

PW13 Lineage of a New Zealand isolate of the influenza virus by mass spectrometry

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influenza, virus, hemagglutinin, mass mapping, peptide

mass mapping of hemagglutinin of a type A influenza Auckland strain establishes its lineage

1995-1999 represents a period of significant antigenic change in the hemagglutinin antigen of type A forms of the influenza virus that necessitated the reformulation of the H1N1 vaccine strain three times in a row. Multiple sequence alignments of the hemagglutinin antigen derived from type A (H1N1) influenza viruses isolated in New Zealand between 1983 and 2007 demonstrate that all isolates after 1998 are of the A/Beijing/262/95-like lineage of the viruses. In contrast, circulating influenza H1N1 viruses in New Zealand prior to 1999 were of the A/Bayern/7/95-like lineage.

The peptide mass fingerprint of the tryptic digested hemagglutinin derived from the 1998 strain A/Auckland/12/98 is in accord with predicted *in silico* digests for strains from the A/Bayern/7/95-like lineage based on the occurrence of a conserved peptide which indicates the absence of a characteristic amino acid substitution (E153G) found in 95% A/Beijing/262/95-like viruses. This confirms that strain A/Auckland/12/98 is still of the A/Bayern/7/95-like lineage of influenza A (H1N1) strains. These findings are in agreement with the deposited sequence of another influenza strain (A/Auckland/18/98) isolated in Auckland during the same influenza season. The presence of a signature peptide characteristic for the H1 isoform of hemagglutinin [1] further authenticates the strain to be of the H1N1 subtype of influenza A viruses.

1. A.B. Schwahn, J.W.H. Wong, K.M. Downard, submitted for publication