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A predictive fitness model for influenza.

Luksza M, Lässig M.
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Recommendations:

Very Good 03 Mar 2014

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GOOD FOR TEACHING | NEW FINDING

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This article provides the most elaborate effort to date to predict genetic drift in influenza A evolution; in particular, it is relevant to strain selection for vaccines. Using the data on genetic divergence, the authors predict the fitness – i.e. rate of future frequency increase – of clades (groups of closely related strains). Rather simple assumptions lead to surprisingly good predictions. Some of the model assumptions may be questioned (most importantly, the use of non-synonymous Hamming distance at epitopic sites as proxy for antigenic distance, and the assumption that substitutions outside epitopes are deleterious); however, the fitness-flux framework provided by the authors allows incorporating more sophisticated assumptions.

Disclosures
None declared

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Abstract:

ABSTRACT

The seasonal human influenza A/H3N2 virus undergoes rapid evolution, which produces significant year-to-year sequence turnover in the population of circulating strains. Adaptive mutations respond to human immune challenge and occur primarily in antigenic epitopes, the antibody-binding domains of the viral surface protein haemagglutinin. Here we develop a fitness model for haemagglutinin that predicts the evolution of the viral population from one year to the next. Two factors are shown to determine the fitness of a strain: adaptive epitope... more »
changes and deleterious mutations outside the epitopes. We infer both fitness components for the strains circulating in a given year, using population-genetic data of all previous strains. From fitness and frequency of each strain, we predict the frequency of its descendent strains in the following year. This fitness model maps the adaptive history of influenza A and suggests a principled method for vaccine selection. Our results call for a more comprehensive epidemiology of influenza and other fast-evolving pathogens that integrates antigenic phenotypes with other viral functions coupled by genetic linkage.

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