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RESEARCH ARTICLE | INFLUENZA

Evolution-informed forecasting of seasonal influenza A (H3N2)

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Foreseeing future flu

Although two strains of influenza A have been circulating globally for decades, these strains mutate quickly to try to escape host immunity. Many models exist to predict influenza seasons, but Du *et al.* have now incorporated evolutionary information to try to forecast upcoming H3N2 seasons in advance. After developing the model, they used it to predict that H3N2 in the pending 2016/2017 season will be at a higher incidence than has been seen recently and will involve substantial antigenic change in the hemagglutinin. Being able to predict this type of information could affect influenza countermeasures worldwide.

Abstract

Interpandemic or seasonal influenza A, currently subtypes H3N2 and H1N1, exacts an enormous annual burden both in terms of human health and economic impact. Incidence prediction ahead of season remains a challenge largely because of the virus' antigenic evolution. We propose a forecasting approach that incorporates evolutionary change into a mechanistic epidemiological model. The proposed models are simple enough that their parameters can be estimated from retrospective surveillance data. These models link amino acid sequences of hemagglutinin epitopes with a transmission model for seasonal H3N2 influenza, also informed by H1N1 levels. With a monthly time series of H3N2 incidence in the United States for more than 10 years, we demonstrate the feasibility of skillful prediction for total cases ahead of season, with a tendency to underpredict monthly peak epidemic size, and an accurate real-time forecast for the 2016/2017 influenza season.

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