Laboratory Bulletin

Date: **November 25, 2011**

To: **Dr. Andre Corriveau, Dr. Gerry Predy, AHW Medical Officers of Health, AHS Medical Officers of Health, Infectious Diseases Physicians, Dr. Mark Joffe (for IPC Physicians)**

From: **Provincial Laboratory for Public Health (ProvLab)**

Re: **Analysis of influenza A hemagglutinin gene from recent outbreak strains**

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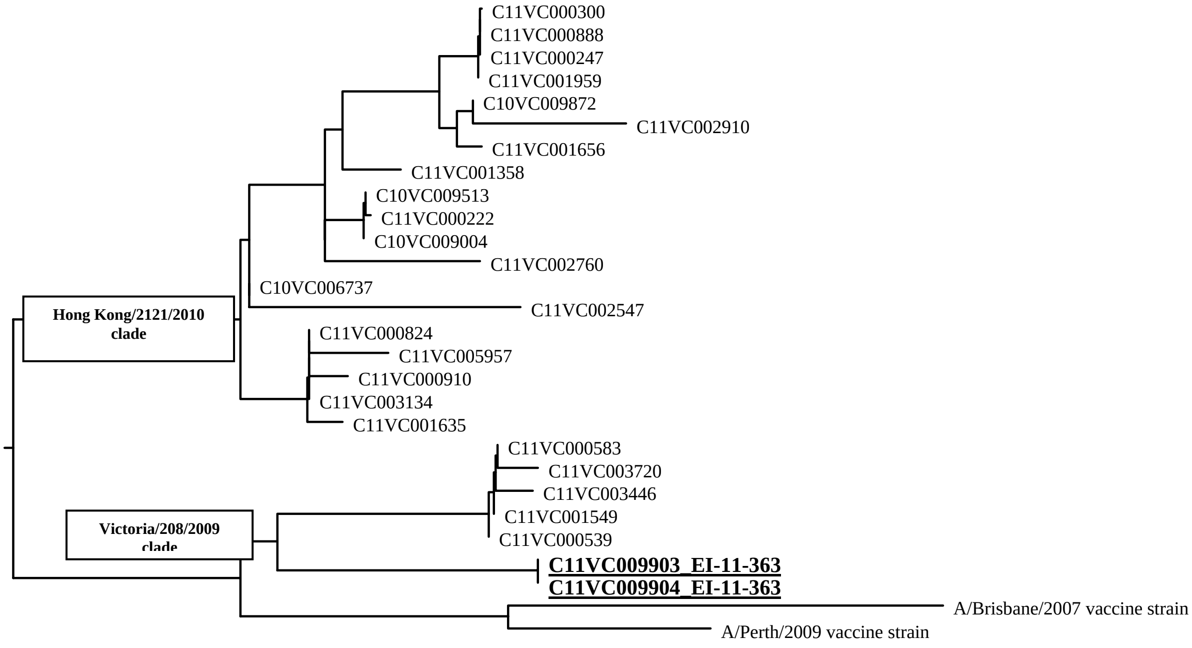
ProvLab has sequenced the full HA gene of the two influenza A H3 subtype strains from a recent outbreak (EI-11-363) occurring in the Calgary zone.

The phylogenetic tree below, shows that while both strains can still be classified as belonging to the Victoria clade that circulated last year, they have since evolved to be a separate branch (outbreak strains are bolded and underlined). Influenza A H3 subtype strains sequenced last season are shown for additional comparison.



In Table 1, the corresponding amino acid changes mapped on the HA gene for the H3 component of the vaccine strain, the Victoria and Hong Kong clades and the two outbreak strains are illustrated to show their respective locations and extent of change.

Table 1: Comparison of amino acid changes at the corresponding antigenic sites of the HA gene for the two clades, current vaccine and outbreak strains

Amino Acid at antigenic sites	**64**	**69**	**73**	**78**	**108**	**110**	**158**	**160**	**215**	**224**	**228**	**230**	**246**	**296**	**328**
A/Perth/16/2009 vaccine	**T**	**D**	**Q**	**K**	**K**	**Y**	**R**	**K**	**S**	**R**	**T**	**S**	**I**	**E**	**N**
A/Victoria/208/ 2009 clade	**-**	**-**	**-**	**E**	**-**	**-**	**-**	**N**	**-**	**-**	**A**	**I**	**-**	**-**	**-**
A/HongKong/2121/ clade	**-**	**N**	**-**	**E**	**-**	**H**	**-**	**N**	**-**	**-**	**A**	**I**	**V**	**A**	**-**
C11VC009903 (EI-11-363)	**-**	**-**	**-**	**E**	**-**	**-**	**-**	**N**	**-**	**-**	**A**	**I**	**-**	**-**	**S**
C11VC009904 (EI-11-363)	**-**	**-**	**-**	**E**	**-**	**-**	**-**	**N**	**-**	**-**	**A**	**I**	**-**	**-**	**S**

Sequence analysis, interpretations, diagrams and charts provided by Kanti Pabbaraju and Sallene Wong, ProvLab.

Last year two influenza H3 clades circulated in Alberta, namely the Victoria clade and the Hong Kong clade, with respective similarities of 94.98% and 93.42% to the current vaccine strain (A/Perth/2009) based upon nucleotide sequence. The A/Perth/2009 strain was also used in the 2010/2011 influenza vaccine, whereas in the 2009/2010 vaccine, A/Brisbane/2007 was the strain used for the H3 component.

As the A/Victoria/208/2009 clade shares 94.98% similarity to the current vaccine strain (A/Perth/2009) it is fair to say that strains from this clade are reasonably well covered by this year's vaccine. However we are waiting for serological characterization results from the National Microbiology Laboratory (NML) to assess if there is a significant antigenic change with the two outbreak strains.

ProvLab will continue to sequence newly emerging strains to assess similarity to the vaccine and which clade they can be assigned.

Inquiries and feedback regarding the content of this bulletin may be directed to:

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This bulletin has been reviewed and approved by Dr. Marie Louie, Acting Medical Director, ProvLab.