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## Genetic drift of influenza A viruses in a subtropical city Hong Kong, 2013-2014

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In subtropical and tropical regions such as Hong Kong, influenza shows less clear seasonal patterns, with multiple peaks observed throughout the year. Antigenic variation of influenza viruses has been proposed to play an important role in regulating influenza seasonality. We conducted a comprehensive study to understand the characterization of the antigenicity and explore the temporal trend of antigenic changes of influenza A virus (both A/H1N1 and A/H3N2 subtypes) in Hong Kong from January 2013 to December 2014. Clinical samples from 1,013 patients with confirmed A/H1N1 and A/H3N2 influenza viruses were collected from two public hospitals which cover over 80% of total hospitalizations in Hong Kong Island during the study period. 379 specimens were randomly selected for a hemagglutinin amino acids (HA) sequence analysis. Based on sequence analysis, all influenza viruses for both A/H1N1 and A/H3N2 subtypes were characterized by at least 4 fixed amino acid mutations for A/H1N1: P100S, S220T, R240Q, and I338V, and at least 8 fixed amino acid mutations for A/H3N2: H9Y, Q49R, N161S, Q172H, V202G, Y235S, and N294K, with respect to WHO recommended vaccine composition strains A/California/07/2009 (for A/H1N1) and A/Victoria/361/2011 (for A/H3N2) in 2013-2014. We further randomly selected 128 specimens (56 A/H1N1 and 72 A/H3N2) for hemagglutinin-inhibition (HI) test. Almost all the HI titer results for both A/H1N1 and A/H3N2 were over 320, which indicated that there were no significant differences between our samples and WHO reference strains. Our study may contribute to develop the knowledge of the evolution of influenza A virus circulated in Hong Kong.

### Biography

Peihua Cao is a PhD candidate in School of Public Health, The University of Hong Kong (2011-present). He has a BS in Biostatistics from Southern Medical University in China and was awarded the Outstanding Graduate Student in 2011. His research interests include evolution and epidemiology of influenza viruses, transmission dynamics of infectious diseases, and situation awareness of disease activity using multiple surveillance data sources. He is now working on a multidisciplinary project to integrate influenza epidemiology and genetic data in a subtropical city Hong Kong.

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