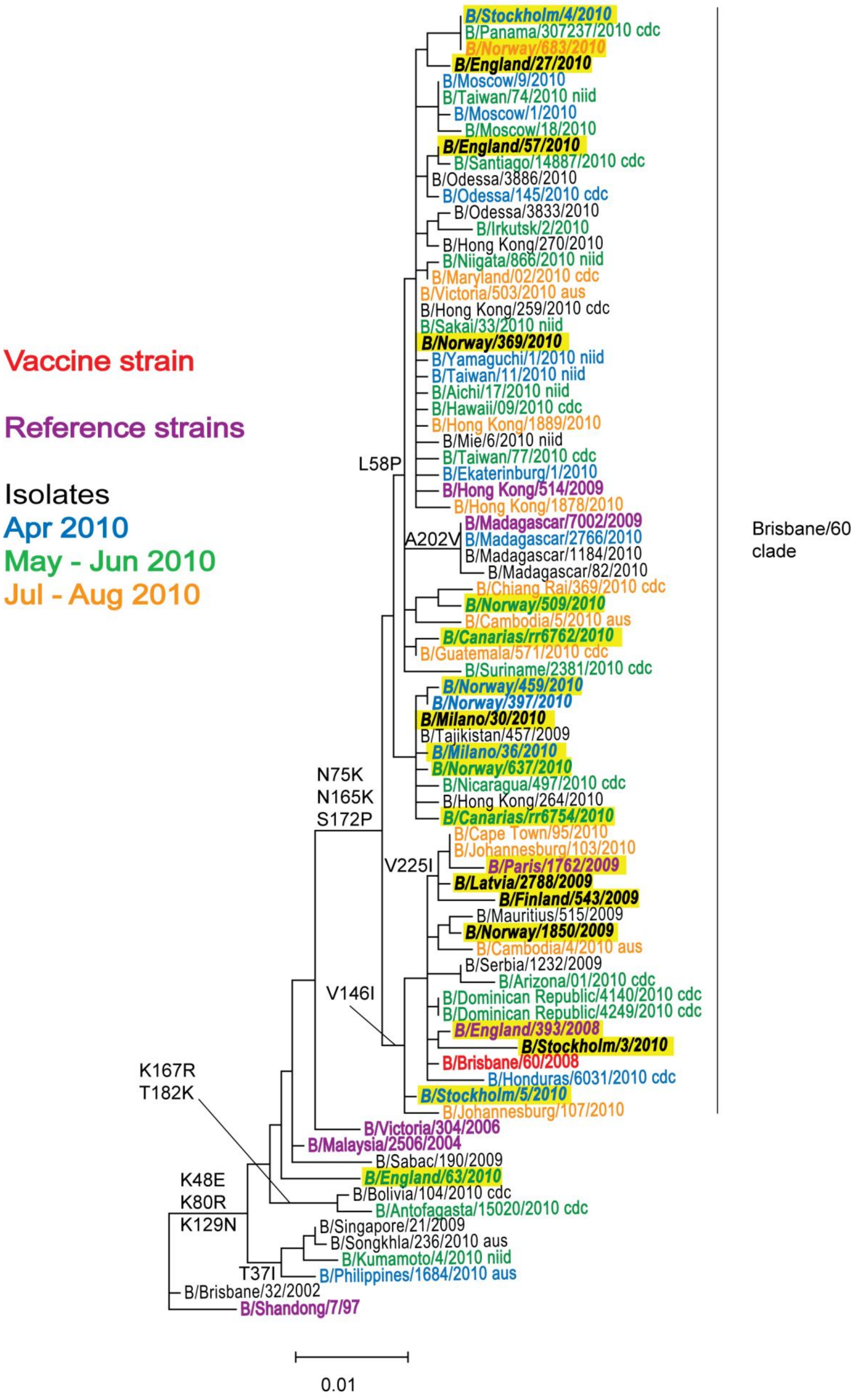


Figure 3. **Phylogenetic comparison of influenza B HA1 genes (Yamagata-lineage)**

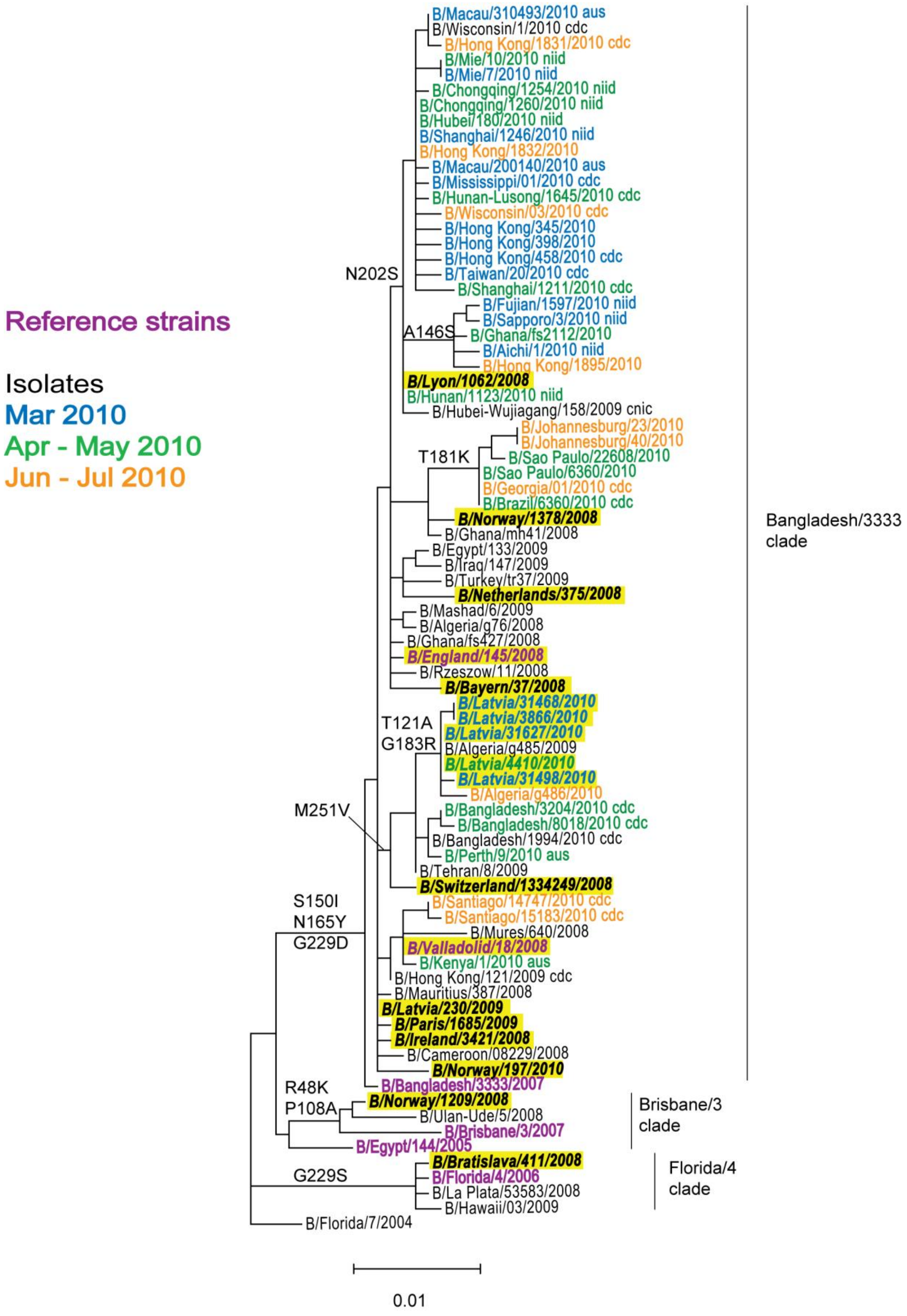
