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Outbreak of influenza A H3N2 and influenza B virus mixed infection post-mass vaccination during 2009-2010 in central Taiwan

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Background: A pandemic outbreak of the A/H1N1 swine-origin influenza virus occurred in 2009. In response, Taiwan authorities approved a national vaccination program at the end of 2009. To investigate their vaccination effect after the end of 2009, non-H1N1 influenza epidemic, and transmission relationships were investigated in Taiwan. **Methods :** Patients with specific respiratory symptoms were recruited from a university hospital in central Taiwan. Respiratory tract specimens were analyzed using rapid diagnostic influenza A & B tests and virus subtyping. A phylogenetic analysis was performed to clarify transmission relationships. **Finding:** A neighbor-joining phylogenetic tree constructed from the 92 influenza A H3N2 and 75 influenza B sequences in Taiwan central that were the focus of this study. In the H3N2 tree, all central Taiwan cases belong to a large clade that also contains the A/Perth/2009/CY081428.1 vaccine strain under statistic. According to results from a neighbor-joining analysis, 14/18 Taiwan H3N2 sequences separated into 3 major monophyletic clusters with statistical significance. According to the influenza B neighbor-joining tree, all 14 sequences displayed 3 monophyletic clusters. In terms of HA sequences, 12 strains were Victoria-like and 2 Yamagata-like. Note the central Taiwan founder clusters of influenza A H3N2 and influenza B outbreaks following the late-2009 H1 vaccination program. **Conclusions:** According to our phylogenetic data, at least 11 independent introductions of influenza A and B viruses continue to sustain transmission in central Taiwan.

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Learning Objectives: To demonstrate their vaccination effect after the end of 2009, non-H1N1 influenza epidemic, and transmission relationships were investigated in Taiwan.

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Qualified on the content I am responsible for because: I analyzed data in this study.

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