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Variations of Influenza A H3N2 Virus in Hong Kong in 2014 Winter

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Perspective

On January 28th, 2015, an H3N2 epidemic was reported by the Centre for Health Protection, Hong Kong. From January to 24th, 2015, it had reported 122 severe cases with influenza, including 64 deaths, among which the elder suffered more severely [1].

Surveillances on the proportions of pathogens causing winter seasonal flu (from December to next February) in Hong Kong showed that the ratios of subtype H3 and H1 (mostly, the pdm09 H1N1) were 468/707, 1815/3156, and 3746/16 respectively in recent three consecutive winters during 2012 ~ 2014 (the winter of 2014 is as of January 28th, 2015). Therefore, subtype H3 flu accounted for a large proportion in Hong Kong continuously, and H3N2 especially dominated the 2014 winter flu [1,2].

Every year, Hong Kong launched a government funded vaccination project for the elder and children against seasonal flu. For example, there were 212,000 injections as of January 18th, 2015 for the winter flu of 2014 (the elder 158,000 and children 54,000). From 2012 to 2014, the vaccine composition of H3N2 recommended by WHO for use in northern hemisphere influenza season was a cell-propagated prototype virus A/Victoria/361/2011(H3N2) and its antigen-like strain A/Texas/50/2012(H3N2) [2,3].

Phylogenetic analyses among 15 H3N2 isolates, including 11 established in 2013 winter and 4 in 2014 winter, and two above-mentioned vaccine strains displayed that isolates responsible for epidemics in the past two years were highly homologous (Figure 1). However, HA sequences of two isolates established in 2014 winter, i.e., A/Hong Kong/7622/2014(H3N2) and A/Hong Kong/7624/2014(H3N2), proved notably divergent. Alignment of deduced amino acid residues also confirmed that E78K, K99R, *N138D*, *L173S*, *Q213H*, *R277Q*, *V363K* sited on HA of A/Hong Kong/7622/2014(H3N2), and *K2R, A154S, S159T, F175S, K342R* sited on HA of A/Hong Kong/7624/2014(H3N2) were of unique variations compared to isolates established in 2013 winter and two recommended vaccine strains. Especially the former, 1000 Max target sequences carried out by protein-protein BLAST demonstrated that *K*99R, *N*138*D*, and *Q*213*H* were of rare and/or novel variations. *N*138*D* located on a conserved receptor binding site (RBS), while *Q*213*H* located between two other conserved RBS domains known as 190-helix and 220-loop [4]. Similarly, variations of *M*51*V*, *V*143*G*, *V*263*I*, *T*434*N* were detected on NA of A/Hong Kong/7622/2014(H3N2), and *M*51*V*, *V*143*G* were also rare and/or novel.

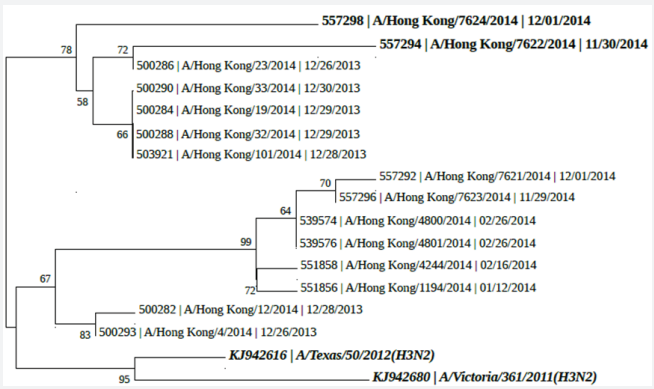

Figure 1a

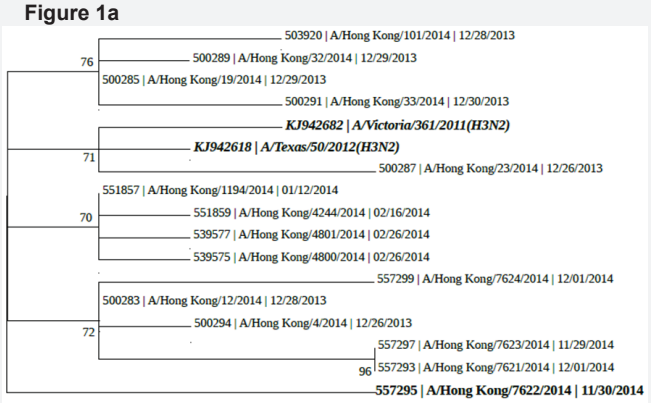

Figure 1b

Figure 1: Phylogenetic trees of deduced proteins of HA and NA affiliated to influenza A H3N. Variants of 2014 winter flu are in bold, and vaccine strains recommended by WHO are in bold and italic (1a, HA; 1b, NA). Evolutionary distances were calculated with the use of the maximum likelihood method.

As we know, Hong Kong is a constant epidemic area of influenza a virus, from where the pandemic influenza H3N2 in 1968 spreading around Asia with more than 1,000,000 infections derived [5]. And thus, it is strongly needed to clarify what roles these variations played for the virulence and pathogenicity in this H3N2 epidemic through laboratory study, and to monitor its epidemic status as well as genetic characteristics.

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