

Clinical and Molecular Evidence of Influenza Transmission Within Households

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Background: Influenza virus is associated with significant morbidity and mortality, causing 83 pediatric deaths during the 2007-08 season. The understanding of influenza transmission is critical to pandemic influenza preparedness. This report focuses on the transmission of influenza virus within households, as children are the primary source of family infections.

Methods: Children with influenza-like illness during the 2007-08 influenza season had nasal washings submitted for EIA, culture and PCR. Accompanying parents or siblings, regardless of clinical illness were also enrolled. Transmission was defined as 2 or more family members developing influenza with onset at least one day apart.

Results: 118 children (114 symptomatic) and 104 adults (56 symptomatic) from a 89 families were enrolled in the study. Forty-four families had at least one member who was influenza PCR-positive (1 H1N1, 27 H3N2 and 16 Influenza B), including 3 families with one asymptomatic influenza-positive person. Suspected transmission of influenza was noted in 16/28(57%) families with influenza A versus 4/16(25%) families with influenza B (p=0.05). Transmission was molecularly confirmed (conserved sequence homology in two PCR-positive family members) in 14/28(50%) families with influenza A versus 2/16(12.5%) families with influenza B (P=0.02). 11/16(68%) of confirmed transmissions originated from a child (ages 10m-17y, mean 6.6y).

Conclusions: Influenza is highly transmissible within families, with young children being the most common source. Transmission of influenza A was significantly more common than influenza B. Subclinical influenza infections occur in contacts of clinically ill patients, and molecular diagnostics have the potential to identify pre-symptomatic patients during an influenza pandemic.