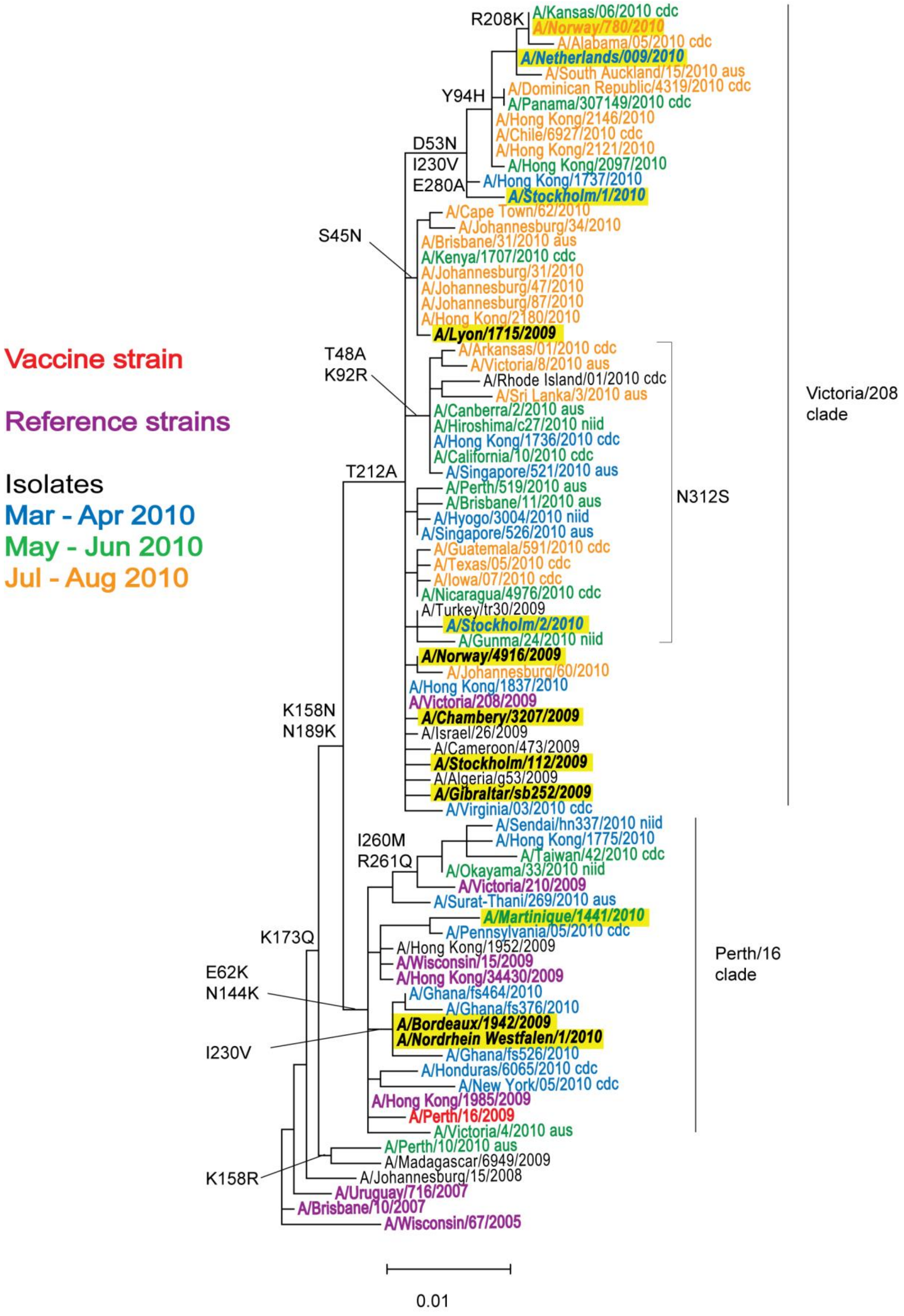


Figure 4. **Phylogenetic comparison of influenza A (H3N2) HA1 genes**



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 and highlighted in yellow. Sequences for some of the viruses from non-European countries were recovered from GISAID and we acknowledge all laboratories submitting sequences.