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Analysis of full-length genome sequences of the first H7N9 imported case in Taiwan

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An outbreak of a novel avian-origin reassortant H7N9 virus in China has raised great concerns due to the rapidly progressive lower respiratory tract infections in infected individuals in 2013. In this study, H7N9 viruses were isolated from the Day 0420, Day 0422, Day 0425 sputum and Day 0425 throat swab of the first imported case in Taiwan. Hem-Agglutinin (HA), neuraminidase and Matrix (M) full-length genome sequences were determined by using PacBio RS II platform. Two mutations, D19G and K330E, in the HA sequence were found in Day 0425 sputum and were speculated to have higher binding ability to human receptor compared with the wild type HA through calculating protein binding affinity. Half of the analyzed NA sequences amplified from four specimens have R289K, the oseltamivir-resistant mutation. Other oseltamivir-resistant mutations such as E115V and I219R were also identified. None of the amino acid mutations were detected in the M gene in all specimens. In conclusion, the population with higher human receptor binding affinity and drug resistance were identified after high dose oseltamivir treatment and might become the major group.

Biography

Tai-Ling Chao is a PhD student studied in Dr. Sui-Yuan Chang 's lab in the department of clinical laboratory science medical biotechnology of National Taiwan University. The major study topics of Dr. Chang's laboratory are molecular virology of HIV and influenza virus. The first imported H7N9 case in Taiwan was identified and investigated in our lab, and the result was published in Clinical Infectious Disease in 2014. (Clin Infect Dis. (2014) 58 (2):242-246.)

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