Phylogenetic Exploration of Nosocomial Transmission Chains of 2009 Influenza A/H1N1 among Children Admitted at Red Cross War Memorial Children's Hospital, Cape Town, South Africa in 2011

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Background/Objective
Traditional modes of investigating influenza nosocomial transmission have entailed a combination of confirmatory molecular diagnostic testing and epidemiological investigation. Common hospital-acquired infections like influenza require a discerning ability to distinguish between viral isolates to accurately identify patient transmission chains. We assessed whether influenza hemagglutinin sequence phylogenies can be used to enrich epidemiological data when investigating the extent of nosocomial transmission over a four month period within a paediatric Hospital in Cape Town South Africa.

Method
Possible transmission chains/channels were initially determined through basic patient admission data combined with Maximum likelihood and time-scaled Bayesian phylogenetic analyses.

Result
These analyses suggested that most instances of potential hospital acquired infections resulted from multiple introductions of Influenza A into the hospital, which included instances where virus hemagglutinin sequences were identical between different patients. Furthermore, a general inability to establish epidemiological transmission linkage of patients/viral isolates implied that identified isolates could have originated from asymptomatic hospital patients, visitors or hospital staff. In contrast a traditional epidemiological investigation that used no viral phylogenetic analyses, based on patient co-admission into specific wards during a particular time-frame suggested that multiple hospital-acquired infection instances may have stemmed from a limited number of identifiable index viral isolates/patients. This traditional epidemiological analysis by itself would incorrectly suggest linkage between unrelated cases, underestimate the number of unique infections and overlook the diffuse nature of hospital transmission, which was shown by sequencing data to be caused by multiple unique introductions of influenza A isolates into individual hospital wards.

Conclusion
We have demonstrated a functional role for viral sequence data in nosocomial transmission investigation through its ability to enrich traditional, non-molecular observational epidemiological investigation by teasing out the transmission pathways and more accurately enumerating the number of possible transmission events.