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Abstract (poster session)

**Sequencing of influenza A(H1N1)pdm viruses in the Philippines**

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Objective: Few studies have been done on the genetic characteristics of influenza strains in the Philippines. Mutations for drug resistance in local influenza isolates have also not been widely studied. This study is part of a larger project in collaboration with the Department of Health and Department of Science and Technology to develop a web-based genomic library for the surveillance of influenza A in the Philippines. Our aim is to generate a genomic library and resistance profile of local influenza strains by sequencing the matrix (M), neuraminidase (NA) and haemagglutinin (HA) genes. Methods: RNA extracts of confirmed influenza A (H1N1) and seasonal influenza A (H3N2) from 2009 to 2011 were obtained from a tertiary hospital, The Medical City, Pasig City, Philippines. Matrix 1 and 2 (M), neuraminidase (NA), and haemagglutinin (HA) genes of influenza A were amplified using gene-specific primers. The amplification products were electrophoresed to determine the presence of amplified product. The amplified products were then sequenced. Results: Of the samples sequenced, 33 have been sent to Genbank. None of the neuraminidase genes tested showed mutations for resistance to oseltamivir. However, all of the matrix genes had resistance mutations for adamantanes. Phylogenetic analysis did not yield any distinct clades of influenza A. However, this may be due to the fact that only one site was involved in the pilot project. Conclusion: The results indicate that resistance mutations for adamantane are likely to be widespread in the Philippines, and the drug should not be used to treat influenza. Resistance mutations for oseltamivir, on the other hand, are likely to be rare. The pilot project will now be scaled up and integrated into all influenza A surveillance specimens in the Philippines.