

# Evolutionary analysis improves ability to predict the spread of flu

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With flu season around the corner, getting a seasonal vaccine might be one of the best ways to prevent people from getting sick. These vaccines only work, however, if their developers have accurately predicted which strains of the virus are likely to be active in the coming season because vaccines must be developed in advance of the upcoming flu season. Recently, a team of scientists from Germany and the United Kingdom have improved the prediction methods used to determine which strains of the flu virus to include in the current season's vaccine. The research describing this advance is published in the October 2012 issue of *Genetics*.

"Seasonal influenza kills about half a million people per year, but improved vaccines can curb this number," said Michael Lässig, Ph.D., a researcher involved in the work from the Institute for Theoretical Physics at the University of Cologne in Köln, Germany. "Although this study is some distance from direct applications, it is a necessary step toward improved prediction methods. We hope that it helps yield better vaccines against influenza," Lässig added.

To make this advance, scientists analyzed the [DNA sequences](#) of thousands of [influenza strains](#) isolated from patients worldwide, dating to 1968. By analyzing this dataset, researchers were able to determine which strains were most successful at expanding into the entire population, and which mutations were least successful in spreading. Using a new statistical method, the researchers found that many more mutations than we thought initially succeed in replicating and surviving.

These mutations compete; some make it into the entire population, others die out. This analysis of the virus enables prediction of trends which can help vaccine developers understand the rules of flu [virus evolution](#). This knowledge, in turn, can be used to predict which strains of the virus are most likely to spread through a human population.

"Every year, new concerns emerge about 'super flus' that have the potential to kill many people," said Mark Johnston, Editor-in-Chief of the journal *Genetics*. "This research itself will not stop any people from getting sick, but it could give us a heads up to particularly dangerous strains that might be on the horizon. With that information, we may be able to develop increasingly effective vaccines."

**More information:** Natalja Strelkova and Michael Lässig Clonal Interference in the Evolution of Influenza, *Genetics*, October 2012 192:671-682

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