

Research predicts future evolution of flu viruses

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New research from the University of Pennsylvania is beginning to crack the code of which strain of flu will be prevalent in a given year, with major implications for global public health preparedness. The findings will be published on February 17 in the open-access journal *PLoS Genetics*.

Joshua Plotkin and Sergey Kryazhimskiy, both at the University of Pennsylvania, conducted the research with colleagues at McMaster University and the Institute for Information Transmission Problems of the Russian Academy of Sciences. Plotkin believes that his group's computational study of 40 years of flu genomes offers a new way of looking at mutations: by cataloging pairs of [genetic changes](#) that have occurred in rapid succession, observing that a mutation in one half of the pair can act as an early warning sign of a mutation about to occur in the other.

Tracking single mutations in a vacuum is not always enough to understand how the [flu virus](#) evolves. "Sometimes a mutation is functional or adaptive only if it's in the context of a certain genetic background – that is, if the protein already has some other mutation," Plotkin said. The influence such combinations have on an organization's adaptive fitness is known as epistasis.

"If you see a mutation occur in Site A and then very soon after you see a mutation in Site B, and this pattern happens repeatedly, then you have some evidence that A and B influence fitness epistatically," Plotkin said.

"The first mutation might be useless on its own, but it might be a prerequisite for the second mutation to be useful. The first mutation is like giving you a nail, and the second one is like giving you a hammer."

Because the studied mutations generally affect the surface proteins that determine whether the virus can enter and infect human cells, being able to predict what [mutations](#) are likely to happen in the near future has lifesaving applications. Tens of thousands of Americans, and hundreds of thousands worldwide, die of seasonal flu complications every year. Flu vaccine production is labor intensive and time consuming; to have enough supplies ready for the [flu](#) season, public health groups like the Centers for Disease Control and the World Health Organization must make an educated guess as to which strain is likely to be the most active several months in advance. Observing the leading site of an epistatic pair could give them a head start.

More information: Kryazhimskiy S, Dushoff J, Bazykin GA, Plotkin JB (2011) Prevalence of Epistasis in the Evolution of Influenza A Surface Proteins. PLoS Genet 7(2): e1001301.
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