

Genetic Analysis of Influenza A (H3N2) Viruses from Index Patients and Family Contacts

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Background/Aims: Influenza hemagglutinin (HA) is a highly evolving surface glycoprotein responsible for viral attachment and entry. Mutational HA drift among circulating human viruses during the 2007/08 season prompted a change in HA proteins used in the current 2008/09 vaccine. Analysis of influenza genes from index patients and family contacts were performed to: 1) evaluate genetic homology to vaccine strains, and 2) determine the extent of genetic mutation in confirmed family transmissions. **Methods:** Genetic analysis of the influenza HA1 hemagglutinin and matrix genes (MA) were performed on viruses obtained from seven families, including an index patient and at least one influenza-positive household family contact. **Results:** All index and transmission strains were genetically more similar to the 2008/09 vaccine Strain, A/Brisbane/10/2007 compared to previous H3N2 vaccine strains. HA analysis of viral strains revealed 100% protein homology from index patient to family contact in four of seven families. Of the three families with HA1 sequence variation, two exhibited one amino acid change, and one family revealed 5 amino acid changes compared to the index strain. The MA and M2 ectodomain were highly conserved among family transmissions, and all strains contained the mutation conferring resistance to adamantane drugs. **Conclusions:** Genetic analysis reveals that all family strains from this cohort are similar to the current A/Brisbane/10/2007 vaccine strain compared to last season's A/Wisconsin/67/2005 strain. HA changes were observed between families and within family transmissions. The results of this study suggest that the HA protein is highly evolving and can drift within a single human transmission.

Results. Genetic analysis of the influenza HA1 hemagglutinin and matrix genes were performed on viruses obtained from seven families. The analysis includes seven confirmed pediatric (index) patients and at least one influenza-positive household family (transmission) contact. Gene comparisons of viral strains were analyzed for mutation (genetic drift) among and within families comprising this cohort, and also compared to current and older vaccine reference strains. All index and transmission strains were