Researchers devise computer model for projecting severity of flu season

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Researchers have developed a statistical model for projecting how many people will get sick from seasonal influenza based on analyses of flu viruses circulating that season. The research, conducted by scientists at the National Institutes of Health, appears today in the open-access publication *PLoS Currents: Influenza*.

Building on other research that has shown that severity of infections with the Influenza A virus is related to its novelty (i.e., how much the virus has changed, or mutated, from prior seasons), the study evaluated the correlation between virus novelty and the epidemiologic severity of influenza from the 1993/1994 flu season through the 2008/2009 season. Virus novelty was assessed through analysis of genetic data (sequences of hemagglutinin proteins from virus samples) and serological data (hemagglutinin inhibition results). The research focused on H3N2 influenza, the influenza subtype responsible for the most severe influenza seasons during inter-pandemic periods.

The results showed that more than 90% of the variation in influenza severity over the periods studied could be explained by the novelty of the virus' hemagglutinin protein.

The researchers also assessed whether influenza sequence and serological data for viruses isolated in the Southern Hemisphere influenza season correlated with influenza severity that occurred in the later influenza season in the Northern Hemisphere. Results showed that the projections explained 66% of the variance in severity in the Northern

Hemisphere.

The ability to accurately predict influenza severity suggests that with appropriate surveillance methods, scientists could make more informed decisions in planning for influenza, including the selection of vaccines. For example, in selecting a vaccine for the coming season, it would be helpful to know that one circulating virus in the current season was likely to produce much more severe influenza than the other circulating viruses.

Edward Holmes (The Pennsylvania State University), an expert on the evolution of flu viruses, and one of the Editors of *PLoS Currents: Influenza* commented: "this paper represents a major step forward in our ability to predict the behavior of influenza and simultaneously opens up a new field of study".

More information: Wolf, Yuri I; Nikolskaya, Anastasia; Cherry, Joshua L.; Viboud, Cecile; Koonin, Eugene; Lipman, David J. Projection of seasonal influenza severity from sequence and serological data. PLoS Currents: Influenza. 2010 Dec 6th. Link to the freely available article, published today: knol.google.com/k/yuri-i-wolf/ … enza/agr0htar1u6r/22

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