Public Health England

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Hospital-associated influenza transmission and its management in a UK teaching hospital

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Introduction

Seasonal influenza is a major cause of morbidity. However, its impact and potential for transmission in secondary care are poorly understood. In this study we combine clinical, epidemiological and genomic data to investigate the burden of influenza-associated morbidity and the extent of transmission within a UK teaching hospital. We also describe the impact of changes in clinical practice implemented in response to suspected nosocomial outbreaks.

Methods

All patients attending Cambridge University Hospitals (CUH) with influenza A detected by PCR between August 2016-April 2017 were included in this study. An epidemiological investigation was conducted in parallel with genetic analysis of samples to develop independent evidence of transmission pathways. Algorithms were developed to interrogate ward movement data to detect co-location of a potentially infectious patient with a susceptible one. A ward-time cluster was defined as a sequence of two or more patients on the same ward where there was an overlap of the intervals of infectiousness and of susceptibility. Genome sequencing was attempted using RNA extracted directly from samples. Whole and partial genome sequences were included in phylogenetic analyses to infer transmission networks. Ward movement, prescribing and laboratory data were derived from electronic records for all confirmed influenza cases for 2016-17 and compared to a second cohort from August 2017-May 2018. Further clinical data were manually abstracted, including judgement of whether infection was community- or hospital-acquired based on symptom duration and length of stay at time of swabbing.

Results

In 2016-17 influenza A was diagnosed in 326 patients, median age 76 years. Of these, 313 (96.0%) were admitted to hospital; 98/313 (31.3%) infections were acquired during the admission. All-cause mortality during the admission was 10.2%; 11/32 deaths were associated with hospital-acquired influenza.

The majority of inpatients (58.8%) were linked in 33 ward-time clusters (figure 1). Whole genome sequences were available for 180/313 cases and partial genomes for a further 29 cases. Using whole genomes, 64.4% of isolates were phylogenetically linked within 22 putative clusters (figure 2); this rose to 73.8% within 31 clusters using partial genomes. Combining epidemiologic and genomic data demonstrated that 43/61 (70.5%) hospital-acquired cases fell within 7 transmission networks (range 2-22 patients) across 10 wards. Additionally, we identified clusters imported into hospital, including transmission in 3 outpatient units and 3 care homes.

In response to influenza transmission, programmes of staff education and reviews of operational and clinical management of influenza were undertaken prior to the 2017-18 winter. These interventions focused on the prompt isolation, testing and treatment of possible influenza cases. The impact of these interventions is summarised in Table 1.

	2016-17	2017-18
Total influenza cases	340	763
Influenza A	326 (96%)	373 (48.9%)
Proportion admitted to side rooms	50%	79%
Median time from admission to sample collection	9.7 hrs	5.2 hrs
Median time from admission to first antiviral dose	45.2 hrs	10.1 hrs

Table 1 – Summary of confirmed influenza cases and improvements in management of inpatients at CUH over two winters.

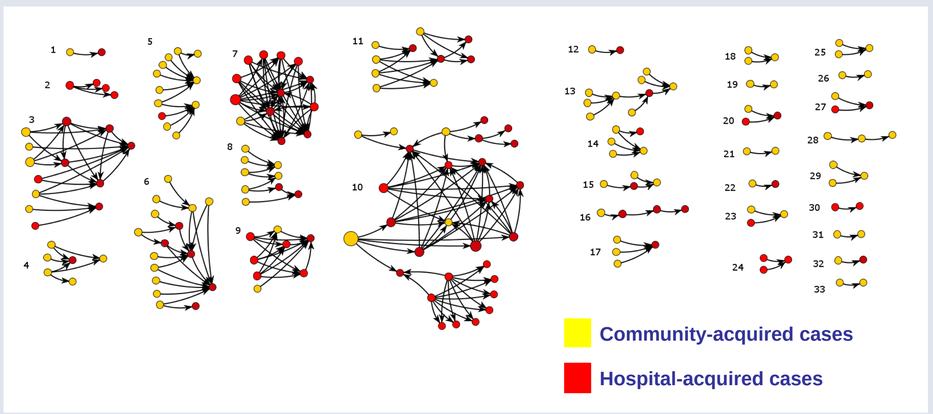

Figure 1 – Ward-time clusters. Each circle represents a single patient; each intervening line demonstrates co-location in the same ward with an overlap between one patient's potential to transmit influenza and another's susceptibility to infection

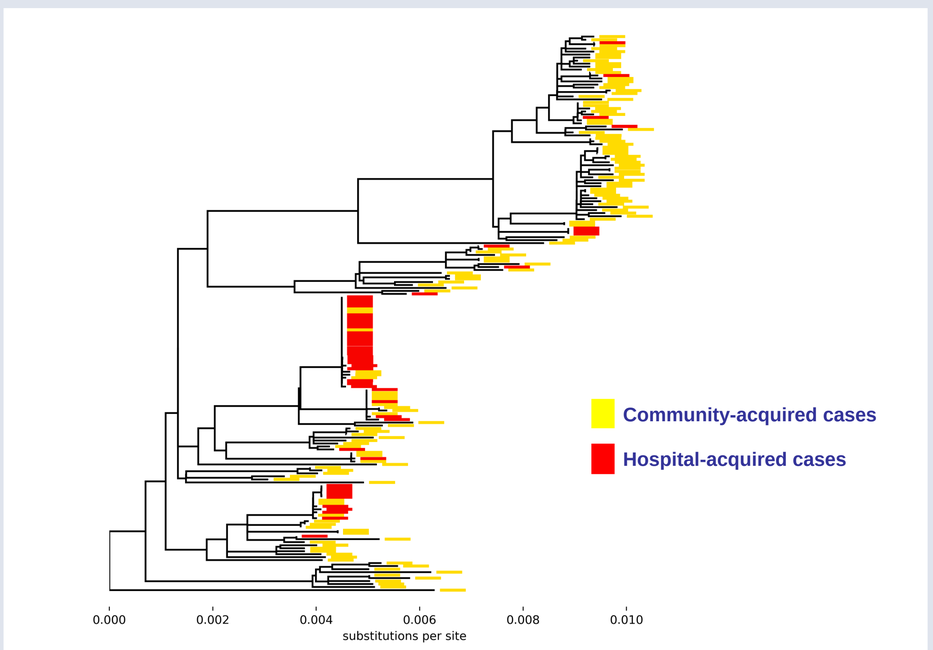

Figure 2 – Phylogenetic tree of 191 influenza isolates, demonstrating clusters of highly genetically similar isolates implicated in transmission networks

Discussion

We have demonstrated that influenza is an important but poorly recognised cause of morbidity and mortality in secondary care. A substantial proportion of influenza cases were acquired during the patient admission and are therefore likely to be amenable to changes in infection control measures. We have demonstrated that better use of existing resources can lead to considerable improvement in patient management.

Combining genomic and epidemiologic approaches provides a powerful and tractable tool for assessing influenza transmission, a critical step in guiding infection control practices. However, these approaches also highlight the complexity of transmission: their individual use can over-estimate patient clustering, while combined they reveal gaps in networks which may represent asymptomatic or untested patients, healthcare workers and hospital visitors.

Although we have studied a single centre, similar transmission is likely to occur throughout secondary care. Responding to this problem requires the engagement of many disciplines, utilising a range of approaches to better understand, manage and prevent transmission.

Acknowledgements

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