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Heterogeneity in antibody range is required for the antigenic drift of influenza A viruses

In this paper we explore the consequences for the evolution of a rapidly mutating virus of a heterogeneous immune response in the population. We show that several features of the incidence and phylogenetic patterns typical of influenza A may be understood in this framework. Limited diversity and rapid drift of the circulating viral strains result from the interplay of two interacting subpopulations with two different types of immune response, narrow or broad, upon infection. The subpopulation with the narrow immune response acts as a reservoir where consecutive neutral mutations escape immunity and can persist. Strains with a number of accumulated mutations escape immunity in the other subpopulation as well, causing larger epidemic peaks in the whole population, and reducing strain diversity. These recurrent larger epidemics have been identified in the data and associated in the modelling literature with "cluster jumps", or mutations whose antigenic effect is larger and generate strains for which the pool of susceptibles in the population is also larger. Our model reproduces the observed epidemic peak height variation and antigenic drift patterns without any assumption of punctuated antigenic evolution.