

Evolution of influenza A virus

An understanding of the evolutionary dynamics of the influenza virus determines scientists' ability to survey and control the virus.

In a new study, published online in the open-access journal *PLoS Pathogens* (<http://dx.doi.org/10.1371/journal.ppat.0020125>), Dr. Eddie C. Holmes of the Department of Biology at Pennsylvania State University and colleagues at the National Institutes of Health, the Wordsworth Center and the Institute for Genomic Research used genomic analysis to investigate the evolutionary properties of the H3N2 subtype of human influenza A virus.

The authors, in the first population-based study of its kind, collected a sample group of 413 complete influenza genomes from across New York State. Comparative analysis of the samples revealed genetically distinct viral strains circulate across the state within any one season and occasionally exchange genes through reassortment.

These results indicate that adaptive evolution occurs only sporadically in influenza virus, and that influenza virus diversity and evolution is strongly affected by chance events, such as reassortment between strains co-infecting a host or the introduction of a particular variant from elsewhere. These factors make predicting future patterns of influenza virus evolution more difficult, as vaccine strain selection then becomes dependent upon intensive surveillance, whole-genome sequencing, and phenotypic analysis.

Source: Public Library of Science

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